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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 09:49:30 ; Search time 25 Seconds
(without alignments)
3.564 Million cell updates/sec

Title: US-10-633-163-47
Perfect score: 4267
Sequence: 1 ggtatctgtgcgcagcag.....tgcagcgtgattaaaaaaa 4267

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 525 seqs, 10440 residues

Total number of hits satisfying chosen parameters: 1050

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 567 summaries

Database : fetchrnpb47.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	0.8	33	1	US-09-750-401-29
2	33	0.8	33	1	US-10-309-788-29
3	33	0.8	33	1	US-10-238-306B-29
4	33	0.8	33	1	US-10-629-453-29
5	25	0.6	25	1	US-09-750-401-31
6	25	0.6	25	1	US-10-309-788-31
7	25	0.6	25	1	US-10-238-306B-31
8	25	0.6	25	1	US-10-189-267-14
9	25	0.6	25	1	US-10-629-453-31
10	25	0.6	25	1	US-10-719-900-43634
11	25	0.6	25	1	US-10-719-900-79674
12	25	0.6	25	1	US-10-719-900-80968
13	25	0.6	25	1	US-10-719-900-105991
14	25	0.6	25	1	US-10-719-900-115675
15	25	0.6	25	1	US-10-719-900-125985
16	25	0.6	25	1	US-10-719-900-164292
17	25	0.6	25	1	US-10-719-900-219322
18	25	0.6	25	1	US-10-719-900-226895
19	25	0.6	25	1	US-10-719-900-324991
20	25	0.6	25	1	US-10-719-900-350767
21	25	0.6	25	1	US-10-719-900-366993
22	25	0.6	25	1	US-10-719-900-443782
23	25	0.6	25	1	US-10-719-900-508233
24	25	0.6	25	1	US-10-719-900-547596
25	25	0.6	25	1	US-10-719-900-548689
26	25	0.6	25	1	US-10-719-900-548629
27	25	0.6	25	1	US-10-719-900-553274
28	25	0.6	25	1	US-10-719-900-563977
29	25	0.6	25	1	US-10-719-900-600913
30	25	0.6	25	1	US-10-719-900-605442
31	25	0.6	25	1	US-10-719-900-661249
32	25	0.6	25	1	US-10-719-900-664806
33	25	0.6	25	1	US-10-719-900-678709

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Sequence 219321,	25	US-10-719-900-219321	23.4	0.5	53
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Sequence 324990,	25	US-10-719-900-324990	23.4	0.5	55
Sequence 350766,	25	US-10-719-900-350766	23.4	0.5	56
Sequence 366992,	25	US-10-719-900-366992	23.4	0.5	57
Sequence 443781,	25	US-10-719-900-443781	23.4	0.5	58
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Sequence 548828,	25	US-10-719-900-548828	23.4	0.5	61
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Sequence 726399,	25	US-10-719-900-726399	23.4	0.5	71
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Sequence 813290,	25	US-10-719-900-813290	23.4	0.5	74
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c 254	20	0.5	20	1	US-10-633-163-64	Sequence 64, Appl	327	16.8	0.4	20	1	US-10-017-995-520	Sequence 520, App
c 255	20	0.5	20	1	US-10-633-163-65	Sequence 65, Appl	c 328	16.8	0.4	20	1	US-10-017-995-520	Sequence 520, App
c 256	20	0.5	20	1	US-10-633-163-66	Sequence 66, Appl	329	16.8	0.4	20	1	US-10-017-995-769	Sequence 769, App
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c 258	20	0.5	20	1	US-10-633-163-68	Sequence 68, Appl	c 331	16.8	0.4	20	1	US-10-209-608-42	Sequence 42, Appl
c 259	19.2	0.4	24	1	US-09-894-799-22	Sequence 22, Appl	332	16.8	0.4	20	1	US-10-367-470-13	Sequence 13, Appl
c 260	19.2	0.4	24	1	US-09-954-556-13	Sequence 13, Appl	333	16.8	0.4	20	1	US-10-367-470-14	Sequence 14, Appl
c 261	19.2	0.4	24	1	US-10-648-984-22	Sequence 22, Appl	334	16.8	0.4	20	1	US-10-314-578-520	Sequence 520, App
c 262	19.2	0.4	19	1	US-10-189-267-13	Sequence 13, Appl	335	16.8	0.4	20	1	US-10-314-578-520	Sequence 520, App
c 263	19	0.4	20	1	US-10-189-267-74	Sequence 74, Appl	336	16.8	0.4	20	1	US-10-314-578-769	Sequence 769, App
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c 265	18.8	0.4	22	1	US-10-155-407A-18	Sequence 18, Appl	338	16.8	0.4	20	1	US-10-189-267-7	Sequence 7, Appl1
c 266	18.8	0.4	22	1	US-10-155-407A-18	Sequence 18, Appl	c 339	16.8	0.4	20	1	US-10-189-267-35	Sequence 35, Appl
c 267	18.4	0.4	20	1	US-09-823-634A-15	Sequence 15, Appl	c 340	16.8	0.4	20	1	US-10-189-267-41	Sequence 41, Appl
c 268	18.4	0.4	20	1	US-09-823-647B-15	Sequence 15, Appl	c 341	16.8	0.4	20	1	US-10-189-267-41	Sequence 41, Appl
c 269	18.4	0.4	20	1	US-10-367-470-15	Sequence 15, Appl	c 342	16.8	0.4	20	1	US-10-189-267-44	Sequence 44, Appl
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c 271	18.4	0.4	20	1	US-10-189-267-39	Sequence 39, Appl	c 344	16.8	0.4	20	1	US-10-189-267-71	Sequence 71, Appl
c 272	18.4	0.4	20	1	US-10-189-267-42	Sequence 42, Appl	345	16.8	0.4	20	1	US-10-189-267-174	Sequence 174, App
c 273	18.4	0.4	20	1	US-10-189-267-49	Sequence 49, Appl	346	16.8	0.4	20	1	US-10-189-267-181	Sequence 181, App
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c 276	18.4	0.4	20	1	US-10-189-267-76	Sequence 76, Appl	c 349	16.8	0.4	20	1	US-10-683-386-42	Sequence 42, Appl
c 277	18.4	0.4	20	1	US-10-189-267-78	Sequence 78, Appl	c 350	16.8	0.4	20	1	US-10-633-163-69	Sequence 69, Appl
c 278	18.4	0.4	20	1	US-10-189-267-180	Sequence 180, App	351	16.8	0.4	20	1	US-10-831-778-520	Sequence 520, App
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c 280	18.4	0.4	20	1	US-10-189-267-193	Sequence 193, App	c 353	16.8	0.4	20	1	US-10-831-778-769	Sequence 769, App
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c 284	18	0.4	18	1	US-10-028-158-9	Sequence 9, Appl1	357	16.8	0.4	20	1	US-10-838-659-76	Sequence 76, Appl
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c 289	17.4	0.4	20	1	US-10-189-267-43	Sequence 43, Appl	362	16.4	0.4	19	1	US-09-766-450-48	Sequence 48, Appl
c 290	17.4	0.4	20	1	US-10-189-267-58	Sequence 58, Appl	c 363	16.4	0.4	19	1	US-10-683-990-59	Sequence 59, Appl
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c 301	16.8	0.4	20	1	US-09-823-634A-13	Sequence 13, Appl	374	16	0.4	16	1	US-10-028-158-17	Sequence 17, Appl
c 302	16.8	0.4	20	1	US-09-823-634A-14	Sequence 14, Appl	c 375	16	0.4	16	1	US-10-146-058-105	Sequence 105, App
c 303	16.8	0.4	20	1	US-09-823-647B-13	Sequence 13, Appl	c 376	16	0.4	16	1	US-10-146-058-113	Sequence 113, App
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c 306	16.8	0.4	20	1	US-09-888-326-192	Sequence 192, App	379	16	0.4	17	1	US-10-238-700-8	Sequence 8, Appl1
c 307	16.8	0.4	20	1	US-09-888-326-193	Sequence 193, App	c 380	16	0.4	18	1	US-09-775-479-9	Sequence 9, Appl1
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c 315	16.8	0.4	20	1	US-09-776-479-769	Sequence 769, App	c 388	15.8	0.4	19	1	US-10-112-653-131	Sequence 131, App
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c 319	16.8	0.4	20	1	US-09-965-101-22	Sequence 22, Appl	392	15.8	0.4	19	1	US-10-314-578-138	Sequence 138, App
c 320	16.8	0.4	20	1	US-09-965-101-76	Sequence 76, Appl	c 393	15.8	0.4	19	1	US-10-314-578-138	Sequence 138, App
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c 323	16.8	0.4	20	1	US-10-112-653-497	Sequence 497, App	396	15.8	0.4	19	1	US-10-831-778-138	Sequence 138, App
c 324	16.8	0.4	20	1	US-10-112-653-497	Sequence 497, App	c 397	15.8	0.4	19	1	US-10-831-778-138	Sequence 138, App
c 325	16.8	0.4	20	1	US-10-112-653-742	Sequence 742, App	c 398	15.6	0.4	22	1	US-09-750-401-32	Sequence 32, Appl

c 399	15.6	0.4	22	1	US-10-309-788-32	Sequence 32, Appl	c 472	14.4	0.3	17	1	US-10-287-949A-3612	Sequence 3612, Ap
c 400	15.6	0.4	22	1	US-10-238-306B-32	Sequence 32, Appl	c 473	14.4	0.3	17	1	US-10-287-949A-6425	Sequence 6425, Ap
c 401	15.6	0.4	22	1	US-10-629-453-32	Sequence 32, Appl	c 474	14.4	0.3	17	1	US-10-287-949A-7146	Sequence 7146, Ap
c 402	15.4	0.4	17	1	US-10-156-306-526	Sequence 526, Appl	c 475	14.4	0.3	17	1	US-10-287-949A-7538	Sequence 7538, Ap
c 403	15.4	0.4	17	1	US-10-156-306-527	Sequence 527, Appl	c 476	14.4	0.3	17	1	US-10-712-672-716	Sequence 716, App
c 404	15.4	0.4	17	1	US-10-238-700-9	Sequence 9, Appl	c 477	14.4	0.3	17	1	US-10-712-672-717	Sequence 717, App
c 405	15.4	0.4	18	1	US-09-725-265-18	Sequence 18, Appl	c 478	14.4	0.3	17	1	US-10-713-633-4	Sequence 4, Appl
c 406	15.4	0.4	18	1	US-09-891-517-18	Sequence 18, Appl	c 479	14.4	0.3	17	1	US-10-713-633-551	Sequence 551, App
c 407	15.4	0.4	18	1	US-10-146-058-112	Sequence 112, Appl	c 480	14.4	0.3	17	1	US-10-498-462-47	Sequence 47, Appl
c 408	15.4	0.4	18	1	US-10-209-608-18	Sequence 18, Appl	c 481	14.4	0.3	17	1	US-10-498-462-48	Sequence 48, Appl
c 409	15.4	0.4	18	1	US-10-232-881-3	Sequence 3, Appl	c 482	14.4	0.3	18	1	US-09-725-265-15	Sequence 15, Appl
c 410	15.4	0.4	18	1	US-10-232-881-5	Sequence 5, Appl	c 483	14.4	0.3	18	1	US-09-725-265-16	Sequence 16, Appl
c 411	15.4	0.4	18	1	US-10-683-386-18	Sequence 18, Appl	c 484	14.4	0.3	18	1	US-09-725-265-17	Sequence 17, Appl
c 412	15.4	0.4	18	1	US-10-760-940-3	Sequence 3, Appl	c 485	14.4	0.3	18	1	US-09-725-265-19	Sequence 19, Appl
c 413	15.4	0.4	18	1	US-10-473-126-1002	Sequence 1002, Ap	c 486	14.4	0.3	18	1	US-09-891-517-15	Sequence 15, Appl
c 414	15.4	0.4	19	1	US-09-569-193A-3	Sequence 3, Appl	c 487	14.4	0.3	18	1	US-09-891-517-16	Sequence 16, Appl
c 415	15.4	0.4	19	1	US-09-865-044-3	Sequence 3, Appl	c 488	14.4	0.3	18	1	US-09-891-517-17	Sequence 17, Appl
c 416	15.4	0.4	19	1	US-10-057-813-3	Sequence 3, Appl	c 489	14.4	0.3	18	1	US-09-891-517-19	Sequence 19, Appl
c 417	15.4	0.4	19	1	US-10-397-887-3	Sequence 3, Appl	c 490	14.4	0.3	18	1	US-09-904-744-2	Sequence 2, Appl
c 418	15.4	0.4	19	1	US-10-349-143-4619	Sequence 4619, Ap	c 491	14.4	0.3	18	1	US-09-961-077-1157	Sequence 1157, Ap
c 419	15.4	0.4	19	1	US-10-701-550-3	Sequence 3, Appl	c 492	14.4	0.3	18	1	US-09-994-311-7	Sequence 7, Appl
c 420	15.4	0.4	19	1	US-10-670-011-33	Sequence 33, Appl	c 493	14.4	0.3	18	1	US-10-077-383-27	Sequence 27, Appl
c 421	15.4	0.4	19	1	US-10-670-011-129	Sequence 129, Appl	c 494	14.4	0.3	18	1	US-10-209-608-15	Sequence 15, Appl
c 422	15.4	0.4	20	1	US-10-663-189-7	Sequence 7, Appl	c 495	14.4	0.3	18	1	US-10-209-608-16	Sequence 16, Appl
c 423	15	0.4	17	1	US-10-156-306-523	Sequence 523, Appl	c 496	14.4	0.3	18	1	US-10-209-608-17	Sequence 17, Appl
c 424	15	0.4	17	1	US-10-735-592-47	Sequence 47, Appl	c 497	14.4	0.3	18	1	US-10-209-608-19	Sequence 19, Appl
c 425	15	0.4	18	1	US-09-775-479-8	Sequence 8, Appl	c 498	14.4	0.3	18	1	US-10-145-857-19	Sequence 19, Appl
c 426	14.8	0.3	18	1	US-09-725-265-20	Sequence 20, Appl	c 499	14.4	0.3	18	1	US-10-683-386-15	Sequence 15, Appl
c 427	14.8	0.3	18	1	US-09-891-517-20	Sequence 20, Appl	c 500	14.4	0.3	18	1	US-10-683-386-16	Sequence 16, Appl
c 428	14.8	0.3	18	1	US-09-969-373-2296	Sequence 2296, Ap	c 501	14.4	0.3	18	1	US-10-683-386-17	Sequence 17, Appl
c 429	14.8	0.3	18	1	US-09-904-744-3	Sequence 3, Appl	c 502	14.4	0.3	18	1	US-10-683-386-19	Sequence 19, Appl
c 430	14.8	0.3	18	1	US-09-949-305B-2	Sequence 2, Appl	c 503	14.4	0.3	18	1	US-10-473-126-652	Sequence 652, App
c 431	14.8	0.3	18	1	US-10-146-058-72	Sequence 72, Appl	c 504	14.4	0.3	18	1	US-10-872-984-7	Sequence 7, Appl
c 432	14.8	0.3	18	1	US-10-146-058-79	Sequence 79, Appl	c 505	14.4	0.3	18	1	US-10-845-667-682	Sequence 682, App
c 433	14.8	0.3	18	1	US-10-146-058-85	Sequence 85, Appl	c 506	14.4	0.3	18	1	US-10-845-667-1432	Sequence 1432, Ap
c 434	14.8	0.3	18	1	US-10-146-058-96	Sequence 96, Appl	c 507	14.4	0.3	25	1	US-10-719-900-164291	Sequence 164291, A
c 435	14.8	0.3	18	1	US-10-146-058-115	Sequence 115, Appl	c 508	14.4	0.3	14	1	US-09-263-959-816	Sequence 816, App
c 436	14.8	0.3	18	1	US-10-146-058-128	Sequence 128, Appl	c 509	14	0.3	14	1	US-10-146-058-57	Sequence 57, Appl
c 437	14.8	0.3	18	1	US-10-146-058-132	Sequence 132, Appl	c 510	14	0.3	14	1	US-10-146-058-63	Sequence 63, Appl
c 438	14.8	0.3	18	1	US-10-085-906-135	Sequence 135, Appl	c 511	14	0.3	14	1	US-10-146-058-67	Sequence 71, Appl
c 439	14.8	0.3	18	1	US-10-209-608-20	Sequence 20, Appl	c 512	14	0.3	14	1	US-10-146-058-74	Sequence 74, Appl
c 440	14.8	0.3	18	1	US-10-352-704-24	Sequence 24, Appl	c 513	14	0.3	14	1	US-10-146-058-75	Sequence 75, Appl
c 441	14.8	0.3	18	1	US-10-220-033-4	Sequence 4, Appl	c 514	14	0.3	14	1	US-10-146-058-91	Sequence 91, Appl
c 442	14.8	0.3	18	1	US-10-328-578-142	Sequence 142, Appl	c 515	14	0.3	14	1	US-10-146-058-101	Sequence 101, Appl
c 443	14.8	0.3	18	1	US-10-297-068-282	Sequence 282, Appl	c 516	14	0.3	14	1	US-10-146-058-103	Sequence 103, App
c 444	14.8	0.3	18	1	US-10-683-386-20	Sequence 20, Appl	c 517	14	0.3	14	1	US-10-146-058-106	Sequence 106, App
c 445	14.8	0.3	18	1	US-10-623-371-142	Sequence 142, Appl	c 518	14	0.3	14	1	US-10-146-058-122	Sequence 122, App
c 446	14.8	0.3	18	1	US-10-849-072-22	Sequence 22, Appl	c 519	14	0.3	14	1	US-10-146-058-136	Sequence 136, App
c 447	14.8	0.3	18	1	US-10-949-072-24	Sequence 24, Appl	c 520	14	0.3	14	1	US-10-343-710-146	Sequence 146, App
c 448	14.8	0.3	18	1	US-10-701-347-6	Sequence 6, Appl	c 521	14	0.3	14	1	US-10-468-753-45	Sequence 45, Appl
c 449	14.8	0.3	18	1	US-10-701-347-11	Sequence 11, Appl	c 522	14	0.3	14	1	US-10-468-753-46	Sequence 46, Appl
c 450	14.4	0.3	16	1	US-09-882-945A-280	Sequence 280, App	c 523	14	0.3	14	1	US-10-468-753-48	Sequence 48, Appl
c 451	14.4	0.3	16	1	US-10-146-058-94	Sequence 94, Appl	c 524	14	0.3	14	1	US-10-468-753-49	Sequence 49, Appl
c 452	14.4	0.3	16	1	US-10-146-058-107	Sequence 107, Appl	c 525	14	0.3	14	1	US-10-855-595-17	Sequence 17, Appl
c 453	14.4	0.3	16	1	US-10-807-114-280	Sequence 280, App	c 526	14	0.3	14	1	US-10-855-595-21	Sequence 21, Appl
c 454	14.4	0.3	17	1	US-10-156-306-526	Sequence 526, App	c 527	14	0.3	14	1	US-10-855-532-17	Sequence 17, Appl
c 455	14.4	0.3	17	1	US-10-156-306-527	Sequence 527, App	c 528	14	0.3	14	1	US-10-855-532-21	Sequence 21, Appl
c 456	14.4	0.3	17	1	US-09-780-533A-233	Sequence 233, App	c 529	14	0.3	15	1	US-09-504-231A-321	Sequence 321, App
c 457	14.4	0.3	17	1	US-09-776-474-942	Sequence 942, App	c 530	14	0.3	15	1	US-09-504-231A-322	Sequence 322, App
c 458	14.4	0.3	17	1	US-09-930-423-998	Sequence 998, App	c 531	14	0.3	15	1	US-09-274-553D-321	Sequence 321, App
c 459	14.4	0.3	17	1	US-09-930-423-1179	Sequence 1179, Ap	c 532	14	0.3	15	1	US-09-274-553D-322	Sequence 322, App
c 460	14.4	0.3	17	1	US-09-745-237A-998	Sequence 998, App	c 533	14	0.3	15	1	US-10-027-632-52311	Sequence 52311, A
c 461	14.4	0.3	17	1	US-09-745-237A-1179	Sequence 1179, Ap	c 534	14	0.3	15	1	US-10-027-632-52311	Sequence 52311, A
c 462	14.4	0.3	17	1	US-10-041-856-35	Sequence 35, Appl	c 535	14	0.3	15	1	US-10-230-007B-17	Sequence 17, Appl
c 463	14.4	0.3	17	1	US-10-156-306-528	Sequence 528, App	c 536	14	0.3	15	1	US-10-647-982A-17	Sequence 17, Appl
c 464	14.4	0.3	17	1	US-10-238-700-7	Sequence 7, Appl	c 537	14	0.3	17	1	US-10-041-856-35	Sequence 35, Appl
c 465	14.4	0.3	17	1	US-10-339-793-439	Sequence 439, App	c 538	14	0.3	17	1	US-09-090-672B-105	Sequence 105, App
c 466	14.4	0.3	17	1	US-10-138-674-1773	Sequence 1773, Ap	c 539	14	0.3	17	1	US-09-780-533A-857	Sequence 857, App
c 467	14.4	0.3	17	1	US-10-138-674-1773	Sequence 1773, Ap	c 540	14	0.3	17	1	US-09-780-533A-2399	Sequence 2399, Ap
c 468	14.4	0.3	17	1	US-10-138-674-3612	Sequence 3612, Ap	c 541	14	0.3	17	1	US-09-780-533A-2400	Sequence 2400, Ap
c 469	14.4	0.3	17	1	US-10-138-674-6452	Sequence 6425, Ap	c 542	14	0.3	17	1	US-09-730-559B-107	Sequence 107, App
c 470	14.4	0.3	17	1	US-10-138-674-7146	Sequence 7146, Ap	c 543	14	0.3	17	1	US-10-163-552-948	Sequence 948, App
c 471	14.4	0.3	17	1	US-10-138-674-7538	Sequence 7538, Ap	c 544	14	0.3	17	1	US-10-156-306-522	Sequence 522, App
c 472	14.4	0.3	17	1	US-10-287-949A-1773	Sequence 1773, Ap	c 545	14	0.3	17	1		

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; CURRENT APPLICATION NUMBER: US/10/309,788
; CURRENT FILING DATE: 2003-06-18
; PRIORITY APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; PRIORITY APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 33
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR consensus sequence of TGF beta 2
US-10-309-788-29

Query Match          0.8%; Score 33; DB 1; Length 33;
Best Local Similarity 33.3%; Pred. No. 7.6;
Matches 11; Conservative 22; Mismatches 0; Indels

Qy      3264   TTTTTCCTTTTAAATGTAATGGTGCTTT 3296
Db       1    UUUUUUUUCCUUUAUUAAAUGGUUUUU 33

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RESULT 3

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; sequence 29, Application US/10/238306B
; Publication No. US20030235830A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; TITLE OF INVENTION: Methods for isolating and characterizing
; FILE OF INVENTION: complexes
; FILE REFERENCE: RBN-001CN
; CURRENT APPLICATION NUMBER: US/10/238,306B
; CURRENT FILING DATE: 2002-09-10
; PRIORITY APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 33
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
; US-10-238-306B-29

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Query Match      0.8%; Score 33; DB 1; Length 333
Best Local Similarity 33.3%; Pred. No. 7.8;
Matches 11; Conservative 22; Mismatches 0; Indels

QY      3264  TTTTTCCTTTTAAATGTAATGTCCTTT 3296
Db      1  UUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33

RESULT 4
US-10-629-453-29
; Sequence 29, Application US/10629453
; Publication No. US20040096878A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing
; complexes
; FILE REFERENCE: RBN-001DV
; CURRENT APPLICATION NUMBER: US/10/629.453

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US-10-238-306B-31

Best Local Similarity 36.0%; Pred. No. 42;
Matches 9; Conservative 16; Mismatches 0; Indels

Db 1 UUCAUUUUUUUAUAUACUAUCUU 25

US-10-189-267-14
; Sequence 14, Application US/10189267

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; APPLICANT: Phelps, William C.
; TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Targets
; FILE REFERENCE: RBN-001CP
; CURRENT APPLICATION NUMBER: US/10/309,788
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-189-267-14

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1789 AAACAGAGCGGAGGCTGAATGGCT 1813
Db 1 AAACAGAGCGGAGGCTGAATGGCT 25

RESULT 9
US-10-629-453-31
; Sequence 31, Application US/10629453
; Publication No. US20040096878A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001DV
; CURRENT APPLICATION NUMBER: US/10/629,453
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3 -UTR sequence of TGF beta 2
US-10-629-453-31

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 36.0%; Pred. No. 42;
Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 3693 TTCAATTTTATATATATCTT 3717
Db 1 UUCAUUUUUUUAUAUACUACUU 25

RESULT 10
US-10-719-900-43634
; Sequence 43634, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43634
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-43634

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2115 AAGAAGCGGCTTTGGATGCTGCT 2139
Db 1 AAGAAGCGGCTTTGGATGCTGCT 25

RESULT 11
US-10-719-900-79674
; Sequence 79674, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 79674
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-79674

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3748 AATGACATGAGCTACCTGGTCCAT 3772
Db 1 AATGACATGAGCTACCTGGTCCAT 25

RESULT 12
US-10-719-900-80968
; Sequence 80968, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 80968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-80968

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2452 AATGCAGCTAAAGTCTTGGGAAG 2476
Db 1 AATGCAGCTAAAGTCTTGGGAAG 25

RESULT 13
US-10-719-900-105991
; Sequence 105991, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900

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; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-105991

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2054 ACATCTCTGCTAAATGTTGTTGCC 2078
Db 1 ACATCTCTGCTAAATGTTGTTGCC 25

RESULT 14

US-10-719-900-115675
; Sequence 115675, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115675

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-115675

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3357 ACCGTGAAGTGGCTGTGATCTACA 3381
Db 1 ACCGTGAAGTGGCTGTGATCTACA 25

RESULT 15

US-10-719-900-125985
; Sequence 125985, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 125985

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-125985

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3979 ACTCAGAGTCTTAGTGGCTA 4003
Db 1 ACTCAGAGTCTTAGTGGCTA 25

RESULT 16

US-10-719-900-164292

; Sequence 164292, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 164292

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-164292

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3172 AGCAAAACAGTGTCTGCGAAGCTT 3196
Db 1 AGCAAAACAGTGTCTGCGAAGCTT 25

RESULT 17

US-10-719-900-219322

; Sequence 219322, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 219322

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-219322

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3849 AGTGTTCAGCCTTTCTGCGTCAG 3873
Db 1 AGTGTTCAGCCTTTCTGCGTCAG 25

RESULT 18

US-10-719-900-226895

; Sequence 226895, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-226895

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4189 ATAAATTCATCCATTATTTCCCTGA 4213
|||||
DB 1 ATAAATTCATCCATTATTTCCCTGA 25

RESULT 19
US-10-719-900-324991
; Sequence 324991, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-324991

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3787 CAGTTCCTTCTATTTTCCAAAGAT 3811
|||||
DB 1 CAGTTCCTTCTATTTTCCAAAGAT 25

RESULT 20
US-10-719-900-350767
; Sequence 350767, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 350767
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-350767

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3312 CCGGTGAATGTTGACCTGTTTGA 3336

DB 1 CCGGTGAATGTTGACCTGTTTGA 25
|||||

RESULT 21
US-10-719-900-366993
; Sequence 366993, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-366993

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3138 CTAAGCAAGTCTCTGCGAAAAAT 3162
|||||
DB 1 CTAAGCAAGTCTCTGCGAAAAAT 25

RESULT 22
US-10-719-900-443782
; Sequence 443782, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443782
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-443782

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2514 GACAACGATGACGACCATGATGTTT 2538
|||||
DB 1 GACAACGATGACGACCATGATGTTT 25

RESULT 23
US-10-719-900-508233
; Sequence 508233, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-508233

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2414 GATCGAACAGCTTCCAAATATGATT 2438
|||||

Db 1 GATCGAACAGCTTCCAAATATGATT 25
|||||

RESULT 24

US-10-719-900-547596
; Sequence 547596, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; CURRENT APPLICATION NUMBER: US/10/719,900
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 547596
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-547596

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4167 GCCAGCACTCGTCATTTTATTCATA 4191
|||||

Db 1 GCCAGCACTCGTCATTTTATTCATA 25
|||||

RESULT 25

US-10-719-900-548688
; Sequence 548688, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548688
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548688

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3297 GCCAGTTTAAGCAAGCGGTGAAT 3321
|||||

Db 1 GCCAGTTTAAGCAAGCGGTGAAT 25
|||||

RESULT 26

US-10-719-900-548829
; Sequence 548829, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548829
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548829

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3204 GCCATATGCCCAAGGCGCTGTAA 3228
|||||

Db 1 GCCATATGCCCAAGGCGCTGTAA 25
|||||

RESULT 27

US-10-719-900-553274
; Sequence 553274, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 553274
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-553274

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4044 GCCGTTCAAAAGCACACAGTTCAAA 4068
|||||

Db 1 GCCGTTCAAAAGCACACAGTTCAAA 25
|||||

RESULT 28

US-10-719-900-563977
; Sequence 563977, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20


```
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 563977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-563977

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3959 GCTAGGTTTAAAGTCTCAACTCA 3983
Db 1 GCTAGGTTTAAAGTCTCAACTCA 25

RESULT 29
US-10-719-900-600913
; Sequence 600913, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 600913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-600913

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2090 GGAGTCACAAAGTCCAGCGGGG 2114
Db 1 GGAGTCACAAAGTCCAGCGGGG 25

RESULT 30
US-10-719-900-605442
; Sequence 605442, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 605442
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-605442

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2129 GGATGCTGCTACTGCTTTAGAAAT 2153
Db 1 GGATGCTGCTACTGCTTTAGAAAT 25
```

```
RESULT 31
US-10-719-900-661249
; Sequence 661249, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 661249
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-661249

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3283 GTAAATGGTCTTTGCCAGTTTAAG 3307
Db 1 GTAAATGGTCTTTGCCAGTTTAAG 25

RESULT 32
US-10-719-900-664806
; Sequence 664806, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 664806
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-664806

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2315 GTACAACACCAATAATCCCGAAGCT 2339
Db 1 GTACAACACCAATAATCCCGAAGCT 25

RESULT 33
US-10-719-900-678709
; Sequence 678709, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 678709
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-678709

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3340 GTATTGTCAGACTTTTGACCGTGA 3364
Db 1 GTATTGTCAGACTTTTGACCGTGA 25

RESULT 34
US-10-719-900-707594
; Sequence 707594, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 707594
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-707594

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3153 GTGGAAAAATCAAGCCCGAGCAA 3177
Db 1 GTGGAAAAATCAAGCCCGAGCAA 25

RESULT 35
US-10-719-900-718938
; Sequence 718938, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 718938
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-718938

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2356 GTGTGTCAGGATCTGGACCACT 2380
Db 1 GTGTGTCAGGATCTGGACCACT 25

RESULT 36
US-10-719-900-726398
; Sequence 726398, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 726398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-726398

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2281 GTTCAGACACTCAACACACCAAGT 2305
Db 1 GTTCAGACACTCAACACACCAAGT 25

RESULT 37
US-10-719-900-739550
; Sequence 739550, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 739550
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-739550

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4010 GTTCTTTAACTCCTATATTATGG 4034
Db 1 GTTCTTTAACTCCTATATTATGG 25

RESULT 38
US-10-719-900-779378
; Sequence 779378, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

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; SEQ ID NO 779378
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-779378

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3833 TAGGTTTGAGCTCCACAGGTTTCA 3857
Db 1 TAGGTTTGAGCTCCACAGGTTTCA 25

RESULT 39
US-10-719-900-813289
; Sequence 813289, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 813289
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-813289

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4198 TCATTATTTCCTGATTTTCATTGA 4222
Db 1 TCATTATTTCCTGATTTTCATTGA 25

RESULT 40
US-10-719-900-858151
; Sequence 858151, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 858151
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-858151

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3373 TGATCTACAATACAGGTTTTCCTT 3397
Db 1 TGATCTACAATACAGGTTTTCCTT 25

```

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RESULT 41
US-10-719-900-868129
; Sequence 868129, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 868129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-868129

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3186 TGCCGAAGCTTCATGACGCCATAT 3210
Db 1 TGCCGAAGCTTCATGACGCCATAT 25

RESULT 42
US-10-719-900-877801
; Sequence 877801, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 877801
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-877801

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 TGGAAACCACTGACCATTTCTTATTA 2395
Db 1 TGGAAACCACTGACCATTTCTTATTA 25

RESULT 43
US-10-719-900-926328
; Sequence 926328, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 926328

```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-926328

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4029 TTATGACTCTCTTTCGGGTCAA 4053
Db 1 TTATGACTCTCTTTCGGGTCAA 25

RESULT 44
US-10-719-900-970882
; Sequence 970882, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970882
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-970882

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3862 TTTCGCGTCAGTGTCAGTCATGTG 3886
Db 1 TTTCGCGTCAGTGTCAGTCATGTG 25

RESULT 45
US-10-189-267-6/c
; Sequence 6, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; PRIOR FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-189-267-6

Query Match          0.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2142 TGCCTTAGAAATGTGCAGGATAATT 2166
Db 25 TGCCTTAGAAATGTGCAGGATAATT 1

RESULT 46
US-10-719-900-43633
; Sequence 43633, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43633
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-43633

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2115 AAGAAGCGCGCTTTGGATGCTGCCT 2139
Db 1 AAGAAGCGCGCTATGATGCTGCCT 25

RESULT 47
US-10-719-900-79673
; Sequence 79673, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 79673
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-79673

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3748 AATGACATGAGCTACCTGGGTCCAT 3772
Db 1 AATGACATGAGCAACCTGGGTCCAT 25

RESULT 48
US-10-719-900-80967
; Sequence 80967, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 80967
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-80967

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2452 AATGCAGCTAAAGTCTCTTGGAAG 2476
      |||||
Db 1 AATGCAGCTAAACTCTTGGGAAG 25

RESULT 49
US-10-719-900-105992
; Sequence 105992, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105992
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-105992

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2054 ACATCTCTCGCTAAATGTTGTC 2078
      |||||
Db 1 ACATCTCTCGCTATATGTTGTC 25

RESULT 50
US-10-719-900-115676
; Sequence 115676, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115676
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-115676

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3357 ACCGTGAAGTGGTGTGTGATCTACA 3381
      |||||
Db 1 ACCGTGAAGTGGTGTGTGATCTACA 25

RESULT 51
US-10-719-900-125986
; Sequence 125986, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 125986
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-125986

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3979 ACTCAGAGTCTTAGTGACTGGGCTA 4003
      |||||
Db 1 ACTCAGAGTCTTTGTGACTGGGCTA 25

RESULT 52
US-10-719-900-164291
; Sequence 164291, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 164291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-164291

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3172 ACNAAACAGTGTCTGCCGAGCTT 3196
      |||||
Db 1 ACNAAACAGTGTCTGCCGAGCTT 25

RESULT 53
US-10-719-900-219321
; Sequence 219321, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219321
; LENGTH: 25
```

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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-219321

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3849 AGTGTTCAGCCTTTCGCTCAG 3873
      |||||
Db 1 AGTGTTCAGCCATTTCGCTCAG 25

RESULT 54
US-10-719-900-226896
; Sequence 226896, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-226896

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4189 ATAATTTCATCATTTATTTCCCTGA 4213
      |||||
Db 1 ATAATTTCATCTTTATTTCCCTGA 25

RESULT 55
US-10-719-900-324990
; Sequence 324990, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324990
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-324990

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3787 CAGTTCCTTCTATTTTCCAAAGAT 3811
      |||||
Db 1 CAGTTCCTTCTAATTTCCAAAGAT 25

RESULT 56
US-10-719-900-350766
; Sequence 350766, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 350766
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-350766

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3312 CCGGTGAAATGTTGACCTGTTTGA 3336
      |||||
Db 1 CCGGTGAAATGTAGACCTGTTTGA 25

RESULT 57
US-10-719-900-366992
; Sequence 366992, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366992
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-366992

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3138 CTAAGCAAGTCTTCTGTGAAAAAT 3162
      |||||
Db 1 CTAAGCAAGTCTACTGTGAAAAAT 25

RESULT 58
US-10-719-900-443781
; Sequence 443781, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443781
; LENGTH: 25
; TYPE: DNA
```

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; ORGANISM: Mus musculus
US-10-719-900-443781

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2514 GACAACGATGACGACCATGATGTTT 2538
      ||||||| ||||||| ||||||| |||||||
Db 1 GACAACGATGACCAACCATGATGTTT 25

RESULT 59
US-10-719-900-508232
; Sequence 508232, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-508232

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2414 GATCGAACAGCTTTCGAATGATT 2438
      ||||||| ||||||| ||||||| |||||||
Db 1 GATCGAACAGCTTTCGAATGATT 25

RESULT 60
US-10-719-900-547597
; Sequence 547597, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 547597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-547597

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4167 GCAGCACTCGCATTTTATTCATA 4191
      ||||||| ||||||| ||||||| |||||||
Db 1 GCAGCACTCGGATTTATTCATA 25

RESULT 61
US-10-719-900-548689
; Sequence 548689, Application US/10719900
```

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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548689
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548689

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3297 GCCAGTTTAAGCAAGCGGTGAAT 3321
      ||||||| ||||||| ||||||| |||||||
Db 1 GCCAGTTTAAGCTAGCCGGTGAAT 25

RESULT 62
US-10-719-900-548828
; Sequence 548828, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548828

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3204 GCCATATGCCAGAGGCGCTGTAA 3228
      ||||||| ||||||| ||||||| |||||||
Db 1 GCCATATGCCACAGGCGCTGTAA 25

RESULT 63
US-10-719-900-553275
; Sequence 553275, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 553275
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
```

```
US-10-719-900-553275
Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4044 GCCGTTCAAAGACACAGTTCAAA 4068
      |||||
Db 1 GCCGTTCAAAGAGACAGTTCAAA 25

RESULT 64
US-10-719-900-563976
; Sequence 563976, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 563976
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-563976

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3959 GCTAGGGTTAAGAAATCTCAACTCA 3983
      |||||
Db 1 GCTAGGGTTAACAATCTCAACTCA 25

RESULT 65
US-10-719-900-600912
; Sequence 600912, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 600912
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-600912

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2090 GGAGTCACAACAGTCCAGCGCGG 2114
      |||||
Db 1 GGAGTCACAACAGTCCAGCGCGG 25

RESULT 66
US-10-719-900-605443
; Sequence 605443, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 605443
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-605443

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2129 GGATGCTGCTACTGCTTTAGAAAT 2153
      |||||
Db 1 GGATGCTGCTAGTCTTTAGAAAT 25

RESULT 67
US-10-719-900-661248
; Sequence 661248, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 661248
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-661248

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3283 GTAAATGGTTCTTCCAGTTTAAAG 3307
      |||||
Db 1 GTAAATGGTTCTATGCCAGTTTAAAG 25

RESULT 68
US-10-719-900-664807
; Sequence 664807, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 664807
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-664807
```


Query Match 0.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 66;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2315 GTACACACCAATTAATCCCGAAGCT 2339
 |||||
 Db 1 GTACACACCAATTAATCCCGAAGCT 25

RESULT 69
 US-10-719-900-678708
 ; Sequence 678708, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 678708
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-678708

Query Match 0.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 66;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3340 GTATTGTCAGACTTTGACCGTGAA 3364
 |||||
 Db 1 GTATTGTCAGACTTTGACCGTGAA 25

RESULT 70
 US-10-719-900-707595
 ; Sequence 707595, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 707595
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-707595

Query Match 0.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 66;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3153 GTGGAAAAATCAAGCCCGCAGCAA 3177
 |||||
 Db 1 GTGGAAAAATCATAGCCCCGAGCAA 25

RESULT 71
 US-10-719-900-718939
 ; Sequence 718939, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 718939
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-718939

Query Match 0.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 66;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2356 GTGTGTCGCCAGGATCTGGAACCACT 2380
 |||||
 Db 1 GTGTGTCGCCAGGTTCTGGAACCACT 25

RESULT 72
 US-10-719-900-726399
 ; Sequence 726399, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 726399
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-726399

Query Match 0.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 66;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2281 GTTCAGACACTCAACACACCAAAAGT 2305
 |||||
 Db 1 GTTCAGACACTCTACACACCAAAAGT 25

RESULT 73
 US-10-719-900-739552
 ; Sequence 739552, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 739552
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-739552

```

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4010 GTTCTTTTAACTCCCTATATTATGG 4034
Db 1 GTTCTTTTAACTGCTATATTATGG 25

RESULT 74
US-10-719-900-779379
; Sequence 779379, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 779379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-779379

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3833 TAGGTTTGAGCTCCACAGTGTTCA 3857
Db 1 TAGGTTTGAGCTGCACAGTGTTCA 25

RESULT 75
US-10-719-900-813290
; Sequence 813290, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 813290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-813290

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4198 TCCATTATTTCCCTGATTTCAATGA 4222
Db 1 TCCATTATTTCCCTGATTTCAATGA 25

RESULT 76
US-10-719-900-858152
; Sequence 858152, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou

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; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 858152
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-858152

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3373 TGATCTACAATACAGGTTTTTCCTT 3397
Db 1 TGATCTACAATAGAGGTTTTTCCTT 25

RESULT 77
US-10-719-900-868130
; Sequence 868130, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 868130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-868130

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3186 TGCCGAAGCTTCATGAGCGCCATAT 3210
Db 1 TGCCGAAGCTTCTTGAGCGCCATAT 25

RESULT 78
US-10-719-900-877802
; Sequence 877802, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 877802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-877802

Query Match          0.5%; Score 23.4; DB 1; Length 25;

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Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2371 TGAACCACTGACCATTTCTCTATT 2395
Db 1 TGAACCACTGACCATTTCTCTATT 25

RESULT 79
US-10-719-900-926327
; Sequence 926327, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 926327
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-926327

Query Match 0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTTCGCGTTCAAA 4053
Db 1 TTATGGACTCTCTTTCGCGTTCAAA 25

RESULT 80
US-10-719-900-970881
; Sequence 970881, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970881
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-970881

Query Match 0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3862 TTTCGCGTCAGTGTGAGTCATGTG 3886
Db 1 TTTCGCGTCAGTGTGAGTCATGTG 25

RESULT 81
US-09-750-401-32
; Sequence 32, Application US/09750401
; Publication No. US20020004211A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.

; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-32

Query Match 0.5%; Score 22; DB 1; Length 22;
Best Local Similarity 22.7%; Pred. No. 75;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAAATGGTTT 4099
Db 1 UUUUUCUUAAUUGUUUUU 22

RESULT 82
US-10-309-788-32
; Sequence 32, Application US/10309788
; Publication No. US20030211466A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; APPLICANT: Phelps, William C.
; TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Targets
; FILE REFERENCE: RBN-001CP
; CURRENT APPLICATION NUMBER: US/10/309,788
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR consensus sequence of TGF beta 2
US-10-309-788-32

Query Match 0.5%; Score 22; DB 1; Length 22;
Best Local Similarity 22.7%; Pred. No. 75;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAAATGGTTT 4099
Db 1 UUUUUCUUAAUUGUUUUU 22

RESULT 83
US-10-238-306B-32
; Sequence 32, Application US/10238306B
; Publication No. US20030235830A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; APPLICANT: complexes

```

; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 522556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-522556

Query Match          0.5%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3937 AGTTCGCACAAATGTAGGCTTAGC 3960
          ||||||||||||||||||||
DB      2 ATTGGCGACAAATGTAGGCTTAGC 25

RESULT 86
US-09-948-002-48/c
; Sequence 48, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-48

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      34 GAGCTGCTGAACCTGCGGC 53
          ||||||||||||||||
DB      20 GAGCTGCTGAACCTGCGGC 1

RESULT 87
US-09-948-002-49/c
; Sequence 49, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-49

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 AAGCTAGGAGGCTGCGAG 278
Db 20 AAGCTAGGAGGCTGCGAG 1

RESULT 88
US-09-948-002-50/c
; Sequence 50, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-50

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 TGGCCGCTGGAGCAAGAA 381
Db 20 TGGCCGCTGGAGCAAGAA 1

RESULT 89
US-09-948-002-51/c
; Sequence 51, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-51

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GGGATCCTCGCGCTGCTC 512
Db 20 GGGATCCTCGCGCTGCTC 1

RESULT 90
US-09-948-002-52/c
; Sequence 52, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-52

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 ACACGTGTGGAAGCAGGCG 690
Db 20 ACACGTGTGGAAGCAGGCG 1

RESULT 91
US-09-948-002-53/c
; Sequence 53, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-53

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 830 TCAGATCAGCCACTCGCAC 849
TCAGATCAGCCACTCGCAC 1

```
Db      20 TCAGATCAGCCACTCGCAC 1
RESULT 92
US-09-948-002-54/c
; Sequence 54, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-54
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1016 TTGGGAACGCTTGCATTTT 1035
Db      20 TTGGGAACGCTTGCATTTT 1
RESULT 93
US-09-948-002-55/c
; Sequence 55, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-55
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1247 GCTCCTGCATCTGGTCCCGG 1266
Db      20 GCTCCTGCATCTGGTCCCGG 1
RESULT 94
US-09-948-002-56/c
; Sequence 56, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-56
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1451 GCAGGAGAGGCAAGCCGGA 1470
Db      20 GCAGGAGAGGCAAGCCGGA 1
RESULT 95
US-09-948-002-57/c
; Sequence 57, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-57
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1668 GTCTTCCGCTTGCAAAACCC 1687
Db      20 GTCTTCCGCTTGCAAAACCC 1
RESULT 96
US-09-948-002-58/c
; Sequence 58, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
```

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-58

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1754 TCCACCCAGCGCTACATCG 1773
Db 20 TCCACCCAGCGCTACATCG 1

RESULT 97
US-09-948-002-59/c
; Sequence 59, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-59

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2032 AAAAAACCAAGTGGGAAGACC 2051
Db 20 AAAAAACCAAGTGGGAAGACC 1

RESULT 98
US-09-948-002-60/c
; Sequence 60, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
```

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; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-60

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2321 CACCATAAATCCGGAAGCTT 2340
Db 20 CACCATAAATCCGGAAGCTT 1

RESULT 99
US-09-948-002-61/c
; Sequence 61, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-61

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2478 CAGGACACGAAAATCACGGT 2497
Db 20 CAGGACACGAAAATCACGGT 1

RESULT 100
US-09-948-002-62/c
; Sequence 62, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
```

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; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-62

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2854 ACGTATTGTTCCAGCCGC 2873
Db 20 ACGTATTGTTCCAGCCGC 1

RESULT 101
US-09-948-002-63/c
; Sequence 63, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-63

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3075 GAACTCAATAAGCCAGGGG 3094
Db 20 GAACTCAATAAGCCAGGGG 1

RESULT 102
US-09-948-002-64/c
; Sequence 64, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-64

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3297 GCCAGTTTAAGCAAGCCGGT 3316
Db 20 GCCAGTTTAAGCAAGCCGGT 1

RESULT 103
US-09-948-002-65/c
; Sequence 65, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-65

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3352 TTTTGACCGTGAAGTGGCTG 3371
Db 20 TTTTGACCGTGAAGTGGCTG 1

RESULT 104
US-09-948-002-66/c
; Sequence 66, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-66

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3753 CATGAGCTACCTGGGTCCAT 3772
Db 20 CATGAGCTACCTGGGTCCAT 1

RESULT 105

US-09-948-002-67/c

; Sequence 67, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-948-002-67

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3874 TGTGAGTCATGTGGCGGTG 3893
Db 20 TGTGAGTCATGTGGCGGTG 1

RESULT 106

US-09-948-002-68/c

; Sequence 68, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-948-002-68

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4097 TTTGGTCTCATGGGTGTA 4116
Db 20 TTTGGTCTCATGGGTGTA 1

RESULT 107

US-10-028-158-8

; Sequence 8, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TITLE OF INVENTION: TROPICBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-028-158-8

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 CATCTGGTCCCGGTGGCGCT 1273
Db 1 CATCTGGTCCCGGTGGCGCT 20

RESULT 108

US-10-189-267-12

; Sequence 12, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-189-267-12

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1757 CACCCAGCGCTACATCGATA 1776
Db 1 CACCCAGCGCTACATCGATA 20

RESULT 109

US-10-189-267-21/c

; Sequence 21, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; OTHER INFORMATION: Antisense Oligonucleotide		; OTHER INFORMATION: Antisense Oligonucleotide	
US-10-189-267-47		US-10-189-267-47	
Query Match		Query Match	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;		Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1412 GGAGTGATTTCCATCTACA 1431		QY 1412 GGAGTGATTTCCATCTACA 1431	
Db 20 GGAGTGATTTCCATCTACA 1		Db 20 GGAGTGATTTCCATCTACA 1	
RESULT 112		RESULT 112	
US-10-189-267-94/c		US-10-189-267-94/c	
; Sequence 94, Application US/10189267		; Sequence 94, Application US/10189267	
; Publication No. US20040006030A1		; Publication No. US20040006030A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Brett P. Monia		; APPLICANT: Brett P. Monia	
; APPLICANT: Susan M. Freier		; APPLICANT: Susan M. Freier	
; APPLICANT: Kenneth W. Dobie		; APPLICANT: Kenneth W. Dobie	
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION		; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION	
; FILE REFERENCE: PTS-0038		; FILE REFERENCE: PTS-0038	
; CURRENT APPLICATION NUMBER: US/10/189,267		; CURRENT APPLICATION NUMBER: US/10/189,267	
; CURRENT FILING DATE: 2002-07-02		; CURRENT FILING DATE: 2002-07-02	
; NUMBER OF SEQ ID NOS: 284		; NUMBER OF SEQ ID NOS: 284	
; SEQ ID NO 94		; SEQ ID NO 94	
; LENGTH: 20		; LENGTH: 20	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Artificial Sequence		; ORGANISM: Artificial Sequence	
; FEATURE:		; FEATURE:	
; OTHER INFORMATION: Antisense Oligonucleotide		; OTHER INFORMATION: Antisense Oligonucleotide	
US-10-189-267-94		US-10-189-267-94	
Query Match		Query Match	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;		Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 133 TAGGGTTTAAAGAGCCATTC 152		QY 133 TAGGGTTTAAAGAGCCATTC 152	
Db 20 TAGGGTTTAAAGAGCCATTC 1		Db 20 TAGGGTTTAAAGAGCCATTC 1	
RESULT 113		RESULT 113	
US-10-189-267-95/c		US-10-189-267-95/c	
; Sequence 95, Application US/10189267		; Sequence 95, Application US/10189267	
; Publication No. US20040006030A1		; Publication No. US20040006030A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Brett P. Monia		; APPLICANT: Brett P. Monia	
; APPLICANT: Susan M. Freier		; APPLICANT: Susan M. Freier	
; APPLICANT: Kenneth W. Dobie		; APPLICANT: Kenneth W. Dobie	
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION		; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION	
; FILE REFERENCE: PTS-0038		; FILE REFERENCE: PTS-0038	
; CURRENT APPLICATION NUMBER: US/10/189,267		; CURRENT APPLICATION NUMBER: US/10/189,267	
; CURRENT FILING DATE: 2002-07-02		; CURRENT FILING DATE: 2002-07-02	
; NUMBER OF SEQ ID NOS: 284		; NUMBER OF SEQ ID NOS: 284	
; SEQ ID NO 95		; SEQ ID NO 95	
; LENGTH: 20		; LENGTH: 20	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Artificial Sequence		; ORGANISM: Artificial Sequence	
; FEATURE:		; FEATURE:	
; OTHER INFORMATION: Antisense Oligonucleotide		; OTHER INFORMATION: Antisense Oligonucleotide	
US-10-189-267-95		US-10-189-267-95	
Query Match		Query Match	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;		Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 860 ACACGAACTCCATTTCTTC 879		QY 860 ACACGAACTCCATTTCTTC 879	
Db 20 ACACGAACTCCATTTCTTC 1		Db 20 ACACGAACTCCATTTCTTC 1	
RESULT 114		RESULT 114	

; APPLICANT: Brett P. Monia		; APPLICANT: Brett P. Monia	
; APPLICANT: Susan M. Freier		; APPLICANT: Susan M. Freier	
; APPLICANT: Kenneth W. Dobie		; APPLICANT: Kenneth W. Dobie	
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION		; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION	
; FILE REFERENCE: PTS-0038		; FILE REFERENCE: PTS-0038	
; CURRENT APPLICATION NUMBER: US/10/189,267		; CURRENT APPLICATION NUMBER: US/10/189,267	
; CURRENT FILING DATE: 2002-07-02		; CURRENT FILING DATE: 2002-07-02	
; NUMBER OF SEQ ID NOS: 284		; NUMBER OF SEQ ID NOS: 284	
; SEQ ID NO 21		; SEQ ID NO 21	
; LENGTH: 20		; LENGTH: 20	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Artificial Sequence		; ORGANISM: Artificial Sequence	
; FEATURE:		; FEATURE:	
; OTHER INFORMATION: Antisense Oligonucleotide		; OTHER INFORMATION: Antisense Oligonucleotide	
US-10-189-267-21		US-10-189-267-21	
Query Match		Query Match	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;		Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1965 TTTGCAGGTATTGATGGCAC 1984		QY 1965 TTTGCAGGTATTGATGGCAC 1984	
Db 20 TTTGCAGGTATTGATGGCAC 1		Db 20 TTTGCAGGTATTGATGGCAC 1	
RESULT 110		RESULT 110	
US-10-189-267-38/c		US-10-189-267-38/c	
; Sequence 38, Application US/10189267		; Sequence 38, Application US/10189267	
; Publication No. US20040006030A1		; Publication No. US20040006030A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Brett P. Monia		; APPLICANT: Brett P. Monia	
; APPLICANT: Susan M. Freier		; APPLICANT: Susan M. Freier	
; APPLICANT: Kenneth W. Dobie		; APPLICANT: Kenneth W. Dobie	
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION		; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION	
; FILE REFERENCE: PTS-0038		; FILE REFERENCE: PTS-0038	
; CURRENT APPLICATION NUMBER: US/10/189,267		; CURRENT APPLICATION NUMBER: US/10/189,267	
; CURRENT FILING DATE: 2002-07-02		; CURRENT FILING DATE: 2002-07-02	
; NUMBER OF SEQ ID NOS: 284		; NUMBER OF SEQ ID NOS: 284	
; SEQ ID NO 38		; SEQ ID NO 38	
; LENGTH: 20		; LENGTH: 20	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Artificial Sequence		; ORGANISM: Artificial Sequence	
; FEATURE:		; FEATURE:	
; OTHER INFORMATION: Antisense Oligonucleotide		; OTHER INFORMATION: Antisense Oligonucleotide	
US-10-189-267-38		US-10-189-267-38	
Query Match		Query Match	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;		Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1337 CCGCGGGCAGATCCTGAGCA 1356		QY 1337 CCGCGGGCAGATCCTGAGCA 1356	
Db 20 CCGCGGGCAGATCCTGAGCA 1		Db 20 CCGCGGGCAGATCCTGAGCA 1	
RESULT 111		RESULT 111	
US-10-189-267-47/c		US-10-189-267-47/c	
; Sequence 47, Application US/10189267		; Sequence 47, Application US/10189267	
; Publication No. US20040006030A1		; Publication No. US20040006030A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Brett P. Monia		; APPLICANT: Brett P. Monia	
; APPLICANT: Susan M. Freier		; APPLICANT: Susan M. Freier	
; APPLICANT: Kenneth W. Dobie		; APPLICANT: Kenneth W. Dobie	
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION		; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION	
; FILE REFERENCE: PTS-0038		; FILE REFERENCE: PTS-0038	
; CURRENT APPLICATION NUMBER: US/10/189,267		; CURRENT APPLICATION NUMBER: US/10/189,267	
; CURRENT FILING DATE: 2002-07-02		; CURRENT FILING DATE: 2002-07-02	
; NUMBER OF SEQ ID NOS: 284		; NUMBER OF SEQ ID NOS: 284	
; SEQ ID NO 47		; SEQ ID NO 47	
; LENGTH: 20		; LENGTH: 20	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Artificial Sequence		; ORGANISM: Artificial Sequence	
; FEATURE:		; FEATURE:	

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US-10-189-267-96/c
; Sequence 96, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 96
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-96
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTCCAGGAGAA 933
Db 20 CCTCTCCCTCCAGGAGAA 1
|||||

RESULT 115
US-10-189-267-97/c
; Sequence 97, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-97
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTCCAGGAGAA 933
Db 20 CCTCTCCCTCCAGGAGAA 1
|||||

US-10-189-267-99/c
; Sequence 99, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 99
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-99
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1094 CTTTGCAAAAGTTTCGTATT 1113
Db 20 CTTTGCAAAAGTTTCGTATT 1
|||||

RESULT 117
US-10-189-267-100/c
; Sequence 100, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-100
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1133 CCGCTCTGAGAATTACTAGT 1152
Db 20 CCGCTCTGAGAATTACTAGT 1
|||||

RESULT 118
US-10-189-267-100/c
; Sequence 100, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-100
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1138 CTGAGAATTACTAGTTCTT 1157
Db 20 CTGAGAATTACTAGTTCTT 1157
|||||
```

10

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1269 GCGCTCAGTCTGTCTACCTG 1288
|||||
Db 20 GCGCTCAGTCTGTCTACCTG 1

RESULT 124

US-10-189-267-106/c
; Sequence 106, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-106

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1314 ATCGGCAAGAGGATCGAGGC 1333
|||||
Db 20 ATCGGCAAGAGGATCGAGGC 1

RESULT 125

US-10-189-267-107/c
; Sequence 107, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 107
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-107

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1321 AGAGGATCGAGGCATCCGC 1340
|||||
Db 20 AGAGGATCGAGGCATCCGC 1

RESULT 126

US-10-189-267-108/c
; Sequence 108, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 108
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-108

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1335 ATCGCGGCAGATCCTGAG 1354
|||||
Db 20 ATCGCGGCAGATCCTGAG 1

RESULT 127

US-10-189-267-109/c
; Sequence 109, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-109

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 CCGGAAGACTATCCGGAGC 1395
|||||
Db 20 CCGGAAGACTATCCGGAGC 1

RESULT 128

US-10-189-267-110/c
; Sequence 110, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 110
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

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US-10-189-267-110
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CCGGAGGTGATTCCATCT 1428
Db      20 CCGGAGGTGATTCCATCT 1

RESULT 129
US-10-189-267-111/c
; Sequence 111, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 111
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-111

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCTACAC 1433
Db      20 AGGTGATTTCCTACAC 1

RESULT 130
US-10-189-267-112/c
; Sequence 112, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 112
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-112

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1422 TCCATCTACACAGTACCAG 1441
Db      20 TCCATCTACACAGTACCAG 1

RESULT 131
US-10-189-267-113/c
; Sequence 113, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 113
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-113

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1463 AAGCCGAGGCGAGCGCCT 1482
Db      20 AAGCCGAGGCGAGCGCCT 1

RESULT 132
US-10-189-267-114/c
; Sequence 114, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 114
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-114

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAGAGGTT 1526
Db      20 AGTACTACGCCAAGAGGTT 1

RESULT 133
US-10-189-267-115/c
; Sequence 115, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 115
; LENGTH: 20
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-115

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1515 GCCAAGGAGGTTTATAAAT 1534
Db 20 GCCAAGGAGGTTTATAAAT 1

RESULT 134
US-10-189-267-116/c
; Sequence 116, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-116

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 TTTATAAATCGACATGCCG 1544
Db 20 TTTATAAATCGACATGCCG 1

RESULT 135
US-10-189-267-117/c
; Sequence 117, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 117
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-117

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTCCGAAATGCCATCCCG 1574
Db 20 CCTCCGAAATGCCATCCCG 1
```

```
RESULT 136
US-10-189-267-118/c
; Sequence 118, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-118

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 CCACCTTCTACAGACCCCTAC 1595
Db 20 CCACCTTCTACAGACCCCTAC 1

RESULT 137
US-10-189-267-119/c
; Sequence 119, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-119

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 TTTCTACAGACCCCTACTTCA 1599
Db 20 TTTCTACAGACCCCTACTTCA 1

RESULT 138
US-10-189-267-120/c
; Sequence 120, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
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; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 120
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-120

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1584 TACAGACCTACTTCAGAAT 1603
Db 20 TACAGACCTACTTCAGAAT 1

RESULT 139
US-10-189-267-121/c
; Sequence 121, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-121

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TACTTCAGAATCGTCGCTT 1612
Db 20 TACTTCAGAATCGTCGCTT 1

RESULT 140
US-10-189-267-122/c
; Sequence 122, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 122
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-122

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 CACAAAGACAGGAACCTGGG 1873
Db 20 CACAAAGACAGGAACCTGGG 1

RESULT 141
US-10-189-267-123/c
; Sequence 123, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 123
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-123

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1877 TAAATAAGTTTACACTGCC 1896
Db 20 TAAATAAGTTTACACTGCC 1

RESULT 142
US-10-189-267-124/c
; Sequence 124, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 124
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-124

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1962 AGATTTCAGGTATTGATGG 1981
Db 20 AGATTTCAGGTATTGATGG 1

RESULT 143
US-10-189-267-125/c
; Sequence 125, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
```


; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-125

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 TGCAGGTATTGATGGACCT 1986
Db 20 TGCAGGTATTGATGGACCT 1
|||||

RESULT 144
US-10-189-267-126/c
; Sequence 126, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-126

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1996 CCAGTGGTGATCAGAAACT 2015
Db 20 CCAGTGGTGATCAGAAACT 1
|||||

RESULT 145
US-10-189-267-127/c
; Sequence 127, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 127
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-127

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2000 TGGTGATCAGAAACTATAA 2019
Db 20 TGGTGATCAGAAACTATAA 1
|||||

RESULT 146
US-10-189-267-128/c
; Sequence 128, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 128
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-128

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 AAACATATAAGTCCACTAGG 2030
Db 20 AAACATATAAGTCCACTAGG 1
|||||

RESULT 147
US-10-189-267-129/c
; Sequence 129, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 129
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-129

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 CCCACATCTCTGCTAAATGT 2070
Db 20 CCCACATCTCTGCTAAATGT 1
|||||

RESULT 148
US-10-189-267-130/c
; Sequence 130, Application US/10189267

```

; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-130

Query Match
Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTTGTCGCCT 2079
|||||
Db 20 CCTGCTAATGTTGTCGCCT 1

RESULT 149
US-10-189-267-131/c
; Sequence 131, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 131
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-131

Query Match
Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2075 GCCCTCCTACAGACTGGAGT 2094
|||||
Db 20 GCCCTCCTACAGACTGGAGT 1

RESULT 150
US-10-189-267-132/c
; Sequence 132, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 132
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-132

Query Match
Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2075 GCCCTCCTACAGACTGGAGT 2094
|||||
Db 20 GCCCTCCTACAGACTGGAGT 1

RESULT 151
US-10-189-267-133/c
; Sequence 133, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-133

Query Match
Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2151 AATGTGCAGGATAATTGCTG 2170
|||||
Db 20 AATGTGCAGGATAATTGCTG 1

RESULT 152
US-10-189-267-134/c
; Sequence 134, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 134
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-134

Query Match
Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TGCCTTCGCCCTCTTTACAT 2188
|||||
Db 20 TGCCTTCGCCCTCTTTACAT 1

```

```
RESULT 153
US-10-189-267-135/c
; Sequence 135, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-135
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CTTTACATTGATTTTAAGAG 2200
|||||
Db 20 CTTTACATTGATTTTAAGAG 1

RESULT 154
US-10-189-267-136/c
; Sequence 136, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-136
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GATTTTAAGAGGATCTTGG 2209
|||||
Db 20 GATTTTAAGAGGATCTTGG 1

RESULT 155
US-10-189-267-137/c
; Sequence 137, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
```

```
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-137
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TGGATCCATGAACCCAAAGG 2236
|||||
Db 20 TGGATCCATGAACCCAAAGG 1

RESULT 156
US-10-189-267-138/c
; Sequence 138, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-138
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2226 GAACCCAAAGGTTACAATGC 2245
|||||
Db 20 GAACCCAAAGGTTACAATGC 1

RESULT 157
US-10-189-267-139/c
; Sequence 139, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 139
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-139
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 139
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-139
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2487 AAAATCAGGTGACAAATGAC 2506
      |||||
Db 20 AAAATCAGGTGACAAATGAC 1

RESULT 163
US-10-189-267-145/c
; Sequence 145, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 145
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-145

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2635 GTTCTGTTGTTAAACTGG 2654
      |||||
Db 20 GTTCTGTTGTTAAACTGG 1

RESULT 164
US-10-189-267-146/c
; Sequence 146, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 146
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-146

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTGTAAACTGGCATCT 2659
      |||||
Db 20 GTTGTAAACTGGCATCT 1

RESULT 165
US-10-189-267-147/c
; Sequence 147, Application US/10189267
; Publication No. US20040006030A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 147
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-147

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2970 TGTGTTACTATATGAAC 2989
      |||||
Db 20 TGTGTTACTATATGAAC 1

RESULT 166
US-10-189-267-148/c
; Sequence 148, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 148
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-148

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2977 CTATATAATGAACCTTTTCAT 2996
      |||||
Db 20 CTATATAATGAACCTTTTCAT 1

RESULT 167
US-10-189-267-149/c
; Sequence 149, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 149
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-149

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2988 ACCTTTCATTACCCCTGGAA 3007
      |||||||
Db 20 ACCTTTCATTACCCCTGGAA 1

RESULT 168
US-10-189-267-150/c
; Sequence 150, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-150

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3049 AAATCATGATGGCTTAAG 3068
      |||||||
Db 20 AAATCATGATGGCTTAAG 1

RESULT 169
US-10-189-267-151/c
; Sequence 151, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 151
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-151

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3073 TTGAACCTCAAAATAGCCAGG 3092
      |||||||
Db 20 TTGAACCTCAAAATAGCCAGG 1

RESULT 170
US-10-189-267-152/c
; Sequence 152, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-152

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3122 GTGAGTTGTTATAGGACTAA 3141
      |||||||
Db 20 GTGAGTTGTTATAGGACTAA 1

RESULT 171
US-10-189-267-153/c
; Sequence 153, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 153
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-153

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 AATTGTAATGTTCTTTGC 3298
      |||||||
Db 20 AATTGTAATGTTCTTTGC 1

RESULT 172
US-10-189-267-154/c
; Sequence 154, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
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; SEQ ID NO 154
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
;
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-154

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3292 TCCTTCCAGTTTAAGCAAG 3311
      |||||
Db 20 TCCTTCCAGTTTAAGCAAG 1

RESULT 173
US-10-189-267-155/c
; Sequence 155, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 155
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-155

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3505 ACAGTAACACTTTACATGT 3524
      |||||
Db 20 ACAGTAACACTTTACATGT 1

RESULT 174
US-10-189-267-156/c
; Sequence 156, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-156

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3512 CTACTTTACATGTAATGTGT 3531
      |||||
Db 20 CTACTTTACATGTAATGTGT 1

RESULT 175
US-10-189-267-157/c
; Sequence 157, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 157
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-157

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3520 CATGTAATGTGTAGATCTTA 3539
      |||||
Db 20 CATGTAATGTGTAGATCTTA 1

RESULT 176
US-10-189-267-158/c
; Sequence 158, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 158
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-158

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3642 GCTGGCCAGTACCTTTGAAT 3661
      |||||
Db 20 GCTGGCCAGTACCTTTGAAT 1

RESULT 177
US-10-189-267-159/c
; Sequence 159, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
```

1

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 172
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-172

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1965 TTTCAGGTATTGATGCAC 1984
|||||
Db 1 TTTCAGGTATTGATGCAC 20

RESULT 183
US-10-189-267-184
; Sequence 184, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 184
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-184

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 CCGCGGCAGATCCTGAGCA 1356
|||||
Db 1 CCGCGGCAGATCCTGAGCA 20

RESULT 184
US-10-189-267-190
; Sequence 190, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 190
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-190

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1412 GGAGGTGATTTCCATCTACA 1431
|||||
Db 1 GGAGGTGATTTCCATCTACA 20

RESULT 185
US-10-189-267-225
; Sequence 225, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 225
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-225

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 AACTGAACCTCCATTTCTTC 879
|||||
Db 1 AACTGAACCTCCATTTCTTC 20

RESULT 186
US-10-189-267-226
; Sequence 226, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 226
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-226

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTTCCAGGAGAAA 933
|||||
Db 1 CCTCTCCCTTCCAGGAGAAA 20

RESULT 187
US-10-189-267-227
; Sequence 227, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 232
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-232

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1269 GCGCTCAGTCTGTCTACCTG 1288
|||||
Db 1 GCGCTCAGTCTGTCTACCTG 20

RESULT 193
US-10-189-267-233
; Sequence 233, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 233
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-233

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1314 ATCGCGAAGAGGATCGAGGC 1333
|||||
Db 1 ATCGCGAAGAGGATCGAGGC 20

RESULT 194
US-10-189-267-234
; Sequence 234, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 234
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-234

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1321 AGAGGATCGAGGCCATCCGC 1340
|||||
Db 1 AGAGGATCGAGGCCATCCGC 20

RESULT 195
US-10-189-267-235
; Sequence 235, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-235

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1335 ATCGCGGCGCAGATCCTGAG 1354
|||||
Db 1 ATCGCGGCGCAGATCCTGAG 20

RESULT 196
US-10-189-267-236
; Sequence 236, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 236
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-236

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 CCCGGAAGACTATCCGAGC 1395
|||||
Db 1 CCCGGAAGACTATCCGAGC 20

RESULT 197
US-10-189-267-237
; Sequence 237, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie

/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189,267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 237
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: M. musculus
/ FEATURE:
US-10-189-267-237

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CCGGAGGTGATTCATCT 1428
Db 1 CCGGAGGTGATTCATCT 20
|||||

RESULT 198
US-10-189-267-238
/ Sequence 238, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189,267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 238
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: M. musculus
/ FEATURE:
US-10-189-267-238

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTCATCTACAAC 1433
Db 1 AGGTGATTCATCTACAAC 20
|||||

RESULT 199
US-10-189-267-239
/ Sequence 239, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189,267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 239
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: M. musculus
/ FEATURE:
US-10-189-267-239

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1422 TCATCTACACAGTACCAG 1441
Db 1 TCATCTACACAGTACCAG 20
|||||

RESULT 200
US-10-189-267-240
/ Sequence 240, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189,267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 240
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: M. musculus
/ FEATURE:
US-10-189-267-240

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1463 AAGCCGAGGCGCGCCT 1482
Db 1 AAGCCGAGGCGCGCCT 20
|||||

RESULT 201
US-10-189-267-241
/ Sequence 241, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189,267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 241
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: M. musculus
/ FEATURE:
US-10-189-267-241

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTAGCCCAAGGAGTT 1526
Db 1 AGTACTAGCCCAAGGAGTT 20
|||||

RESULT 202
US-10-189-267-242
/ Sequence 242, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION

; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 242
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-242

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1515 GCCAAGGAGGTTATATAAT 1534
Db 1 GCCAAGGAGGTTATATAAT 20

RESULT 203

US-10-189-267-243
; Sequence 243, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:

US-10-189-267-243

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 TTTATAAAATCGACATGCCG 1544
Db 1 TTTATAAAATCGACATGCCG 20

RESULT 204

US-10-189-267-244
; Sequence 244, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 244
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:

US-10-189-267-244

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTCCGAAATCCCATCCCG 1574
Db 1 CCTCCGAAATCCCATCCCG 20

RESULT 205

US-10-189-267-245
; Sequence 245, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 245
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:

US-10-189-267-245

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 CCACCTTTCTACAGACCCCTAC 1595
Db 1 CCACCTTTCTACAGACCCCTAC 20

RESULT 206

US-10-189-267-246
; Sequence 246, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 246
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:

US-10-189-267-246

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 TTTCTACAGACCCCTACTTCA 1599
Db 1 TTTCTACAGACCCCTACTTCA 20

RESULT 207

US-10-189-267-247
; Sequence 247, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038

; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 247

; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-247

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1584 TACAGACCTACTTCAGAAAT 1603
Db 1 TACAGACCTACTTCAGAAAT 20

RESULT 208

US-10-189-267-248
; Sequence 248, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobbie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 248

; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-248

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TACTTCAGAAATCGTCGCTT 1612
Db 1 TACTTCAGAAATCGTCGCTT 20

RESULT 209

US-10-189-267-249
; Sequence 249, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobbie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 249

; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-249

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1854 CACAAAGACAGGAACCTGGG 1873

Db 1 CACAAAGACAGGAACCTGGG 20

RESULT 210

US-10-189-267-250
; Sequence 250, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobbie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 250

; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-250

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1877 TAAATAAGTTTACACTGCC 1896
Db 1 TAAATAAGTTTACACTGCC 20

RESULT 211

US-10-189-267-251
; Sequence 251, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobbie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 251

; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-251

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 TGCAGGTATTGATGGCACCT 1986
Db 1 TGCAGGTATTGATGGCACCT 20

RESULT 212

US-10-189-267-252
; Sequence 252, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobbie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267

```
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 252
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-252

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1996 CCAAGTGGTGATCAGAAAAC 2015
      |||||
Db 1 CCAAGTGGTGATCAGAAAAC 20

RESULT 213
US-10-189-267-253
; Sequence 253, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 253
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-253

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2000 TGCTGATCAGAAAACATATA 2019
      |||||
Db 1 TGCTGATCAGAAAACATATA 20

RESULT 214
US-10-189-267-254
; Sequence 254, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 254
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-254

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTTGTCCT 2079
      |||||
Db 1 CCTGCTAATGTTGTCCT 20

RESULT 215
US-10-189-267-255
; Sequence 255, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 255
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-255

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2075 GCCCTCCTACAGACTGGAGT 2094
      |||||
Db 1 GCCCTCCTACAGACTGGAGT 20

RESULT 216
US-10-189-267-256
; Sequence 256, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 256
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-256

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2142 TGCCTTAGAAATGTCAGGA 2161
      |||||
Db 1 TGCCTTAGAAATGTCAGGA 20

RESULT 217
US-10-189-267-257
; Sequence 257, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
```

```
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 257
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-257

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TGCCTTCGCCCTCTTACAT 2188
Db 1 TGCCTTCGCCCTCTTACAT 20

RESULT 218
US-10-189-267-258
; Sequence 258, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 258
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-258

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GATTTTAAGAGGATCTTGG 2209
Db 1 GATTTTAAGAGGATCTTGG 20

RESULT 219
US-10-189-267-259
; Sequence 259, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 259
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-259

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TGGATCCATGAACCCCAAGG 2236
Db 1 TGGATCCATGAACCCCAAGG 20
```

```
RESULT 220
US-10-189-267-260
; Sequence 260, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 260
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-260

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2226 GAACCCAAAGGTACAATGC 2245
Db 1 GAACCCAAAGGTACAATGC 20

RESULT 221
US-10-189-267-261
; Sequence 261, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 261
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-261

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2238 TACAATGCTAACTTCTGTGC 2257
Db 1 TACAATGCTAACTTCTGTGC 20

RESULT 222
US-10-189-267-262
; Sequence 262, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
```



```
/ SEQ ID NO 262
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: M. musculus
/ FEATURE:
US-10-189-267-262

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2349 CCTTGTCTGTGTCTCCAGGA 2368
      |||||
Db 1 CCTTGTCTGTGTCTCCAGGA 20

RESULT 223
US-10-189-267-263
; Sequence 263, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 263
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-263

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2444 GTCCTGTAATGCAGCTAAA 2463
      |||||
Db 1 GTCCTGTAATGCAGCTAAA 20

RESULT 224
US-10-189-267-264
; Sequence 264, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 264
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-264

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2451 AAATGCAGCTAAAGTCCTTG 2470
      |||||
Db 1 AAATGCAGCTAAAGTCCTTG 20
```

```
RESULT 225
US-10-189-267-265
; Sequence 265, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 265
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-265

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2487 AAAATCACGGTGACAATGAC 2506
      |||||
Db 1 AAAATCACGGTGACAATGAC 20

RESULT 226
US-10-189-267-266
; Sequence 266, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 266
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-266

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2635 GTTCTGTTTGTAAACTGG 2654
      |||||
Db 1 GTTCTGTTTGTAAACTGG 20

RESULT 227
US-10-189-267-267
; Sequence 267, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 267
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-267
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTTGTTAAACTGGCATCT 2659
      |||||||
Db 1 GTTTGTTAAACTGGCATCT 20

RESULT 228
US-10-189-267-268
; Sequence 268, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 268
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-268
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2970 TGTGTTACTATATAATGAAC 2989
      |||||||
Db 1 TGTGTTACTATATAATGAAC 20

RESULT 229
US-10-189-267-269
; Sequence 269, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 269
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-269
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2988 ACCTTTCATTACCTTGGAA 3007
      |||||||
Db 1 ACCTTTCATTACCTTGGAA 20
```

```
RESULT 230
US-10-189-267-270
; Sequence 270, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 270
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-270
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3049 AAATCATGATGGCTTAAG 3068
      |||||||
Db 1 AAATCATGATGGCTTAAG 20

RESULT 231
US-10-189-267-271
; Sequence 271, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 271
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-271
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 AATTGTAATGTTCTTTGC 3298
      |||||||
Db 1 AATTGTAATGTTCTTTGC 20

RESULT 232
US-10-189-267-272
; Sequence 272, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 272
; LENGTH: 20
```

```
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-272
    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3292 TCCTTGCCAGTTTAAGCAAG 3311
    |||||
Db 1 TCCTTGCCAGTTTAAGCAAG 20
    |||||

RESULT 233
US-10-189-267-273
; Sequence 273, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 273
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-273
    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3520 CATGTAATGTGTAGATCTTA 3539
    |||||
Db 1 CATGTAATGTGTAGATCTTA 20
    |||||

RESULT 236
US-10-189-267-276
; Sequence 276, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 276
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-276
    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3505 ACAGTAACACTTTTACATGT 3524
    |||||
Db 1 ACAGTAACACTTTTACATGT 20
    |||||

RESULT 234
US-10-189-267-274
; Sequence 274, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 274
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-274
    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3512 CTACTTTACATGTAATGTGT 3531
    |||||
Db 1 CTACTTTACATGTAATGTGT 20
    |||||

RESULT 235
US-10-189-267-277
; Sequence 277, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 277
; LENGTH: 20
; TYPE: DNA
; FEATURE:
US-10-189-267-277
    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3642 GCTGGCCAGTACCTTTGAAT 3661
    |||||
Db 1 GCTGGCCAGTACCTTTGAAT 20
    |||||

RESULT 237
US-10-189-267-277
; Sequence 277, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 277
; LENGTH: 20
; TYPE: DNA
; FEATURE:
US-10-189-267-277
    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3642 GCTGGCCAGTACCTTTGAAT 3661
    |||||
Db 1 GCTGGCCAGTACCTTTGAAT 20
    |||||
```

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; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-277

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4245 CTTTGAGGCTGATTAATAA 4264
Db      1 CTTTGAGGCTGATTAATAA 20

RESULT 238
US-10-633-163-48/c
; Sequence 48, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-48

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAACTGCCGC 53
Db      20 GAGCTGCTGAACTGCCGC 1

RESULT 239
US-10-633-163-49/c
; Sequence 49, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-49

; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-49

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 AAGCTAGGGAAGGGTGCAG 278
Db      20 AAGCTAGGGAAGGGTGCAG 1

RESULT 240
US-10-633-163-50/c
; Sequence 50, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-50

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 TGGCCGCTGGAGCAAGAA 381
Db      20 TGGCCGCTGGAGCAAGAA 1

RESULT 241
US-10-633-163-51/c
; Sequence 51, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-51

```

US-10-633-163-51

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GGGATCCTCGCGCCTGCTC 512
|||||
DB 20 GGGATCCTCGCGCCTGCTC 1

RESULT 242

US-10-633-163-52/c
; Sequence 52, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-52

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 ACACGTGTGGAAGGCAGGCG 690
|||||
DB 20 ACACGTGTGGAAGGCAGGCG 1

RESULT 243

US-10-633-163-53/c
; Sequence 53, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-53

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 830 TCAGATCAGCCACTCGGCAC 849
|||||
DB 20 TCAGATCAGCCACTCGGCAC 1

RESULT 244

US-10-633-163-54/c
; Sequence 54, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-54

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1016 TTGGGAACGCGTGCATTTT 1035
|||||
DB 20 TTGGGAACGCGTGCATTTT 1

RESULT 245

US-10-633-163-55/c
; Sequence 55, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-55

```
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 GCTCTGTCATCTGGTCCCGG 1266
DB      |||||
        20 GCTCTGTCATCTGGTCCCGG 1

RESULT 246
US-10-633-163-56/c
; Sequence 56, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-56

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 GCAGGAGAGGCAAGCCGGA 1470
DB      |||||
        20 GCAGGAGAGGCAAGCCGGA 1

RESULT 247
US-10-633-163-57/c
; Sequence 57, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-57

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 GCTCTGTCATCTGGTCCCGG 1266
DB      |||||
        20 GCTCTGTCATCTGGTCCCGG 1

RESULT 248
US-10-633-163-58/c
; Sequence 58, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-58

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1754 TCCACCCAGCGCTACATCG 1773
DB      |||||
        20 TCCACCCAGCGCTACATCG 1

RESULT 249
US-10-633-163-59/c
; Sequence 59, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-59

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2032 AAAAAACCAAGTGGGAAGACC 2051
|||||
Db 20 AAAAAACCAAGTGGGAAGACC 1

RESULT 250

US-10-633-163-60/c
; Sequence 60, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-60

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2321 CACCAATAATCCGAAGCTT 2340
|||||
Db 20 CACCAATAATCCGAAGCTT 1

RESULT 251

US-10-633-163-61/c
; Sequence 61, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-61

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2478 CAGGACACGAAATCACGGT 2497
|||||
Db 20 CAGGACACGAAATCACGGT 1

RESULT 252

US-10-633-163-62/c
; Sequence 62, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-62

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2854 ACGTATTGTTTCCAGCCGCG 2873
|||||
Db 20 ACGTATTGTTTCCAGCCGCG 1

RESULT 253

US-10-633-163-63/c
; Sequence 63, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-63

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3075 GAACCTCAATAAGCCAGGG 3094
|||||
Db 20 GAACCTCAATAAGCCAGGG 1

RESULT 254
US-10-633-163-64/c
; Sequence 64, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-64

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3297 GCAGTTTAAGCAAGCCGGT 3316
|||||
Db 20 GCAGTTTAAGCAAGCCGGT 1

RESULT 255
US-10-633-163-65/c
; Sequence 65, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-65

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3352 TTTGACCGTGAAGTGGCTG 3371

Db 20 TTTTGACCGTGAAGTGGCTG 1
|||||

RESULT 256
US-10-633-163-66/c
; Sequence 66, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-66

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3753 CATGAGCTACCTGGGTCCAT 3772
|||||
Db 20 CATGAGCTACCTGGGTCCAT 1

RESULT 257
US-10-633-163-67/c
; Sequence 67, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-67

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3874 TGTGAGTCATGCGGGTGG 3893
|||||

Db 20 TGTGAGTCATGTGGCGGTG 1

RESULT 258

US-10-633-163-68/c
; Sequence 68, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean

; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-633-163-68
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4097 TTTGGTGTCTCATGGGTGTA 4116
|||||

Db 20 TTTGGTGTCTCATGGGTGTA 1

RESULT 259

US-09-894-799-22
; Sequence 22, Application US/09894799
; Publication No. US20030009784A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030009784A1artis

; TITLE OF INVENTION: Expression of trehalose biosynthetic genes in plants
; FILE REFERENCE: trehalose
; CURRENT APPLICATION NUMBER: US/09/894,799
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/262,615
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: CGC1990/PROV
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide

US-09-894-799-22
Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCTCCCTCCCTCCCTCCCAAGCT 991
|||||

Db 1 AGCTTCTCCCTCCCTCCCTCCCAAGCT 24

RESULT 260

US-09-954-556-13
; Sequence 13, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRES
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-954-556-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2927 CCTCCCTCCCTCCCTCCCAAGCT 2950
|||||

Db 1 CCACACCGTCCATCTCCCAAGCT 24

RESULT 261

US-10-648-984-22
; Sequence 22, Application US/10648984
; Publication No. US20040078848A1
; GENERAL INFORMATION:
; APPLICANT: Novartis

; TITLE OF INVENTION: Expression of trehalose biosynthetic genes in plants
; FILE REFERENCE: trehalose
; CURRENT APPLICATION NUMBER: US/10/648,984
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: US/09/894,799
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/262,615
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: CGC1990/PROV
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide

US-10-648-984-22
Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCTCCCTCCCTCCCAAGCT 991
|||||

Db 1 AGCTTCTCCCTCCCTCCCAAGCT 24

RESULT 262

US-10-189-267-13/c
; Sequence 13, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
 ; FILE REFERENCE: PTS-0038
 ; CURRENT APPLICATION NUMBER: US/10/189,267
 ; CURRENT FILING DATE: 2002-07-02
 ; NUMBER OF SEQ ID NOS: 284
 ; SEQ ID NO 13
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR Primer
 US-10-189-267-13

Query Match 0.4%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 CCTTCGACGTGACAGACGC 1834
 Db 19 CCTTCGACGTGACAGACGC 1

RESULT 263
 US-10-189-267-74/c
 ; Sequence 74, Application US/10189267
 ; Publication No. US20040006030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
 ; FILE REFERENCE: PTS-0038
 ; CURRENT APPLICATION NUMBER: US/10/189,267
 ; CURRENT FILING DATE: 2002-07-02
 ; NUMBER OF SEQ ID NOS: 284
 ; SEQ ID NO 74
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-189-267-74

Query Match 0.4%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 GCAAGCTGAAGCTCACCAG 1372
 Db 20 GCAAGCTGAAGCTCACCAG 2

RESULT 264
 US-10-189-267-214
 ; Sequence 214, Application US/10189267
 ; Publication No. US20040006030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
 ; FILE REFERENCE: PTS-0038
 ; CURRENT APPLICATION NUMBER: US/10/189,267
 ; CURRENT FILING DATE: 2002-07-02
 ; NUMBER OF SEQ ID NOS: 284
 ; SEQ ID NO 214
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 US-10-189-267-214

Query Match 0.4%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 GCAAGCTGAAGCTCACCAG 1372
 Db 1 GCAAGCTGAAGCTCACCAG 19

RESULT 265
 US-10-155-407A-18
 ; Sequence 18, Application US/10155407A
 ; Publication No. US20030077267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frenz, John
 ; APPLICANT: Shire, Steven J.
 ; APPLICANT: Silkowski, Mary B.
 ; TITLE OF INVENTION: PURIFIED FORMS OF DNase
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/155,407A
 ; FILING DATE: 22-May-2002
 ; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/638112
 ; FILING DATE: 11-Aug-2000
 ; APPLICATION NUMBER: 08/942561
 ; FILING DATE: 01-OCT-1997
 ; APPLICATION NUMBER: 08/634125
 ; FILING DATE: 19-Apr-1996
 ; APPLICATION NUMBER: 08/409631
 ; FILING DATE: 22-Mar-1995
 ; APPLICATION NUMBER: 08/348284
 ; FILING DATE: 30-No. US20030077267A1-1994
 ; APPLICATION NUMBER: 08/116186
 ; FILING DATE: 02-Sep-1993
 ; APPLICATION NUMBER: 07/895300
 ; FILING DATE: 08-Jun-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Evans, David W.
 ; REGISTRATION NUMBER: NONE
 ; REFERENCE/DOCKET NUMBER: P0747C9
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1739
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22 base pairs
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-155-407A-18
 Query Match 0.4%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCGCGCGCGCGC 636
 Db 1 GCGCGCGCGCGCGCGCGCGC 22

```
RESULT 266
US-10-155-407A-18/C
; Sequence 18, Application US/10155407A
; Publication No. US20030077267A1
; GENERAL INFORMATION:
; APPLICANT: Frenz, John
; Shire, Steven J.
; Sliwowski, Mary B.
; TITLE OF INVENTION: PURIFIED FORMS OF DNase
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,407A
; FILING DATE: 22-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/638112
; FILING DATE: 11-Aug-2000
; APPLICATION NUMBER: 08/942561
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: 08/634125
; FILING DATE: 19-Apr-1996
; APPLICATION NUMBER: 08/409631
; FILING DATE: 22-Mar-1995
; APPLICATION NUMBER: 08/348284
; FILING DATE: 30-No. US20030077267A1-1994
; APPLICATION NUMBER: 08/116186
; FILING DATE: 02-Sep-1993
; APPLICATION NUMBER: 07/895300
; FILING DATE: 08-Jun-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P0747C8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-155-407A-18

Query Match          0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCAGCAGCGCGC 636
DB 22 GCGCGCGCGCGCGCGCGC 1

RESULT 267
US-09-823-634A-15
; Sequence 15, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-634A-15

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
DB 1 AAAAAAAAAATTGGAGAAAAA 20

RESULT 268
US-09-823-647B-15
; Sequence 15, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-647B-15

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
DB 1 AAAAAAAAAATTGGAGAAAAA 20

RESULT 269
US-10-367-470-15
; Sequence 15, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
```

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; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-10-367-470-15

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAATTGGAGAAAAA 20

RESULT 270
US-10-189-267-31/c
; Sequence 31, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-31

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACTGCAGCACCCTCGA 1300
Db 20 TCTACTGCAGCACCCTCGA 1

RESULT 271
US-10-189-267-39/c
; Sequence 39, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-39

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACTGCAGCACCCTCGA 1300
Db 20 TCTACTGCAGCACCCTCGA 1

RESULT 272
US-10-189-267-42/c
; Sequence 42, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-42

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2442 AGTCTTGTAAATGCAGCTA 2461
Db 20 AGTCTTGTAAATGCAGCTA 1

RESULT 273
US-10-189-267-49/c
; Sequence 49, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-49

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2224 ATGAACCCCAAGGGTACAAT 2243
Db 20 ATGAACCCCAAGGGTACAAT 1

RESULT 274
US-10-189-267-50/c
; Sequence 50, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

```

```
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-50

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTGATTTTAAGAGGGATCT 2206
      ||||| ||||| ||||| |||||
Db 20 ATTGATTTCAAGAGGGATCT 1

RESULT 275
US-10-189-267-57/c
; Sequence 57, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-57

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1310 GTTATGCGCAAGAGGATCG 1329
      ||| ||||| ||||| |||||
Db 20 GTTCATGCGCAAGAGGATCG 1

RESULT 276
US-10-189-267-76/c
; Sequence 76, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-76

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACTCTGCAGCACCTCGA 1300
      ||||| ||||| ||||| |||||
Db 1 TCTACTCTGCAGCACACTCGA 20

RESULT 279
US-10-189-267-192

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACTCTGCAGCACCTCGA 1300
      ||||| ||||| ||||| |||||
Db 1 TCTACTCTGCAGCACACTCGA 20

RESULT 277
US-10-189-267-78/c
; Sequence 78, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-78

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2240 CAATGCTAACTTCTGTGCTG 2259
      ||||| ||||| ||||| |||||
Db 20 CAATGCCAACTTCTGTGCTG 1

RESULT 278
US-10-189-267-180
; Sequence 180, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 180
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-180

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
; Sequence 192, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 192
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-192

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2224 ATGAACCCCAAGGGTACAAAT 2243
| | | | | | | | | | | | | | | |
DB 1 ACGAACCCCAAGGGTACAAAT 20
| | | | | | | | | | | | | | | |

RESULT 280
US-10-189-267-193
; Sequence 193, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-193

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTGATTTTAAAGAGGGATCT 2206
| | | | | | | | | | | | | | | |
DB 1 ATTGATTTTCAAGAGGGATCT 20
| | | | | | | | | | | | | | | |

RESULT 281
US-10-189-267-200
; Sequence 200, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 200
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
```

```
; FEATURE:
US-10-189-267-200

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1310 GTTTATGCGCAAGAGGATCG 1329
| | | | | | | | | | | | | | | |
DB 1 GTTCAATGCGCAAGAGGATCG 20
| | | | | | | | | | | | | | | |

RESULT 282
US-10-189-267-216
; Sequence 216, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 216
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-216

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2240 CAATGCTAACTTCTGTGCTG 2259
| | | | | | | | | | | | | | | |
DB 1 CAATGCCAACTTCTGTGCTG 20
| | | | | | | | | | | | | | | |

RESULT 283
US-10-792-280-88
; Sequence 88, Application US/10792280
; Publication No. US20040234517A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Bowman, Michael
; APPLICANT: Follettie, Maximillian
; APPLICANT: Chen, Heng
; APPLICANT: Williams, Cara
; APPLICANT: Ellis, Debra
; APPLICANT: Winkler, Aaron
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR
; FILE REFERENCE: AM101023-2
; CURRENT APPLICATION NUMBER: US/10/792,280
; CURRENT FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 1535
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-792-280-88

Query Match      0.4%; Score 18.4; DB 1; Length 21;
Best Local Similarity 65.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3248 GTGGCAATCTGGAAGATTTT 3267
| : | | | | | | | | | | | | | | | |
```

Db 2 GUGGCAACUGGAAGAUUUU 21

RESULT 284

US-10-028-158-9/c
; Sequence 9, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TITLE OF INVENTION: TROPHOBLAST
; FILE REFERENCE: 11757.38USNO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-028-158-9

Query Match 0.4%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 CCCTACTTCAGATCGTC 1607

Db 18 CCCTACTTCAGATCGTC 1

RESULT 285

US-10-146-058-67/c
; Sequence 67, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-67

Query Match 0.4%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCATCTACA 1431

Db 18 AGGTGATTTCCATCTACA 1

RESULT 286

US-10-146-058-104/c
; Sequence 104, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666

```
;
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-104

Query Match
; Sequence 18; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1

RESULT 287
US-10-789-119-2
; Sequence 2, Application US/10789119
; Publication No. US20040170157A1
; GENERAL INFORMATION:
; APPLICANT: Chung, Yih-Lin
; TITLE OF INVENTION: METHOD FOR INCREASING THERAPEUTIC GAIN
; FILE REFERENCE: 13206-004002
; CURRENT APPLICATION NUMBER: US/10/789,119
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US 10/205,738
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-789-119-2

Query Match
; Sequence 18; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACTACTGTGTGCT 1234
Db 1 CATGCACTACTGTGTGCT 18

RESULT 288
US-10-189-267-33/c
; Sequence 33, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-33
```

```
Query Match
; Sequence 18; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1746 TTAACATCTCCACCACG 1764
Db 19 TTAACATCTCCACCACG 1

RESULT 289
US-10-189-267-43/c
; Sequence 43, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-43

Query Match
; Sequence 18; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2084 CAGACTGCAGTCACAACAG 2102
Db 20 CAGACTGCAGTCACAACAG 2

RESULT 290
US-10-189-267-58/c
; Sequence 58, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-58

Query Match
; Sequence 19; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 800 TCTCGTCCCTTTGGCCGG 818
Db 19 TCTCTCCCTTTGGCCGG 1

RESULT 291
US-10-189-267-70/c
; Sequence 70, Application US/10189267
```



```
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-70

Query Match          0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3027 TCGAGACCAAAATCTTGC 3045
DB 19 TGGAGACCAAAATCTTGC 1

RESULT 292
US-10-189-267-187
; Sequence 187, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-187

Query Match          0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2084 CAGACTGGAGTCACACAG 2102
DB 1 CAGACTTGAGTCACACAG 19

RESULT 293
US-10-189-267-201
; Sequence 201, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 201
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
```

```
; FEATURE:
US-10-189-267-201

Query Match          0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 800 TCTCGTCCCTTTGGCCGG 818
DB 2 TCTCTTCCCTTTGGCCGG 20

RESULT 294
US-10-189-267-211
; Sequence 211, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 211
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-211

Query Match          0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3027 TCGAGACCAAAATCTTGC 3045
DB 2 TGGAGACCAAAATCTTGC 20

RESULT 295
US-10-786-720-12633
; Sequence 12633, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; FILE REFERENCE: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12633
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-786-720-12633

Query Match          0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 63.2%; Pred. No. 2.4e+02;
Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 4 TATCTGCTGGCAGCAGGTT 22
DB 3 UAUCUGUGGCAACAGGUU 21

RESULT 296
US-10-792-280-85
```

; Sequence 85, Application US/10792280
; Publication No. US20040234517A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Bowman, Michael
; APPLICANT: Follettie, Maximilian
; APPLICANT: Chen, Heng
; APPLICANT: Williams, Cara
; APPLICANT: Ellis, Debra
; APPLICANT: Winkler, Aaron
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR
; FILE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES
; FILE REFERENCE: AM101023-2
; CURRENT APPLICATION NUMBER: US/10/792,280
; CURRENT FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 1535
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-792-280-85

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 68.4%; Pred. No. 2.4e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3248 GTGGCAATCTGGAAGATT 3266
|:||||| |:|||||:::
Db 3 GUGGCAACUGGAAGAUU 21

RESULT 297
US-09-953-047-49/c
; Sequence 49, Application US/09953047
; Publication No. US20030087854A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
; FILE REFERENCE: RTS-0157
; CURRENT APPLICATION NUMBER: US/09/953,047
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-047-49

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 TTGCTGTGTGTCGCCAGG 2367
|:||||| |:|||||:::
Db 17 TTGCTGTGTGTCGCCAGG 1

RESULT 298
US-10-630-401-49/c
; Sequence 49, Application US/10630401
; Publication No. US20040048824A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
; FILE REFERENCE: RTS-0157
; CURRENT APPLICATION NUMBER: US/10/630,401
; CURRENT FILING DATE: 2003-07-30

; PRIOR APPLICATION NUMBER: US/09/953,047
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-630-401-49

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 TTGCTGTGTGTCGCCAGG 2367
|:||||| |:|||||:::
Db 17 TTGCTGTGTGTCGCCAGG 1

RESULT 299
US-10-663-189-7/c
; Sequence 7, Application US/10663189
; Publication No. US20050026158A1
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins School of Medicine
; APPLICANT: Nelson, William
; APPLICANT: Tchou, Julia
; APPLICANT: Bakker, Jilia
; APPLICANT: Lin, Xiaohui
; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DISC
; FILE REFERENCE: JHU1660-1
; CURRENT APPLICATION NUMBER: US/10/663,189
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US/09/687,246B
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,168
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer N-F1
US-10-663-189-7

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAATT 2590
|:||||| |:|||||:::
Db 19 TTAAAAAATAAAATT 3

RESULT 300
US-09-725-265-42/c
; Sequence 42, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLI
; FILE REFERENCE: THE METHOD
; CURRENT APPLICATION NUMBER: 199953USOXDIV

```
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-42

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATATTT 1171
Db 20 TTTTATATATATATAT 1

RESULT 301
US-09-823-634A-13
; Sequence 13, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS USING RNASE H
; FILE REFERENCE: 47541-2006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAATTGGAGAAAAA 20

RESULT 302
US-09-823-634A-14
; Sequence 14, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS USING RNASE H
; FILE REFERENCE: 47541-2006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAATTGGAGAAAAA 20

RESULT 303
US-09-823-647B-13
; Sequence 13, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAATTGGAGAAAAA 20

RESULT 304
US-09-823-647B-14
; Sequence 14, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
```

Matches	18;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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Qy 2580 AAAAAAAAAATTGGAGAAAAA 2599
| | | | | | | | | |
pb 1 AAAAAAAAAATTGTAAAAAA 20

```

RESULT 305
US-09-888-326-192
; Sequence 192, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C10397052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: fastSEQ for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0) ... (0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-192

```

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18: Conservative 0; Mismatches 2; Indels

Qy 616 CGCGCGCACGACGCGG 635
pb 1 CGCGCGCGCGCGCGCGG 20

```

RESULT 306
US-09-888-326-192/c
; Sequence 192, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C103977052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-192

```

Query Match	0.4%;	Score 16.8;	DB 1;	Length 20;
Best Local Similarity	90.0%;	Pred. No. 2.5e+02;		
Matches 18: Conservative	0;	Mismatches 2;	Indels	

Qy 616 CGCGCGGCACGCACGCGCG 635
pb 20 CGCGCGCGCGCGCGCGCG 1

```

RESULT 307
US-09-888-326-193
; Sequence 193, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-193

```

Query Match	0.4%	Score 16.8	DB 1	Length 20
Best Local Similarity	90.0%	Pred. No. 2.5e+02		
Matches 18	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

Qy 616 CGCGCGGCACGCACGCG 635
pb 1 CGCGCGCGCGCGCGCG 20

```

RESULT 308
US-09-888-326-193/c
; Sequence 193, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: fastSEQ for Windows Version 3.0
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-193

```

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels

•

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 309

US-09-948-002-69/c
; Sequence 69, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-69

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1247 GCTCTGTCATCTGTCCTCCGG 1266
|||||
Db 20 GATCTGTCATCTGGTCACGG 1

RESULT 310

US-09-776-479-520
; Sequence 520, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 311

US-09-776-479-520/c
; Sequence 520, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 312

US-09-776-479-520
; Sequence 520, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 313

US-09-776-479-520/c
; Sequence 520, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:

; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 314

US-09-776-479-769
; Sequence 769, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 769
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 315

US-09-776-479-769/c
; Sequence 769, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy

; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 769
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 316

US-09-776-479-769
; Sequence 769, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 769
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 317

US-09-776-479-769/c
; Sequence 769, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03

; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 769
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 318
US-09-965-101-22
; Sequence 22, Application US/09965101
; Publication No. US20040186067A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 319
US-09-965-101-22/c
; Sequence 22, Application US/09965101
; Publication No. US20040186067A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649

; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 320
US-09-965-101-76
; Sequence 76, Application US/09965101
; Publication No. US20040186067A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-76

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGCG 634
|||||
Db 1 GCGCGCGCGCGCGCGCGCG 20

RESULT 321
US-09-965-101-76/c
; Sequence 76, Application US/09965101
; Publication No. US20040186067A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or

```
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/WAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-76

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
Db 20 GCGCGCGCGCGCGCGCGC 1

RESULT 322
US-10-146-058-99/c
; Sequence 99, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
```

```
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-99

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCGAATAAAGCG 1947
Db 20 CATCATCCGAATAAAGTG 1

RESULT 323
US-10-112-653-497
; Sequence 497, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Daniel J.
; APPLICANT: Berg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 497
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-497

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGCACGCGCGC 635
Db 1 GCGCGCGCGCGCGCGCGC 20

RESULT 324
US-10-112-653-497/c
; Sequence 497, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Daniel J.
; APPLICANT: Berg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 497
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```



```
;
;
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-497

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGACGCGCG 635
DB      20 CGCGCGCGCGCGCGCGCG 1

RESULT 325
US-10-112-653-742
; Sequence 742, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 742
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-742

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGACGCGCG 635
DB      1 CGCGCGCGCGCGCGCGCG 20

RESULT 326
US-10-112-653-742/c
; Sequence 742, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 742
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-742

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGACGCGCG 635
DB      20 CGCGCGCGCGCGCGCGCG 1

RESULT 327
US-10-017-995-520
; Sequence 520, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-520

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGACGCGCG 635
DB      1 CGCGCGCGCGCGCGCGCG 20

RESULT 328
US-10-017-995-520/c
; Sequence 520, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-520

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGACGCGCG 635
DB      20 CGCGCGCGCGCGCGCGCG 1

RESULT 329
US-10-017-995-769
; Sequence 769, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
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; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-42

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1152 TTTCTTTTATATATATTT 1171
Db      20  TTTTATATATATATAT 1

RESULT 332
US-10-367-470-13
; Sequence 13, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-10-367-470-13

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2580 AAAAAAAATTGCAGAAAAA 2599
Db      1  AAAAAAAATTTGAAAAAAA 20

RESULT 333
US-10-367-470-14
; Sequence 14, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470

```

; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-10-367-470-14

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGGAGAAAAA 2599
||||||| - |||||
Db 1 AAAAAAAATTGTAATAAAA 20

RESULT 334
US-10-314-578-520
; Sequence 520, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
||||||| - |||||
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 335
US-10-314-578-520/c
; Sequence 520, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
||||||| - |||||
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 336
US-10-314-578-769
; Sequence 769, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 769
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
||||||| - |||||
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 337
US-10-314-578-769/c
; Sequence 769, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578


```
RESULT 342
US-10-189-267-44/c
; Sequence 44, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-44
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2127 TTGGATGCTGCCTACTGCTT 2146
Db 20 TTGGATGGCGCCTATTGCTT 1

RESULT 343
US-10-189-267-46/c
; Sequence 46, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-46
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAAGT 2465
Db 20 CTTGCAATGCAGCTAAAT 1

RESULT 344
US-10-189-267-71/c
; Sequence 71, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
```

```
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-71
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3056 TCGATGGCTTAAGGAGTTTG 3075
Db 20 TGGATGGCTTAAGGAACTTG 1

RESULT 345
US-10-189-267-174
; Sequence 174, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 174
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-174
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2349 CCTTGCTGTGTCTCCAGGA 2368
Db 1 CCTTGCTGTGTCTCCAGA 20

RESULT 346
US-10-189-267-181
; Sequence 181, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 181
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-181
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2094 TCACAACAGTCCAGCGCGG 2113
Db 1 TCACAACAGACCAACCGCG 20
```

APPLICANT: FURUSHO, KENTA

```
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-520

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 352
US-10-831-778-520/c
; Sequence 520, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-520

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 353
US-10-831-778-769
; Sequence 769, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
```

```
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 769
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-769

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 354
US-10-831-778-769/c
; Sequence 769, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 769
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-769

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 355
US-10-838-659-22
; Sequence 22, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
```

; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCACGCGCGCG 635
|||||
DB 1 GCGCGCGCGCGCGCGCG 20

RESULT 356
US-10-838-659-22/c
; Sequence 22, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCACGCGCGCG 635
|||||
DB 20 GCGCGCGCGCGCGCGCG 1

RESULT 357
US-10-838-659-76
; Sequence 76, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or

; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-76

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 634
|||||
DB 1 GCGCGCGCGCGCGCGCG 20

RESULT 358
US-10-838-659-76/c
; Sequence 76, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-76

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 634
|||||
DB 20 GCGCGCGCGCGCGCGCG 1

RESULT 359

US-10-146-058-76/c

; Sequence 76, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann

; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/146,058

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/535,249

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-5350

; TELE: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 76:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-10-146-058-76

Query Match

Best Local Similarity 0.4%; Score 16.4; DB 1; Length 18;

; Sequence 133, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann

; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

RESULT 360

US-10-146-058-133/c

; Sequence 133, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann

; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/146,058

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/535,249

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-5350

; TELE: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 133:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-10-146-058-133

Query Match

Best Local Similarity 0.4%; Score 16.4; DB 1; Length 18;

; Sequence 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463

DB 18 CTTGCAATGCAGCTAAA 1

RESULT 361

US-10-789-119-4/c

; Sequence 4, Application US/10789119

; Publication No. US20040170157A1

; GENERAL INFORMATION:

; APPLICANT: Chung, Yih-Lin

; TITLE OF INVENTION: METHOD FOR INCREASING THERAPEUTIC GAIN

; FILE REFERENCE: 13206-004002

; CURRENT APPLICATION NUMBER: US/10/789,119

; CURRENT FILING DATE: 2004-03-11

; PRIOR APPLICATION NUMBER: US 10/205,738

; PRIOR FILING DATE: 2002-07-25

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

FEATURE:
US-10-789-119-4
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2454 TGCAGCTAAAGTCCTGG 2471
DB 18 TGCAGCTAAAGTCCTCGG 1
RESULT 362
US-09-766-450-48
Sequence 48, Application US/09766450
Publication No. US20030022166A1
GENERAL INFORMATION:
APPLICANT: Collins, Colin
APPLICANT: Volik, Stanislav
APPLICANT: Gray, Joe W.
APPLICANT: Albertson, Donna G.
APPLICANT: Pinkel, Daniel
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Repeat-Free Probes for Molecular
FILE REFERENCE: 023071-111800US
CURRENT APPLICATION NUMBER: US/09/766,450
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer 768.348.rl
US-09-766-450-48
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 645 ACACATCCACGCACAC 662
DB 2 ACACATGCACGCACAC 19
RESULT 363
US-10-683-990-59
Sequence 59, Application US/10683990
Publication No. US20040198682A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Usman, Nassim
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
FILE REFERENCE: 400/134 (02-742-H)
CURRENT APPLICATION NUMBER: US/10/683,990
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: PCT/US03/05022
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
SOFTWARE: PatentIn version 3.2
SEQ ID NO 156
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-683-990-156

PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-683-990-59
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 66 GCGAGAGAAAGAGAGAG 83
DB 2 GUGAGAGAAAGAGAGAG 19
RESULT 364
US-10-683-990-156/c
Sequence 156, Application US/10683990
Publication No. US20040198682A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Usman, Nassim
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
FILE REFERENCE: 400/134 (02-742-H)
CURRENT APPLICATION NUMBER: US/10/683,990
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: PCT/US03/05022
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
SOFTWARE: PatentIn version 3.2
SEQ ID NO 156
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-683-990-156

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 GCGAGAGAAAGAGAGAG 83
DB 18 GTGAGAGAAAGAGAGAG 1

RESULT 365
US-09-791-942-10
; Sequence 10, Application US/09791942
; Patent No. US20020147166A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Rothlein
; APPLICANT: Takashi Kei Kishimoto
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0099
; CURRENT APPLICATION NUMBER: US/09/791,942
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-942-10

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3393 TCCTTGCTTGGTATAT 3410
DB 2 TCCTTGCTTGGTATAT 19

RESULT 366
US-10-189-267-27/c
; Sequence 27, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-27

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1693 AACCCCAAGCCAGAGTG 1700
DB 19 AACCCCAAGCCAGAGTG 2

RESULT 367
US-10-189-267-177

; Sequence 177, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 177
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-177

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 AACCCCAAGCCAGAGTG 1700
DB 2 AACCCCAAGCCAGAGTG 19

RESULT 368
US-10-289-762-2628
; Sequence 2628, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2628
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2628

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1055 GCCAGGACGTTTCTA 1072
DB 2 GCCAGGACGTTTCTA 19

RESULT 369
US-10-415-463-10
; Sequence 10, Application US/10415463
; Publication No. US20040110705A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0198
; CURRENT APPLICATION NUMBER: US/10/415,463
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 09/702,251
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-415-463-10

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3393 TCCTTTGCTTGGTATAT 3410
      ||||| ||||| ||||| |||||
Db 2 TCCTTCGCTCTGGTATAT 19

RESULT 370
US-10-728-399-292/c
; Sequence 292, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-292

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588
      ||||| ||||| ||||| |||||
Db 20 TGTTTAAACAAAAA 3

RESULT 371
US-10-728-399-369/c
; Sequence 369, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 369
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-369

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588
      ||||| ||||| ||||| |||||
Db 19 TGTTTAAACAAAAA 2

RESULT 372
US-10-728-399-475/c
; Sequence 475, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-475

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588
      ||||| ||||| ||||| |||||
Db 18 TGTTTAAACAAAAA 1

RESULT 373
US-10-028-158-16/c
; Sequence 16, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TROPICOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human mitoneet antisense
US-10-028-158-16

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACACTACTGTGTG 1232
      ||||| ||||| ||||| |||||
Db 16 CATGCACACTACTGTGTG 1

RESULT 374
US-10-028-158-17
; Sequence 17, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella

```

APPLICANT: Post, Martin
APPLICANT: Lye, Stephen
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TROPICBLAST
FILE REFERENCE: 11757 38USWO
CURRENT APPLICATION NUMBER: US/10/028,158
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/09/380,662
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: PCT/CA98/00180
PRIOR FILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: US 60/039,919
PRIOR FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 16
TYPE: DNA
ORGANISM: Homo sapiens
US-10-028-158-17

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACACTACTGTGTG 1232
Db 1 CATGCACACTACTGTGTG 16

RESULT 375
US-10-146-058-105/c
Sequence 105, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202)638-6666

TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-105

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAA 2035
Db 16 AGTCCACTAGGAAAA 1

RESULT 376
US-10-146-058-113/c
Sequence 113, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)

```
; ANTI-SENSE: YES
US-10-146-058-113

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATGCG 2168
DB 16 TGTGCAGGATAATGCG 1

RESULT 377
US-10-156-306-524/c
; Sequence 524, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-524

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAAATAAAAAA 2588
DB 17 TTTAAAAAATAAAAAA 2

RESULT 378
US-10-156-306-525/c
; Sequence 525, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-525

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAAATAAAAAA 2588
DB 16 TTTAAAAAATAAAAAA 1

RESULT 379
US-10-238-700-8
; Sequence 8, Application US/10238700
```

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; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-8

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 AGGCAGCAGCGCGGC 439
DB 1 AGGCAGCAGCGCGGC 16

RESULT 380
US-09-775-479-3/c
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECIERC, Guy
; APPLICANT: MARTEL, R.mi
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; FILE REFERENCE: 12168-1US-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-9

Query Match          0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAAATAAAAAA 2588
DB 18 TTTAAAAAATAAAAAA 3

RESULT 381
US-10-713-900-164292/c
; Sequence 164292, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 164292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-164292
```

```
Query Match          0.4%; Score 16; DB 1; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3165 AAGCTTCGCGACAGCGTCTGTC 3188
Db 25 AAGCTTCGCGACAGCGTGTGTC 2
```

```
RESULT 382
US-09-888-326-342
; Sequence 342, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-342
```

```
Query Match          0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 633
Db 1 GCGCGCGCGCGCGCGCG 19
```

```
RESULT 383
US-09-888-326-342/c
; Sequence 342, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 342
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-342
```

```
Query Match          0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGCACGCGCGC 634
Db 19 GCGCGCGCGCGCGCGCGC 1
```

```
RESULT 384
US-09-776-479-138
; Sequence 138, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138
```

```
Query Match          0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
Db 1 GCGCGCGCGCGCGCGCGC 19
```

```
RESULT 385
US-09-776-479-138/c
; Sequence 138, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGC 634
    |||||
Db 19 CGCGCGCGCGCGCGCGC 1

RESULT 386
US-09-776-479-138
; Sequence 138, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
    |||||
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 387
US-09-776-479-138/c
; Sequence 138, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
    |||||
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 388
US-10-112-653-131/c
; Sequence 131, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-131

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
    |||||
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 389
US-10-112-653-131/c
; Sequence 131, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-131

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGC 634
    |||||

```



```
Db      19  CGCGCGCGCGCGCGCGC 1

RESULT 390
US-10-017-995-138
; Sequence 138, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      615  GCGCGCGCGCACGCGCGC 633
          |||||
Db      1    GCGCGCGCGCGCGCGCGC 19

RESULT 391
US-10-017-995-138/c
; Sequence 138, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616  CGCGCGCGCACGCGCGC 634
          |||||
Db      19  CGCGCGCGCGCGCGCGC 1

RESULT 392
US-10-314-578-138
; Sequence 138, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616  CGCGCGCGCACGCGCGC 634
          |||||
Db      19  CGCGCGCGCGCGCGCGC 1

RESULT 394
US-10-683-990-97
; Sequence 97, Application US/10683990
; Publication No. US20040198682A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; APPLICANT: McSwiggen, James
```

APPLICANT: Usman, Nassim
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
FILE REFERENCE: 400/134 (02-742-H)
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
SOFTWARE: PatentIn version 3.2
SEQ ID NO 97
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-683-990-97
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.9e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2570 GTGTTTAAAAA 2588
Db 1 GUGUGGAAAAA 19
RESULT 395
US-10-683-990-194/c
Sequence 194, Application US/10683990
Publication No. US20040198682A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Usman, Nassim
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
FILE REFERENCE: 400/134 (02-742-H)
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US/10/683,990
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: PCT/US03/05022
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
SOFTWARE: PatentIn version 3.2
SEQ ID NO 194
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-683-990-194
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2570 GTGTTTAAAAA 2588
Db 19 GTGTGMAAAAAA 1
RESULT 396
US-10-831-778-138
Sequence 138, Application US/10831778
Publication No. US20040235774A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US/10/831,778
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 138
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-831-778-138
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCGCGCGCG 633
Db 1 GCGCGCGCGCGCGCGCG 19
RESULT 397
US-10-831-778-138/c
Sequence 138, Application US/10831778
Publication No. US20040235774A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
FILE REFERENCE: C1037/7013 (HCL/MAT)

; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-138

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGACGCGCGC 634
|||||
DB 19 GCGCGCGCGCGCGCGC 1

RESULT 398
US-09-750-401-32/c
; Sequence 32, Application US/09750401
; Publication No. US20020004211A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAA 2599
|||||
DB 22 AAAAAAACCAATTAAGAAAA 1

RESULT 399
US-10-309-788-32/c
; Sequence 32, Application US/10309788
; Publication No. US20030211466A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; APPLICANT: Phelps, William C.
; TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Target
; FILE REFERENCE: RBN-001CP
; CURRENT APPLICATION NUMBER: US/10/309,788
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/750,401

; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR consensus sequence of TGF beta 2
US-10-309-788-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAA 2599
|||||
DB 22 AAAAAAACCAATTAAGAAAA 1

RESULT 400
US-10-238-306B-32/c
; Sequence 32, Application US/10238306B
; Publication No. US20030235830A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001CN
; CURRENT APPLICATION NUMBER: US/10/238,306B
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-10-238-306B-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAA 2599
|||||
DB 22 AAAAAAACCAATTAAGAAAA 1

RESULT 401
US-10-629-453-32/c
; Sequence 32, Application US/10629453
; Publication No. US20040096878A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001DV
; CURRENT APPLICATION NUMBER: US/10/629,453
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28

Query Match	Best Local Similarity	Score	DB 1	Length
US-10-629-453-32	0.4%;	Score 15.6;	DB 1;	Length 22;
US-10-629-453-32	81.8%;	Pred. No. 3.9e+02;		
Matches 18;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY 2578	AAAAAAAAAATTCGAGAAAAA	2599		
DB 22	AAAAAAAAACCAATTAAAGAAAAA	1		
RESULT 402				
US-10-156-306-526/c				
Sequence 526,	Application US/10156306			
Publication No.	US20030119017A1			
GENERAL INFORMATION:				
APPLICANT:	Ribozyme Pharmaceuticals, Inc.			
APPLICANT:	McSwiggen, James			
TITLE OF INVENTION:	Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to			
FILE REFERENCE:	MHB01-664-A (400/050)			
CURRENT APPLICATION NUMBER:	US/10/156,306			
CURRENT FILING DATE:	2002-05-28			
NUMBER OF SEQ ID NOS:	8013			
SOFTWARE:	PatentIn version 3.0			
SEQ ID NO 526				
LENGTH: 17				
TYPE: RNA				
ORGANISM:	Homo sapiens			
US-10-156-306-526				
Query Match	0.4%;	Score 15.4;	DB 1;	Length 17;
Best Local Similarity	94.1%;	Pred. No. 2.7e+02;		
Matches 16;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 2571	TGTTTAAAAA	2597		
DB 17	TCTTTAAAAA	1		
RESULT 403				
US-10-156-306-527/c				
Sequence 527,	Application US/10156306			
Publication No.	US20030119017A1			
GENERAL INFORMATION:				
APPLICANT:	Ribozyme Pharmaceuticals, Inc.			
APPLICANT:	McSwiggen, James			
TITLE OF INVENTION:	Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to			
FILE REFERENCE:	MHB01-664-A (400/050)			
CURRENT APPLICATION NUMBER:	US/10/156,306			
CURRENT FILING DATE:	2002-05-28			
NUMBER OF SEQ ID NOS:	8013			
SOFTWARE:	PatentIn version 3.0			
SEQ ID NO 527				
LENGTH: 17				
TYPE: RNA				
ORGANISM:	Homo sapiens			
US-10-156-306-527				
Query Match	0.4%;	Score 15.4;	DB 1;	Length 17;
Best Local Similarity	94.1%;	Pred. No. 2.7e+02;		
Matches 16;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 2570	GTGTTTAAAAA	2586		

```
Db      17 TATATATTTTTTCTT 1
RESULT 406
US-09-891-517-18/c
; Sequence 18, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-18
Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1161 TATATATTTTTTCTT 1177
Db      17 TATATATTTTTTCTT 1
RESULT 407
US-10-146-058-112/c
; Sequence 112, Application US/10146058
; Publication No. US2003004099A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
```

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/
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-112
Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2136 GCCTACTGCTTTAGAAA 2152
Db      17 GCCTATTGCTTTAGAAA 1
RESULT 408
US-10-209-608-18/c
; Sequence 18, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-18
Query Match      0.4%; Score 15.4; DB 1; Length 18;
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Best Local Similarity 94.1%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1

RESULT 409
US-10-232-881-3/c
; Sequence 3, Application US/10232881
; Publication No. US2003008088A1
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Capaldi, Daniel
; APPLICANT: Krotz, Achim
; APPLICANT: Cole, Douglas
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric
; FILE REFERENCE: ISIS3380
; CURRENT APPLICATION NUMBER: US/10/232,881
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/288,679
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Phosphorothioate backbone
US-10-232-881-3

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAATTGGG 2

RESULT 410
US-10-232-881-5/c
; Sequence 5, Application US/10232881
; Publication No. US2003008088A1
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Capaldi, Daniel
; APPLICANT: Krotz, Achim
; APPLICANT: Cole, Douglas
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric
; FILE REFERENCE: ISIS3380
; CURRENT APPLICATION NUMBER: US/10/232,881
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/288,679
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial

; FEATURE:
; OTHER INFORMATION: NO. US2003008088A1el Sequence
US-10-232-881-5

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAATTGGG 2

RESULT 411
US-10-683-386-18/c
; Sequence 18, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-18

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1

RESULT 412
US-10-760-940-3/c
; Sequence 3, Application US/10760940
; Publication No. US20040219577A1
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Capaldi, Daniel C.
; APPLICANT: Krotz, Achim
; APPLICANT: Cole, Douglas L.
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: IMPROVED PROCESS FOR THE SYNTHESIS OF OLIGOMERIC COMPOUNDS
; FILE REFERENCE: ISIS-5422
; CURRENT APPLICATION NUMBER: US/10/760,940
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 10/232,881
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 09/288,679
; PRIOR FILING DATE: 1999-04-09

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; PRIOR APPLICATION NUMBER: US 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phosphorothioate backbone
US-10-760-940-3

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2

RESULT 413
US-10-473-126-1002/c
; Sequence 1002, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 1002
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for N-MYC
US-10-473-126-1002

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAAAAACATCAAAAC 2823
Db 18 AAAAAAAAAACCAAAAC 2

RESULT 414
US-09-569-193A-3
; Sequence 3, Application US/09569193A
; Patent No. US20020076697A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Kinase Assays Using Polyclonals
; FILE REFERENCE: 100/07930
; CURRENT APPLICATION NUMBER: US/09/569,193A
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 09/316,447
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/156,366
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/139,562
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-473-126-1002
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; OTHER INFORMATION: PNA probe
US-09-569-193A-3

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 415
US-09-865-044-3
; Sequence 3, Application US/09865044
; Patent No. US20020146703A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Assay Methods and Systems
; FILE REFERENCE: 09316447
; CURRENT APPLICATION NUMBER: US/09/865,044
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/316,447
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-865-044-3

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 416
US-10-057-812-3
; Sequence 3, Application US/10057812
; Publication No. US20020197619A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Kinase Assays Using Polyclonals
; FILE REFERENCE: 100/07930
; CURRENT APPLICATION NUMBER: US/10/057,812
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/569,193A
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/156,366
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/139,562
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-057-812-3

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2123 CGCTTTGGATGCTGCCT 2139
|||||
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 417
US-10-397-887-3
; Sequence 3, Application US/10397887
; Publication No. US20030175815A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Assay Methods and Systems
; FILE REFERENCE: 09316447
; CURRENT APPLICATION NUMBER: US/10/397,887
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/316,447A
; PRIOR FILING DATE: 1999-02-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Nucleic Acid
US-10-397-887-3

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
|||||
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 418
US-10-349-143-4619
; Sequence 4619, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.0200CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4619
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-16399 for SEQ 685,
US-10-349-143-4619

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3126 GTTGTATAGGACTAAG 3142
|||||
Db 2 GTTGTATAGGACTAAG 18

RESULT 419
US-10-701-550-3
; Sequence 3, Application US/10701550
; Publication No. US20040058406A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Kinase Assays Using Polycations
; FILE REFERENCE: 100/07930
; CURRENT APPLICATION NUMBER: US/10/701,550
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 09/569,193
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 09/316,447
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/156,366
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/139,562
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-701-550-3

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
|||||
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 420
US-10-670-011-33/c
; Sequence 33, Application US/10670011
; Publication No. US20040209832A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/132 (MBHB02-742-G)
; CURRENT APPLICATION NUMBER: US/10/670,011
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05


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; PRIOR APPLICATION NUMBER: US60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 427
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
US-10-670-011-33

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 CCTCCCCGGGCTCGCC 601
Db 17 CCTGCCCGGGCTCGCC 1

RESULT 421
US-10-670-011-129
; Sequence 129, Application US/10670011
; Publication No. US20040209832A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/132 (MBH02-742-G)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 427
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-670-011-129

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 585 CCTCCCCGGGCTCGCC 601
Db 3 CCUGCCCGGGCUCGCC 19

RESULT 422
US-10-663-189-7
; Sequence 7, Application US/10663189
; Publication No. US20050026158A1
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins School of Medicine
; APPLICANT: Nelson, William
; APPLICANT: Tchou, Julia
; APPLICANT: Bakker, Jila
; APPLICANT: Lin, Xiaohui
; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS
; FILE REFERENCE: JHU1660-1
; CURRENT APPLICATION NUMBER: US/10/663,189
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US/09/687,246B
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,168
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer N-F1
US-10-663-189-7

Query Match          0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTTTTTTAAG 2758
Db 4 ATTTTTTTTTTTAAG 20

RESULT 423
US-10-156-306-523/c
; Sequence 523, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 523
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-523

Query Match          0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAA 2588
Db 17 TTAAAAAATAAAAAA 3

RESULT 424

```

```
US-10-735-592-47
; Sequence 47, Application US/10735592
; Publication No. US2004017157A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70039US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-47

Query Match          0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2572 GTTTAAAAA 2586
Db 3 GTTTAAAAA 17

RESULT 425
US-09-775-479-8
; Sequence 8, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: MARTEL, Guy
; APPLICANT: LECLERC, Guy
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF PREPARATION AND
; FILE REFERENCE: 12168-IUS-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-8

Query Match          0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAA 2590
Db 3 AAAAAA 17

RESULT 426
US-09-725-265-20/c
; Sequence 20, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGATA, YOIICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KANAGATA, YOIICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS C
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA C
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-20

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
Db 18 ATATATATTTTCTTTC 1
```

```
US-09-725-265-20
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KANAGATA, YOIICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS C
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA C
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
Db 18 ATATATATTTTCTTTC 1

RESULT 427
US-09-891-517-20/c
; Sequence 20, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGATA, YOIICHI
; APPLICANT: KANAGATA, YOIICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS C
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA C
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-20

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
Db 18 ATATATATTTTCTTTC 1
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Db 18 ATATATATTTTTTTTTTC 1

RESULT 428

US-09-969-373-2296

; Sequence 2296, Application US/09969373

; Patent No. US20020133852A1

; GENERAL INFORMATION:

; APPLICANT: Effertz, Roger J.

; APPLICANT: Haug, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679)A

; CURRENT APPLICATION NUMBER: US/09/969,373

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US/09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US/09/855,768

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 2296

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Glycine max

US-09-969-373-2296

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2053 CACATCTCTGCTAATGT 2070

Db 1 CCCATCTCTGCTAAGT 18

RESULT 429

US-09-904-744-3/c

; Sequence 3, Application US/09904744

; Patent No. US20020150905A1

; GENERAL INFORMATION:

; APPLICANT: Barbera-Guillem, Emilio

; APPLICANT: Nelson, M. Bud

; APPLICANT: Castro, Stephanie

; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form

; FILE REFERENCE: B-73

; CURRENT APPLICATION NUMBER: US/09/904,744

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: 09/437076

; PRIOR FILING DATE: 1999-11-09

; PRIOR APPLICATION NUMBER: 60/107828

; PRIOR FILING DATE: 1998-11-10

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthesized

US-09-904-744-3

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCCCC 990

Db 18 CCCCCCCCCCGCCCC 1

RESULT 430

US-09-949-305B-2

; Sequence 2, Application US/09949305B

; Publication No. US20030022318A1

; GENERAL INFORMATION:

; APPLICANT: Lin, Shi-Lung

; APPLICANT: Ying, Shao-yao

; TITLE OF INVENTION: Method for Thermocycling Amplification of Nucleic Acid Sequences

; FILE REFERENCE: 266/014

; CURRENT APPLICATION NUMBER: US/09/949,305B

; CURRENT FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: 09/494,212

; PRIOR FILING DATE: 2000-01-25

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 18

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: poly(C) primer

US-09-949-305B-2

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCCCC 990

Db 1 CCCCCCCCCCGCCCC 18

RESULT 431

US-10-146-058-72/c

; Sequence 72, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Georg-Ferdinand

; APPLICANT: Brysich, Wolfgang

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Schlengersiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS: 137

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/146,058

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/535,249

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-72

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TATAAATCGACATGCCG 1544
DB 18 TACAAATAGACATGCCG 1

RESULT 432

US-10-146-058-79/c
Sequence 79, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlengersiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlengersiepen, Karl-Hermann
APPLICANT: Schlengersiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-79

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1636 ATGCTTCCAATCTGCTGA 1653
DB 18 ATGCTTCCAATTTGCTGA 1

RESULT 433

US-10-146-058-85/c
Sequence 85, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlengersiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlengersiepen, Karl-Hermann
APPLICANT: Schlengersiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-85

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1711 GGATTGAAGTGTATCAGA 1728
|||||||
Db 18 CGATTGAGCTATATCAGA 1

RESULT 434
US-10-146-058-96/c
; Sequence 96, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-96

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1880 AATAAGTTTACACTGCC 1897
|||||||
Db 18 AATAAGCTTACACTGCC 1

RESULT 435
US-10-146-058-115/c
; Sequence 115, Application US/10146058
; Publication No. US20030040499A1

; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-115

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2175 CGCCCTCTTTACATTGAT 2192
|||||||
Db 18 CGTCCACITTACATTGAT 1

RESULT 436
US-10-146-058-128/c
; Sequence 128, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-128

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```

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2375 ACCACTGACCAATCTCTA 2392
DB 18 ACCTCTAACCATTCTCTA 1

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RESULT 437
US-10-146-058-132/c
Sequence 132, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlengersien, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlengersien, Karl-Hermann
APPLICANT: Schlengersien, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-132

```

```

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2439 GTCAAGTCTTGTAAATGC 2456
DB 18 GTAAAGTCTTGCATATGC 1

```

```

RESULT 438
US-10-085-906-135/c
Sequence 135, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 135
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-135

```

```

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```
QY 645 ACATCCACACGACAC 662
    ||||| ||||| |||||
Db 18 ACACACACACGACAC 1

RESULT 439
US-10-209-608-20/c
; Sequence 20, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-20

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
    ||||| ||||| |||||
Db 18 ATATATATTTTCTTTC 1

RESULT 440
US-10-352-704-24
; Sequence 24, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelein, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,704
```

```
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..18
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-352-704-24

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCCCC 990
    ||||| ||||| |||||
Db 1 CCCCCCCCCCGCCCC 18

RESULT 441
US-10-220-033-4/c
; Sequence 4, Application US/10220033
; Publication No. US20030186906A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
; and a molecule binding to an expression product of that
; FILE REFERENCE: P68119US0
; CURRENT APPLICATION NUMBER: US/10/220,033
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: PCT/EP01/02694
; PRIOR FILING DATE: 2001-03-10
; PRIOR APPLICATION NUMBER: EP00105190.3
; PRIOR FILING DATE: 2000-03-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide
US-10-220-033-4

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TATAAATCGACATGCCG 1544
```

```

Db      18 TACAAATAGACATGCG 1
      || ||||| ||||| |||||
RESULT 442
US-10-328-578-142/c
; Sequence 142, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002020
; CURRENT FILING DATE: 2003-05-16
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2002-04-23
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-328-578-142

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      931 AAAAAAAAAACCACTT 948
      ||||| ||||| |||||
Db      18 AAAAAAAAAAAAAACCT 1

RESULT 443
US-10-297-068-282/c
; Sequence 282, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 282
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: capture
US-10-297-068-282

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
```

```

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2914 CTGCAGTGGTGCCTCC 2931
      ||||| ||||| ||||| ||
Db      18 CTGCAGTAGGTGCCACC 1

RESULT 444
US-10-683-386-20/c
; Sequence 20, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; FILE REFERENCE: 0163-0758-0X
; CURRENT FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-20

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1162 ATATATATTTTCTTAC 1179
      ||||| ||||| |||||
Db      18 ATATATATTTTCTTTC 1

RESULT 445
US-10-623-371-142/c
; Sequence 142, Application US/10623371
; Publication No. US20040132677A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; APPLICANT: TUCK, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002021
; CURRENT FILING DATE: 2003-07-18
; PRIOR FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: FastSeq for Windows Version 4.0
```



```
; SEQ ID NO 142
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic construct
US-10-623-371-142

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 AAAAAAAAAAACCACTT 948
Db 18 AAAAAAAAAAAAAAACCCT 1

RESULT 446
US-10-849-072-22
; Sequence 22, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: High density labeling of DNA with modified or
; FILE OF INVENTION: "chromophore" carrying nucleotides and DNA polymerases
; FILE REFERENCE: 4780/00/WO
; CURRENT APPLICATION NUMBER: US/10/849,072
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: second
; OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-22

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 447
US-10-849-072-24/c
; Sequence 24, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: High density labeling of DNA with modified or
; FILE OF INVENTION: "chromophore" carrying nucleotides and DNA polymerases
; FILE REFERENCE: 4780/00/WO
; CURRENT APPLICATION NUMBER: US/10/849,072
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: second
; OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-24

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCCCC 990
Db 18 CCCCCCCCCCCCCCCCCC 1

Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCCCC 990
Db 18 CCCCCCCCCCCCCCCCCC 1

RESULT 448
US-10-701-347-6
; Sequence 6, Application US/10701347
; Publication No. US20050026161A1
; GENERAL INFORMATION:
; APPLICANT: LEUCADIA TECHNOLOGIES, INC.
; TITLE OF INVENTION: DISPLACEMENT SANDWICH IMMUNO-PCR
; FILE REFERENCE: 45283.0002 UTL
; CURRENT APPLICATION NUMBER: US/10/701,347
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: 60/423,173
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-701-347-6

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2344 CTTCCCTTTCTGTGTGT 2361
Db 1 CTTCCCTTTCTGTGTGT 18

RESULT 449
US-10-701-347-11
; Sequence 11, Application US/10701347
; Publication No. US20050026161A1
; GENERAL INFORMATION:
; APPLICANT: LEUCADIA TECHNOLOGIES, INC.
; TITLE OF INVENTION: DISPLACEMENT SANDWICH IMMUNO-PCR
; FILE REFERENCE: 45283.0002 UTL
; CURRENT APPLICATION NUMBER: US/10/701,347
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: 60/423,173
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: PNA backbone
US-10-701-347-11

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2344 CTTCCCTTTCTGTGTGT 2361
Db 1 CTTCCCTTTCTGTGTGT 18
```

```

RESULT 450
US-09-882-945A-280/c
; Sequence 280, Application US/09882945A
; Publication No. US2003014353A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-280

```

```

Query Match          0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred.No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 65 TGGGAGAGAAAGAGAG 80
Db 16 TGGGAGAGAAACAGAG 1

```

```

RESULT 451
US-10-146-058-94/c
; Sequence 94, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs

```

```

; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-94
Query Match          0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred.No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1851 CACCACAAAGACAGGA 1866
Db 16 CACCATTAAGACAGGA 1

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RESULT 452
US-10-146-058-107/c
; Sequence 107, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs

```

;
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-107

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTTGTTG 2075
Db 16 CCTGCTAATGTTATTG 1

RESULT 453
US-10-807-114-280/c
; Sequence 280, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 280
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-807-114-280

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 TGGGAGAGAAAGACAG 80
Db 16 TGGGAGAGAAACAG 1

RESULT 454
US-10-156-306-526
; Sequence 526, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: Levels of IKK-Gamma and PKR
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 526
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-526

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;
QY 2745 TTTTNTTTTAAAGGA 2760
Db 2 UUUUUUUUUUAAAGA 17

RESULT 455
US-10-156-306-527
; Sequence 527, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: Levels of IKK-Gamma and PKR
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 527
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-527

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAGGA 2760
Db 1 UUUUUUUUUUAAAGA 16

RESULT 456
US-09-780-533A-233
; Sequence 233, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 233
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-233

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1587 AGACCTTACTTCAGAA 1602
Db 2 AGAUCUACUUCAGAA 17

RESULT 457
US-09-776-474-942
; Sequence 942, Application US/09776474
; Publication No. US20030087847A1

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaev, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 942
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-942

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 932 AAAAAAAAAACAACCT 947
      |||||
Db 1 AAAAAAAAAACAUAACU 16

RESULT 458
US-09-930-423-998
; Sequence 998, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 998
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-998

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GGGCAGCGCTCAGGA 119
      |||||
Db 1 GGGCAGCGCCAGGGA 16

RESULT 459
US-09-930-423-1179
; Sequence 1179, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 942
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1179

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GGGCAGCGCTCAGGA 119
      |||||
Db 1 GGGCAGCGCCAGGGA 16

RESULT 460
US-09-745-237A-998
; Sequence 998, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 998
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-998

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GGGCAGCGCTCAGGGA 119
      |||||
Db 1 GGGCAGCGCCAGGGA 16

RESULT 461
US-09-745-237A-1179
; Sequence 1179, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1179

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 103 GGGCAGCGCTCAGGG 118
      |||||
Db 2 GGGCAGCGCCAGGG 17

RESULT 462
US-09-745-237A-1179
; Sequence 1179, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1179

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 103 GGGCAGCGCTCAGGG 118
      |||||
```

Db 2 GGGGAGGCCGCCAGG 17

RESULT 462

US-10-041-856-35
; Sequence 35, Application US/10041856
; Publication No. US2002016929A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-041-856-35

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTTCATTTTAAAGGA 2760

Db 2 TTTTTCATTTTTCAGGA 17

RESULT 463

US-10-156-306-528/c
; Sequence 528, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 528
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-528

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2570 GTGTTTAAAAA 2585

Db 16 GTCTTTAAAAA 1

RESULT 464

US-10-238-700-7
; Sequence 7, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700

; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-7

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 422 GCAGGCAGCAGCGCG 437

Db 2 GGAGGCAGCAGCGCG 17

RESULT 465

US-10-339-793-439/c
; Sequence 439, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 439
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-439

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2138 CTACTGCTTTAGAAAT 2153

Db 17 CTACTGCTTTAGAGAT 2

RESULT 466

US-10-138-674-1773
; Sequence 1773, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1773

Query Match		0.3%;	Score 14.4;	DB 1;	Length 17;
Best Local Similarity		62.5%;	Pred. No. 3.4e+02;		
Matches 10;		Conservative 5;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1813	TCTCCTTCGAGTGAC 1828			
		.: : :			
Db	2	UCUCCUCCAGGUGAC 17			
RESULT 467					
US-10-138-674-3612/c					
; Sequence 3612, Application US/10138674					
; Publication No. US20040077565A1					
; GENERAL INFORMATION:					
; APPLICANT: Ribozyme Pharmaceuticals, Inc.					
; APPLICANT: Pavco, Pam					
; APPLICANT: McSwiggen, Jim					
; APPLICANT: Stinchcomb, Dan					
; APPLICANT: Escobedo, Jaime					
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re					
; FILE REFERENCE: MBHB00-876-N (400/049)					
; CURRENT APPLICATION NUMBER: US/10/138,674					
; CURRENT FILING DATE: 2002-05-03					
; NUMBER OF SEQ ID NOS: 20822					
; SOFTWARE: PatentIn version 3.0					
; SEQ ID NO 3612					
; LENGTH: 17					
; TYPE: RNA					
; ORGANISM: Mus musculus					
US-10-138-674-3612					
Query Match		0.3%;	Score 14.4;	DB 1;	Length 17;
Best Local Similarity		93.8%;	Pred. No. 3.4e+02;		
Matches 15;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	2666	ACAGCAACAAACCA 2681			
Db	17	ACAGCAACAAACAA 2			
RESULT 468					
US-10-138-674-6425					
; Sequence 6425, Application US/10138674					
; Publication No. US20040077565A1					
; GENERAL INFORMATION:					
; APPLICANT: Ribozyme Pharmaceuticals, Inc.					
; APPLICANT: Pavco, Pam					
; APPLICANT: McSwiggen, Jim					
; APPLICANT: Stinchcomb, Dan					
; APPLICANT: Escobedo, Jaime					
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re					
; FILE REFERENCE: MBHB00-876-N (400/049)					
; CURRENT APPLICATION NUMBER: US/10/138,674					
; CURRENT FILING DATE: 2002-05-03					
; NUMBER OF SEQ ID NOS: 20822					
; SOFTWARE: PatentIn version 3.0					
; SEQ ID NO 6425					
; LENGTH: 17					
; TYPE: RNA					
; ORGANISM: Homo sapiens					
US-10-138-674-6425					
Query Match		0.3%;	Score 14.4;	DB 1;	Length 17;
Best Local Similarity		62.5%;	Pred. No. 3.4e+02;		
Matches 10;		Conservative 5;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1813	TCTCCTTCGAGTGAC 1828			
		.: : :~			
Db	1	UCUCCUCCAGGUGAC 16			
		.: :~:~:~			

RESULT 469	
US-10-138-674-7146	
; Sequence 7146, Application US/10138674	
; Publication No. US20040077565A1	
; GENERAL INFORMATION:	
; APPLICANT: Ribozyme Pharmaceuticals, Inc.	
; APPLICANT: Pavco, Pam	
; APPLICANT: McSwiggen, Jim	
; APPLICANT: Stinchcomb, Dan	
; APPLICANT: Escobedo, Jaime	
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re	
; FILE REFERENCE: MBHB00-876-N (400/049)	
; CURRENT APPLICATION NUMBER: US/10/138,674	
; CURRENT FILING DATE: 2002-05-03	
; NUMBER OF SEQ ID NOS: 20822	
; SOFTWARE: PatentIn version 3.0	
; SEQ ID NO 7146	
; LENGTH: 17	
; TYPE: RNA	
; ORGANISM: Homo sapiens	
US-10-138-674-7146	
Query Match	
Best Local Similarity	
Matches 14;	
Conservative 1;	
Mismatches 1;	
Indels 0;	
Gaps 0;	
Qy	425
	GGCAGCAGCGCGCT 440
Db	2
	GGCAGCGCGCGCGCU 17
RESULT 470	
US-10-138-674-7538	
; Sequence 7538, Application US/10138674	
; Publication No. US20040077565A1	
; GENERAL INFORMATION:	
; APPLICANT: Ribozyme Pharmaceuticals, Inc.	
; APPLICANT: Pavco, Pam	
; APPLICANT: McSwiggen, Jim	
; APPLICANT: Stinchcomb, Dan	
; APPLICANT: Escobedo, Jaime	
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re	
; FILE REFERENCE: MBHB00-876-N (400/049)	
; CURRENT APPLICATION NUMBER: US/10/138,674	
; CURRENT FILING DATE: 2002-05-03	
; NUMBER OF SEQ ID NOS: 20822	
; SOFTWARE: PatentIn version 3.0	
; SEQ ID NO 7538	
; LENGTH: 17	
; TYPE: RNA	
; ORGANISM: Homo sapiens	
US-10-138-674-7538	
Query Match	
Best Local Similarity	
Matches 15;	
Conservative 0;	
Mismatches 1;	
Indels 0;	
Gaps 0;	
Qy	2671
	AACAACAACCAAAA 2686
Db	2
	AAAAACAACCAAAA 17
RESULT 471	
US-10-287-949A-1773	
; Sequence 1773, Application US/10287949A	
; Publication No. US20040102389A1	
; GENERAL INFORMATION:	
; APPLICANT: Ribozyme Pharmaceuticals, Inc.	
; APPLICANT: Pavco, Pam	
; APPLICANT: McSwiggen, Jim	

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1773

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
      :|::|::|::|::|::|
Db 2 UCUCUCCACGUGAC 17

RESULT 472
US-10-287-949A-3612/c
; Sequence 3612, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3612
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3612

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACAACAACA 2681
      |||||
Db 17 ACAGCAACAACAACA 2

RESULT 473
US-10-287-949A-6425
; Sequence 6425, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 6425
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6425

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
      :|::|::|::|::|::|
Db 1 UCUCUCCACGUGAC 16

RESULT 474
US-10-287-949A-7146
; Sequence 7146, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7146
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7146

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 425 GGCAGCAGCGCGGCT 440
      |||||
Db 2 GGCAGCAGCGCGGCGCU 17

RESULT 475
US-10-287-949A-7538
; Sequence 7538, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7538
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7538

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 97 AGCTCTGGGGCAGGCG 112
Db 16 AGCGTGGGGCAGGCG 1

```

RESULT 478
US-10-712-633-4
; Sequence 4, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MOLECULES
; TITLE OF INVENTION: RECEPTOR FOR THE TGF- $\beta$ 
; FILE REFERENCE: MBH02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
; US-10-712-633-4

```

```

US-10-712-672-717/c
; Sequence 717, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 717
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-717

```

```

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      425  GGCAGCAGCGCGCGCT 440
           ||||| ||||| |||||
DB       2  GGCAGCGCGCGCGCGCU 17

RESULT 479
US-10-712-633-551
; Sequence 551, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASE
; FILE REFERENCE: MBHB02-325FCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772

```



```
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 551
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-551

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2671 AACAAACACACAAAA 2686
Db 2 AAAAACACACAAAA 17

RESULT 480
US-10-498-462-47
; Sequence 47, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 47
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-47

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 CGCGCGGCACGCACG 631
Db 2 CGCGCGCACACGCACG 17

RESULT 481
US-10-498-462-48
; Sequence 48, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aeomica Sequence Listing Engine
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```
; SEQ ID NO 48
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-48

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 CGCGCGGCACGCACG 631
Db 1 CGCGCGCACACGCACG 16

RESULT 482
US-09-725-265-15/c
; Sequence 15, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-15

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTCCTT 1177
Db 18 ATATATATTTTTCCTT 3

RESULT 483
US-09-725-265-16/c
; Sequence 16, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
```

```

; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-365-16

```

```
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1162 ATATATATTTTCTT 1177
|||
pb 18 ATATATTTTTTTT 3

RESULT 484

```

US-09-725-265-17/c
; Sequence 17, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETE
; TITLE OF INVENTION: NUCLEIC ACID P
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199931050XDIV
; CURRENT APPLICATION NUMBER: US/09/7
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US/09/556
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-1
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17

```

```
Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1162 ATATATATTTTCTT 1177
 |||||
 Db 18 ATATATTTTTTTT 3

RESULT 485

US-09-725-265-19/c
; Sequence 19, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI

```

: APPLICANT: YAMADA, KAZUTAKA
: APPLICANT: YOKOMAKU, TOYOKAZU
: APPLICANT: KOYAMA, OSAMU
: APPLICANT: FURUSHO, KENTA
: TITLE OF INVENTION: METHOD FOR DETERMINING
: TITLE OF INVENTION: NUCLEIC ACID PROBES
: TITLE OF INVENTION: THE METHOD
: FILE REFERENCE: 199953USOXDIV
: CURRENT APPLICATION NUMBER: US/09/725,265
: CURRENT FILING DATE: 2000-11-29
: PRIOR APPLICATION NUMBER: US 09/556,127
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: JP 1999-111601
: PRIOR FILING DATE: 1999-04-20
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: Patent In version 3.1
: SEQ ID NO 19
: LENGTH: 18
: TYPE: DNA
: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC DNA
: US-09-725-265-19

```

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15: Conservative 0; Mismatches 1. Indels

Qy 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTTTT 3

RESULT 486

```

US-09-491-517-15/C
; Sequence 15, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINVA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOKOZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PR
; TITLE OF INVENTION: NOVEL NUCLEIC ACID BY USIN
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-491-517-15

```

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15: Conservative 0: Mismatches 1 Indels

Qy 1162 ATATATATTTTCTT 1177

Db 18 ATATATATTTTTTTT 3

RESULT 487

US-09-891-517-16/c
; Sequence 16, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-16

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
|||||
Db 18 ATATATATTTTTTTT 3

RESULT 488

US-09-891-517-17/c
; Sequence 17, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
|||||
Db 18 ATATATATTTTTTTT 3

RESULT 489

US-09-891-517-19/c
; Sequence 19, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
|||||
Db 18 ATATATATTTTTTTT 3

RESULT 490

US-09-904-744-2/c
; Sequence 2, Application US/09904744
; Patent No. US20020150905A1
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; TITLE OF INVENTION: dendrimers in a signal amplification system
; FILE REFERENCE: B-73
; CURRENT APPLICATION NUMBER: US/09/904,744
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/437076

;
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/107828
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-09-904-744-2

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAAACAACC 946
Db 17 AAAAAAAAAAACAACC 2

RESULT 491

US-09-961-077-1157
; Sequence 1157, Application US/09961077
; Publication No. US20030014775A1

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.
Edington, Brent B.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS

NUMBER OF SEQUENCES: 1263

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/961,077

FILING DATE: 21-Sep-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,645

FILING DATE: July 12, 1996

APPLICATION NUMBER: 60/001,135

FILING DATE: July 13, 1995

APPLICATION NUMBER: 08/300,726

FILING DATE: September 2, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 219/247

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

;
; INFORMATION FOR SEQ ID NO: 1157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1157:
US-09-961-077-1157

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 3.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 586 CTCCTCCGGGCTCGCC 601
Db 2 CUCCCCCGCCGCGCC 17

RESULT 492

US-09-994-311-7/c

; Sequence 7, Application US/09994311

; Publication No. US20030082556A1

GENERAL INFORMATION:

APPLICANT: Kaufman, Joseph C.

APPLICANT: Roth, Matthew E.

APPLICANT: Lizardi, Paul M.

APPLICANT: Feng, Li

APPLICANT: Latimer, Darin R.

TITLE OF INVENTION: Binary Encoded Sequence Tags

FILE REFERENCE: AGL 100

CURRENT APPLICATION NUMBER: US/09/994,311

CURRENT FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: US/09/637,751

PRIOR FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-994-311-7

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACA 2816
Db 18 TGAATAAAAAAAAAACA 3

RESULT 493

US-10-077-383-27

; Sequence 27, Application US/10077383

; Publication No. US2003005044A1

GENERAL INFORMATION:

APPLICANT: Haydock, Paul V.

APPLICANT: U'Ren, Jack

APPLICANT: Saigene Corporation

TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and

DNA/RNA Mixed Polymer Intermediate Products

FILE REFERENCE: 018048-001710US

CURRENT APPLICATION NUMBER: US/10/077,383

CURRENT FILING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: US 60/296,812

PRIOR FILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 27

LENGTH: 18

TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: spacer sequence
US-10-077-383-27

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 GGGAGAGAGAGAGAGA 81
Db 1 GGGAGAGAGAGAGAGA 16

RESULT 494
US-10-209-608-15/c
; Sequence 15, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-15

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 495
US-10-209-608-16/c
; Sequence 16, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-15

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 496
US-10-209-608-17/c
; Sequence 17, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-17

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 497
US-10-209-608-19/c
```

```
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-16

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3
```

```
RESULT 496
US-10-209-608-17/c
; Sequence 17, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-17
```

```
Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 497
US-10-209-608-19/c
```

; Sequence 19, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
18 ATATATATTTTCTT 3

Db

RESULT 498
US-10-145-857-19
; Sequence 19, Application US/10145857
; Publication No. US20030092654A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-ALPHA EXPRESSION
; FILE REFERENCE: RTSP-0117
; CURRENT APPLICATION NUMBER: US/10/145,857
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/856,074
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US/09/197,360
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US/09/856,074
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-145-857-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3727 TATTTATGTTGTC 3742
|||||

Db 1 TATTTATGTTATTC 16

RESULT 499

US-10-683-386-15/c
; Sequence 15, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-15

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
18 ATATATATTTTCTT 3

Db

RESULT 500
US-10-683-386-16/c
; Sequence 16, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:

; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-16

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177
| | | | | | | | | | | | | | | | | |
Db 18 ATATATATTTTCTT 3

RESULT 501

US-10-683-386-17/c
; Sequence 17, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177
| | | | | | | | | | | | | | | | | |
Db 18 ATATATATTTTCTT 3

RESULT 502

US-10-683-386-19/c
; Sequence 19, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177
| | | | | | | | | | | | | | | | | |
Db 18 ATATATATTTTCTT 3

RESULT 503

US-10-473-126-652/c
; Sequence 652, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 652
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for ELK1
US-10-473-126-652

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 935 AAAAAACAACCTTC 950
| | | | | | | | | | | | | | | | | |
Db 16 AAAAAACAACCTTC 1

RESULT 504

US-10-473-126-1066/c
; Sequence 1066, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 1066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for ELK1
US-10-473-126-1066

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950
Db 16 AAAAAACAACCTTC 1

RESULT 505
US-10-872-984-7/c
; Sequence 7, Application US/10872984
; Publication No. US2004026588A1
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/10/872,984
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/994,311
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-872-984-7

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACA 2816
Db 18 TGAATAAAAAAAAAAAAAA 3

RESULT 506
US-10-845-667-682
; Sequence 682, Application US/10845667
; Publication No. US20050026183A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Bibikova, Marina
; TITLE OF INVENTION: Methods and Compositions For Diagnosing
; FILE REFERENCE: 67234-091
; CURRENT APPLICATION NUMBER: US/10/845,667
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: 60/471,488
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 1506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 682
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-845-667-682

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3772 TTCTCTCCCAACCCC 3787
Db 1 TTCTCTCTCCCAACCCC 16

RESULT 507
US-10-845-667-1432
; Sequence 1432, Application US/10845667
; Publication No. US20050026183A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Bibikova, Marina
; TITLE OF INVENTION: Methods and Compositions For Diagnosing
; FILE REFERENCE: 67234-091
; CURRENT APPLICATION NUMBER: US/10/845,667
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: 60/471,488
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 1506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1432
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-845-667-1432

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3772 TTCTCTCCCAACCCC 3787
Db 1 TTCTCTCTCCCAACCCC 16

RESULT 508
US-10-719-900-164291/c
; Sequence 164291, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 164291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-164291

Query Match 0.3%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3165 AAGCCCCAGCAACACGTGTCTGC 3188
Db 25 AAGCTTCGCGAGTCACGTGTTCG 2

RESULT 509
US-09-263-959-816/c
; Sequence 816, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 320010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 816:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-816

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GAGAGAAAGAGAGA 81
Db 14 GAGAGAAAGAGAGA 1
|||||

RESULT 510
US-10-146-058-57/c
Sequence 57, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 393-5350
TELEFAX: (202) 393-5350

APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: DNA (genomic)
MOLECULE TYPE: YES
ANTI-SENSE: YES
US-10-146-058-57

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1219 TGCACACTGTGTG 1232
Db 14 TGCACACTGTGTG 1
|||||

RESULT 511
US-10-146-058-63/c
Sequence 63, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 393-5350
TELEFAX: (202) 393-5350

TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-63

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCTGAGCAA 1357
Db 14 CAGATCTGAGCAA 1

RESULT 512

US-10-146-058-71/c
Sequence 71, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (

US-10-146-058-71/c

Sequence 71, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES

US-10-146-058-71

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTAGCCCAAG 1520
Db 14 AGTACTAGCCCAAG 1

RESULT 513

US-10-146-058-74/c
Sequence 74, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (

US-10-146-058-74/c

Sequence 74, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-74

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574
Db 14 AAAATGCCATCCCG 1

RESULT 514
US-10-146-058-75/c
; Sequence 75, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: DNA (genomic)
; MOLECULE TYPE: YES
; ANTI-SENSE: YES
US-10-146-058-75

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTTCTACAG 1588
Db 14 CCCACTTTCTACAG 1

RESULT 515
US-10-146-058-91/c
; Sequence 91, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: DNA (genomic)
; MOLECULE TYPE: YES
; ANTI-SENSE: YES
US-10-146-058-91

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1807 AATGGCTCTCCTTC 1820
Db 14 AATGGCTCTCCTTC 1

RESULT 516
US-10-146-058-101/c
; Sequence 101, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.

;; CITY: Washington D.C
;; COUNTRY: U.S.A.
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/146,058
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/535,249
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93 107 089.0
;; FILING DATE: 30-APR-1993
;; INFORMATION FOR SEQ ID NO: 101:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: DNA (genomic)
;; MOLECULE TYPE: YES
;; ANTI-SENSE: YES
US-10-146-058-101

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCAC 1984
Db 14 GGTATTGATGGCAC 1

RESULT 517
US-10-146-058-103/c
; Sequence 103, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/146,058
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/535,249
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93 107 089.0
;; FILING DATE: 30-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93 107 849.7
;; FILING DATE: 13-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Player, William E.
;; REGISTRATION NUMBER: 31,409
;; REFERENCE/DOCKET NUMBER: 10577/P58418
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)638-6666
;; TELEFAX: (202) 393-5350
;; TELEX: RCA 248593 IDEA UR
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: YES
US-10-146-058-103

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGGTGATCAGA 2010
Db 14 CAGTGGTGATCAGA 1

RESULT 518
US-10-146-058-106/c
; Sequence 106, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta (1
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-106

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AAGACCCCATCT 2059
Db 14 AAGACCCCATCT 1

RESULT 519
US-10-146-058-122/c
; Sequence 122, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666

; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-122
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291
Db 14 GGAGTTCAGACACT 1

RESULT 520
US-10-146-058-136/c
; Sequence 136, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)

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; ANTI-SENSE: YES
US-10-146-058-136

Query Match          0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 521
US-10-343-710-146/c
; Sequence 45, Application US/10343710
; Publication No. US20040087478A1
; GENERAL INFORMATION:
; APPLICANT: GILLEN, Clemens
; APPLICANT: WETZELS, Ingrid
; APPLICANT: WENDT, Stephan
; APPLICANT: WEIHE, E.
; APPLICANT: SCHAEFER, M., K.-H.
; TITLE OF INVENTION: SCREENING METHOD
; FILE REFERENCE: 029310.52022US
; CURRENT APPLICATION NUMBER: US/10/343,710
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP01/09011
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-10-343-710-146

Query Match          0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAA 2587
Db 14 TTAAAAAATAAAAAA 1

RESULT 522
US-10-468-753-45
; Sequence 45, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-10-468-753-45

Query Match          0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAA 2587
Db 14 TTAAAAAATAAAAAA 1

RESULT 523
US-10-468-753-46
; Sequence 46, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-46

Query Match          0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2803 AAAAAAATAAAAAA 2816
Db 1 AAAAAAATAAAAAA 14

RESULT 524
US-10-468-753-48/c
; Sequence 48, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-48
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-48
Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAAAAAAAAA 2588
Db 14 TAAAAAAAAAAAAA 1

RESULT 525
US-10-855-595-17/c
; Sequence 17, Application US/10855595
; Publication No. US20040235057A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/855,595
; FILING DATE: 28-May-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,482
; FILING DATE: 25-Sep-2000
; APPLICATION NUMBER: 08/882,164
; FILING DATE: June 25, 1997
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 17
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17
US-10-855-595-17
Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TAAAAAAAAAAAAA 2587
Db 14 TAAAAAAAAAAAAA 1

RESULT 526
US-10-855-595-21/c
; Sequence 21, Application US/10855595
; Publication No. US20040235057A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/855,595
; FILING DATE: 28-May-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,482
; FILING DATE: 25-Sep-2000
; APPLICATION NUMBER: 08/882,164
; FILING DATE: June 25, 1997
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 21
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21
US-10-855-595-21
Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814
Db 14 TGAIAAAAAAAAAA 1

RESULT 527
US-10-855-532-17/c
; Sequence 17, Application US/10855532
; Publication No. US20040259074A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
```

6,306,624

RESULT 530
US-09-504-231A-322/c
; Sequence 322, Application US/09504231A

RESULT 530
US-09-504-231A-322/c
; Sequence 322, Application US/09504231A

Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-322

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223
Db 14 TGCCCAAGGCCT 1

RESULT 531
US-09-274-553D-321/c
; Sequence 321, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 321
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-321

QY 3210 TGCCCAAGGCCT 3223
Db 15 TGCCCAAGGCCT 2

RESULT 532
US-09-274-553D-322/c
; Sequence 322, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-322

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223
Db 14 TGCCCAAGGCCT 1

RESULT 533
US-10-027-632-52311
; Sequence 52311, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 52311
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52311

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 ATTCTTCCTCTTA 885
   |||||
Db 1 ATTCTTCCTCTTA 14

RESULT 534
US-10-027-632-52311
; Sequence 52311, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52311
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52311

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 ATTCTTCCTCTTA 885
   |||||
Db 1 ATTCTTCCTCTTA 14

RESULT 535
US-10-230-007B-17
; Sequence 17, Application US/10230007B
; Publication No. US20030170667A1
; GENERAL INFORMATION:
; APPLICANT: Kaytes, Paul
; APPLICANT: Teng, Chi-Hse
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Diagnostic for Schizophrenia
; FILE REFERENCE: 00458.PRO1
; CURRENT APPLICATION NUMBER: US/10/230,007B
; CURRENT FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA

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```

; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-230-007B-17

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3718 CCTGCGCTGTATTT 3731
   |||||
Db 1 CCTGCGCTGTATTT 14

RESULT 536
US-10-647-982A-17
; Sequence 17, Application US/10647982A
; Publication No. US20040115699A1
; GENERAL INFORMATION:
; APPLICANT: Kaytes, Paul
; APPLICANT: Teng, Chi-Hse
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Diagnostic for Schizophrenia
; FILE REFERENCE: 01313.PRO1
; CURRENT APPLICATION NUMBER: US/10/647,982A
; CURRENT FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-647-982A-17

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3718 CCTGCGCTGTATTT 3731
   |||||
Db 1 CCTGCGCTGTATTT 14

RESULT 537
US-10-041-856-35/c
; Sequence 35, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 35
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-041-856-35

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
   |||||
Db 14 TGAATAAAAAAAAAA 1

```

6,828,428

RESULT 538
US-09-090-672B-105/c
; Sequence 105, Application US/09090672B
; Patent No. US20020068707A1
; GENERAL INFORMATION:
; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tateunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigenasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
US-09-090-672B-105

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA-857/c
Db 17 TAAAAA-857/c

RESULT 539
US-09-780-533A-857/c
; Sequence 857, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 857
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-857

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCGCTCCGGGCG 578
Db 17 GCGCTCCGGGCG 4

RESULT 540
US-09-780-533A-2399/c
; Sequence 2399, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR APPLICATION NUMBER: 2001-02-09
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2399
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2399

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCGCTCCGGGCG 578
Db 16 GCGCTCCGGGCG 3

RESULT 541
US-09-780-533A-2400/c
; Sequence 2400, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2400
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2400

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCGGCTCCGGGGCG 578
DB 15 GCGGCTCCGGGGCG 2

RESULT 542
US-09-730-559B-107/c
; Sequence 107, Application US/09730559B
; Publication No. US20030207828A1
; GENERAL INFORMATION:
; APPLICANT: ISHIWATA, TETSUYOSHI
; APPLICANT: SAKURADA, MIKIRO
; APPLICANT: KAWABATA, AYAKO
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: NISHI, TATSUNARI
; APPLICANT: KUGA, TETSURO
; APPLICANT: SAWADA, SHIGEMASA
; APPLICANT: TAKEI, MASAMI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: FURUYA, AKIKO
; TITLE OF INVENTION: IGA NEPHROPATHY-ASSOCIATED GENE
; FILE REFERENCE: 766.21 CIP
; CURRENT APPLICATION NUMBER: US/09/730,559B
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
US-09-730-559B-107

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAATGA 2588
DB 17 TAAAAAATAATGA 4

RESULT 543
US-10-163-552-948/c
; Sequence 948, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBH01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 948
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-948

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2362 CCCAGGATCTGGAA 2375

DB 16 CCCAGGATCTGGAA 3

RESULT 544
US-10-156-306-522/c
; Sequence 522, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 522
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-522

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAATGA 2588
DB 17 TAAAAAATAATGA 4

RESULT 545
US-10-156-306-631/c
; Sequence 631, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 631
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-631

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3599 TTTTITTTTAAATGA 3612
DB 17 TTTTITTTTAAATGA 4

RESULT 546
US-10-061-201-2011/c
; Sequence 2011, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannnon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2011
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-2011

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCCCTGCTG 1903
DB 17 CACTGCCCCCTGCTG 4

RESULT 547
US-10-061-201-2012/c
; Sequence 2012, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2012
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-2012
```

```
Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCCCTGCTG 1903
DB 16 CACTGCCCCCTGCTG 3

RESULT 548
US-10-061-201-2013/c
; Sequence 2013, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2013
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-2013

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCCCTGCTG 1903
DB 15 CACTGCCCCCTGCTG 2

RESULT 549
US-10-061-201-2014/c
; Sequence 2014, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
```

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2014
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-2014

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCTGCTG 1903
Db 14 CACTGCCCTGCTG 1

RESULT 550

US-10-309-152A-3/c
; Sequence 3, Application US/10309152A
; Publication No. US20030175759A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi LTD.
; TITLE OF INVENTION: A method for prediction of genes and a method for providing a list
; FILE REFERENCE: H02001031A
; CURRENT APPLICATION NUMBER: US/10/309,152A
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: JP 2002-047297
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligo-d(T) primer by Nippon Flour Mills
US-10-309-152A-3

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588
Db 17 TAAAAA 4

RESULT 551

US-10-220-373-7/c
; Sequence 7, Application US/10220373
; Publication No. US20030180743A1
; GENERAL INFORMATION:
; APPLICANT: NAGASU, Takeshi
; APPLICANT: OSHIDA, Tadashi
; APPLICANT: OBAYASHI, Izumi
; APPLICANT: MATSUI, Keiko
; APPLICANT: SAITO, Hirohisa
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SH2-010US

; CURRENT APPLICATION NUMBER: US/10/220,373
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-61832
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificially
; OTHER INFORMATION: Synthesized Primer Sequence
US-10-220-373-7

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588
Db 17 TAAAAA 4

RESULT 552

US-10-291-808-63/c
; Sequence 63, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-63

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588
Db 17 TAAAAA 4

RESULT 553

US-10-380-255-6/c
; Sequence 6, Application US/10380255
; Publication No. US20040023263A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64935
; CURRENT APPLICATION NUMBER: US/10/380,255

; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08247
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-293021
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-255-6

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAATAAAAAAAAAA 2588
Db 17 TAAATAAAAAAAAAA 4

RESULT 554
US-10-380-254-3/c
; Sequence 3, Application US/10380254
; Publication No. US2004003825A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64773
; CURRENT APPLICATION NUMBER: US/10/380,254
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08246
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-291318
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-254-3

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAATAAAAAAAAAA 2588
Db 17 TAAATAAAAAAAAAA 4

RESULT 555
US-10-398-885A-2/c
; Sequence 2, Application US/10398885A
; Publication No. US20040053282A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; APPLICANT: Takahashi, Eiki
; TITLE OF INVENTION: Method of Testing For Allergic Diseases
; FILE REFERENCE: SHIMIZU-07907

; CURRENT APPLICATION NUMBER: US/10/398,885A
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08937
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-885A-2

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAATAAAAAAAAAA 2588
Db 17 TAAATAAAAAAAAAA 4

RESULT 556
US-10-398-877-18/c
; Sequence 18, Application US/10398877
; Publication No. US20040058351A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07906
; CURRENT APPLICATION NUMBER: US/10/398,877
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08574
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-877-18

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAATAAAAAAAAAA 2588
Db 17 TAAATAAAAAAAAAA 4

RESULT 557
US-10-239-734-3/c
; Sequence 3, Application US/10239734
; Publication No. US20040161746A1
; GENERAL INFORMATION:
; APPLICANT: GENOX RESEARCH, INC.
; APPLICANT: JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF AGENCY OF NATIONAL CENTER FOR
; APPLICANT: CHILD HEALTH AND DEVELOPMENT
; APPLICANT: Matsumoto, Yoshiko
; APPLICANT: Tsujimoto, Gozoh

```
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Sugita, Yuji
; APPLICANT: Oshida, Tadashi
; APPLICANT: Imai, Yukiko
; TITLE OF INVENTION: Method of Testing For Allergic Disease
; FILE REFERENCE: SHIMIZU-07379
; CURRENT APPLICATION NUMBER: US/10/239,734
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/JP01/11286
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 2000-389476 JP
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: "Grt15A", an artificially synthesized primer sequence
US-10-239-734-3
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2575 TAAAAAATAAAAAA 2588
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DB 17 TAAAAAATAAAAAA 4
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RESULT 558
US-10-735-592-17/c
; Sequence 17, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-17
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2803 AAAAAAATAAAAAA 2816
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DB 15 AAAAAAATAAAAAA 2
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RESULT 559
US-10-735-592-46
; Sequence 46, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-46
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2575 TAAAAAATAAAAAA 2588
|||
DB 4 TAAAAAATAAAAAA 17
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RESULT 560
US-10-735-592-56/c
; Sequence 56, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-56
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2803 AAAAAAATAAAAAA 2816
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DB 15 AAAAAAATAAAAAA 2
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RESULT 561
US-10-608-863-3/c
; Sequence 3, Application US/10608863
; Publication No. US20040214192A1
; GENERAL INFORMATION:
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Kagaya, Shinji
; APPLICANT: Yavoi, Yoshihiro
; APPLICANT: Sugita, Yuji
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: METHODS FOR EXAMINATION FOR ALLERGIC DISEASES
; FILE REFERENCE: 3462.1003-000
; CURRENT APPLICATION NUMBER: US/10/608,863
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: JP 2002-188490
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
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; OTHER INFORMATION: Synthesized Primer Sequence	
US-10-608-863-3	
Query Match 0.3%; Score 14; DB 1; Length 17;	
Best Local Similarity 100.0%; Pred. No. 3.8e+02;	
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 2575 TAAAAA	2588
Db 17 TAAAAA	4
RESULT 562	
US-10-156-306-525	
; Sequence 525, Application US/10156306	
; Publication No. US20030119017A1	
; GENERAL INFORMATION:	
; APPLICANT: McSwiggen, James	
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to	
; FILE OF INVENTION: Levels of IKK-Gamma and PKR	
; FILE REFERENCE: MBHB01-664-A (400/050)	
; CURRENT APPLICATION NUMBER: US/10/156,306	
; CURRENT FILING DATE: 2002-05-28	
; NUMBER OF SEQ ID NOS: 8013	
; SOFTWARE: PatentIn version 3.0	
; SEQ ID NO 525	
; LENGTH: 17	
; TYPE: RNA	
; ORGANISM: Homo sapiens	
US-10-156-306-525	
Query Match 0.3%; Score 13.8; DB 1; Length 17;	
Best Local Similarity 17.6%; Pred. No. 4e+02;	
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;	
QY 2743 TCTTTT	2759
: : : : : : : :	
Db 1 UUUUUUUUUUUU	AAG 17
RESULT 563	
US-10-156-306-523	
; Sequence 523, Application US/10156306	
; Publication No. US20030119017A1	
; GENERAL INFORMATION:	
; APPLICANT: McSwiggen, James	
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to	
; FILE OF INVENTION: Levels of IKK-Gamma and PKR	
; FILE REFERENCE: MBHB01-664-A (400/050)	
; CURRENT APPLICATION NUMBER: US/10/156,306	
; CURRENT FILING DATE: 2002-05-28	
; NUMBER OF SEQ ID NOS: 8013	
; SOFTWARE: PatentIn version 3.0	
; SEQ ID NO 523	
; LENGTH: 17	
; TYPE: RNA	
; ORGANISM: Homo sapiens	
US-10-156-306-523	
Query Match 0.3%; Score 13.8; DB 1; Length 17;	
Best Local Similarity 17.6%; Pred. No. 4e+02;	
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;	
QY 2741 CACCTT	2757
: : : : : : :	
Db 1 CUUUUUUUUUUU	UA 17
RESULT 564	
US-10-735-592-47/c	
; Sequence 47, Application US/10735592	

; Publication No. US20040171571A1	
; GENERAL INFORMATION:	
; APPLICANT: Art, Krieg	
; APPLICANT: Joerg, Vollmer	
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use	
; FILE REFERENCE: C1037-70038US01	
; CURRENT APPLICATION NUMBER: US/10/735,592	
; CURRENT FILING DATE: 2003-12-11	
; NUMBER OF SEQ ID NOS: 69	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 47	
; LENGTH: 17	
; TYPE: DNA	
; ORGANISM: Artificial	
; FEATURE:	
; OTHER INFORMATION: Synthetic oligonucleotide	
US-10-735-592-47	
Query Match 0.3%; Score 13.8; DB 1; Length 17;	
Best Local Similarity 88.2%; Pred. No. 4e+02;	
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 1032 TTTTCT	1048
Db 17 TTTTCT	1
RESULT 565	
US-10-156-306-528	
; Sequence 528, Application US/10156306	
; Publication No. US20030119017A1	
; GENERAL INFORMATION:	
; APPLICANT: McSwiggen, James	
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to	
; FILE OF INVENTION: Levels of IKK-Gamma and PKR	
; FILE REFERENCE: MBHB01-664-A (400/050)	
; CURRENT APPLICATION NUMBER: US/10/156,306	
; CURRENT FILING DATE: 2002-05-28	
; NUMBER OF SEQ ID NOS: 8013	
; SOFTWARE: PatentIn version 3.0	
; SEQ ID NO 528	
; LENGTH: 17	
; TYPE: RNA	
; ORGANISM: Homo sapiens	
US-10-156-306-528	
Query Match 0.3%; Score 13.8; DB 1; Length 17;	
Best Local Similarity 29.4%; Pred. No. 4e+02;	
Matches 5; Conservative 10; Mismatches 2; Indels 0; Gaps 0;	
QY 2746 TTTTCT	2762
: : : : : : : :	
Db 1 UUUUUUUUUUUU	AAGACA 17
RESULT 566	
US-10-291-808-63	
; Sequence 63, Application US/10291808	
; Publication No. US20030224382A1	
; GENERAL INFORMATION:	
; APPLICANT: McClelland, Michael	
; APPLICANT: Welsh, John	
; APPLICANT: Trenkle, Thomas	
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of	
; FILE OF INVENTION: Using Same	
; FILE REFERENCE: P-PH 3457	
; CURRENT APPLICATION NUMBER: US/10/291,808	
; CURRENT FILING DATE: 2002-11-07	
; PRIOR APPLICATION NUMBER: US/09/300,958	
; PRIOR FILING DATE: 1999-04-27	
; PRIOR APPLICATION NUMBER: 60/083,331	
; PRIOR FILING DATE: 1998-04-27	

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; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-63
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No.4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3263 ATTTTTCCTTTTAA 3279
Db 1 ATTTTTCCTTTTAA 17
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RESULT 567
US-09-775-479-9
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; APPLICANT: MARTEL, R.m
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-IUS-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-9
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Query Match 0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred.No.4.3e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTAA 3280
Db 1 TTTTTCCTTTTAA 17
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Search completed: February 25, 2005, 09:49:58
Job time : 28 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 09:40:13 ; Search time 17 Seconds
(without alignments)
3.637 Million cell updates/sec

Title: US-10-633-163-47
Perfect score: 4267
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 404 seqs, 7245 residues

Total number of hits satisfying chosen parameters: 808

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 476 summaries

Database : fcrhnr147.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	34.2	0.8	39	1	US-08-789-588-7
5	33	0.8	33	1	US-09-750-401-29
6	25	0.6	25	1	US-09-750-401-31
7	25	0.6	25	1	US-09-396-196G-60887
8	25	0.6	25	1	US-09-396-196G-60888
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21	25	0.6	25	1	US-09-396-196G-60901
22	25	0.6	25	1	US-09-396-196G-60902
23	25	0.6	25	1	US-09-396-196G-60903
24	25	0.6	25	1	US-09-396-196G-60904
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26	25	0.6	25	1	US-09-396-196G-60906
27	22	0.5	22	1	US-09-750-401-32
28	20	0.5	20	1	US-09-380-662-8
29	20	0.5	20	1	US-09-661-753-48
30	20	0.5	20	1	US-09-661-753-49
31	20	0.5	20	1	US-09-661-753-50
32	20	0.5	20	1	US-09-661-753-51
33	20	0.5	20	1	US-09-661-753-52
34	20	0.5	20	1	US-09-661-753-53
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49	20	0.5	20	1	US-09-661-753-68
50	19.2	0.4	24	1	US-08-478-470-13
51	19.2	0.4	24	1	US-08-214-599-13
52	19.2	0.4	24	1	US-08-473-015-13
53	19.2	0.4	24	1	US-08-465-368-13
54	19.2	0.4	24	1	US-08-477-306-13
55	19.2	0.4	24	1	US-08-700-448-13
56	19.2	0.4	24	1	US-08-923-386A-13
57	19.2	0.4	24	1	US-09-655-804B-67
58	19.2	0.4	24	1	US-09-894-799-22
59	19.2	0.4	24	1	US-09-695-437A-27
60	19.2	0.4	24	1	US-09-695-437A-27
61	18.8	0.4	22	1	US-08-458-367-18
62	18.8	0.4	22	1	US-08-458-367-18
63	18.8	0.4	22	1	US-08-482-577B-34
64	18.8	0.4	22	1	US-08-288-508C-25
65	18.8	0.4	22	1	US-08-289-222E-38
66	18.8	0.4	22	1	US-09-218-176-17
67	18.8	0.4	22	1	US-09-054-526B-38
68	18.8	0.4	22	1	US-09-386-450D-25
69	18.4	0.4	20	1	US-09-823-634A-15
70	18.4	0.4	20	1	US-09-823-647B-15
71	18	0.4	18	1	US-09-380-662-9
72	18	0.4	18	1	US-08-535-249-67
73	18	0.4	18	1	US-08-535-249-104
74	17.4	0.4	21	1	US-09-009-913-100
75	17.4	0.4	21	1	US-09-657-472-1948
76	16.8	0.4	20	1	US-08-482-182-68
77	16.8	0.4	20	1	US-08-863-639A-51
78	16.8	0.4	20	1	US-08-863-639A-51
79	16.8	0.4	20	1	US-09-030-701-59
80	16.8	0.4	20	1	US-09-030-701-59
81	16.8	0.4	20	1	US-09-082-649B-22
82	16.8	0.4	20	1	US-09-082-649B-22
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84	16.8	0.4	20	1	US-09-082-649B-76
85	16.8	0.4	20	1	US-08-535-249-99
86	16.8	0.4	20	1	US-09-725-265-42
87	16.8	0.4	20	1	US-09-823-634A-13
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89	16.8	0.4	20	1	US-09-823-647B-13
90	16.8	0.4	20	1	US-09-823-647B-14
91	16.8	0.4	20	1	US-09-556-127-42
92	16.8	0.4	20	1	US-09-965-101-22
93	16.8	0.4	20	1	US-09-965-101-22
94	16.8	0.4	20	1	US-09-965-101-76
95	16.8	0.4	20	1	US-09-965-101-76
96	16.8	0.4	20	1	5221620-13
97	16.8	0.4	20	1	5221620-13
98	16.8	0.4	24	1	US-09-655-804B-67
99	16.6	0.4	24	1	US-08-535-249-76
100	16.4	0.4	18	1	US-08-535-249-133
101	16.4	0.4	18	1	US-09-696-791-3527
102	16.4	0.4	19	1	US-09-696-791-3528
103	16.4	0.4	19	1	US-09-702-251-10
104	16.4	0.4	20	1	US-09-198-452A-2628
105	16.4	0.4	20	1	US-09-380-662-16
106	16	0.4	16	1	Sequence 53, Appl
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					Sequence 191, Appl
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					Sequence 193, Appl
					Sequence 194, Appl

107	16	0.4	16	1	US-09-380-662-17	Sequence 17, Appl	C 180	14.8	0.3	18	1	US-08-535-249-96	Sequence 96, Appl
C 108	16	0.4	16	1	US-08-535-249-105	Sequence 105, App	C 181	14.8	0.3	18	1	US-08-535-249-115	Sequence 115, App
C 109	16	0.4	16	1	US-08-535-249-113	Sequence 113, App	C 182	14.8	0.3	18	1	US-08-535-249-128	Sequence 128, App
C 110	16	0.4	17	1	US-09-601-144-2	Sequence 2, Appl	C 183	14.8	0.3	18	1	US-08-535-249-132	Sequence 132, App
C 111	16	0.4	18	1	US-08-330-000-1	Sequence 1, Appl	C 184	14.8	0.3	18	1	US-09-725-265-20	Sequence 20, Appl
C 112	16	0.4	18	1	US-08-365-908-1	Sequence 1, Appl	C 185	14.8	0.3	18	1	US-09-704-640-122	Sequence 122, App
C 113	16	0.4	19	1	US-09-026-601-25	Sequence 25, Appl	C 186	14.8	0.3	18	1	US-09-556-127-20	Sequence 20, Appl
C 114	16	0.4	20	1	US-08-842-079-4	Sequence 4, Appl	C 187	14.8	0.3	18	1	US-10-352-704-24	Sequence 24, Appl
C 115	16	0.4	20	1	US-09-638-857-4	Sequence 4, Appl	C 188	14.8	0.3	18	1	US-09-904-744-3	Sequence 3, Appl
C 116	16	0.4	24	1	US-08-478-470-13	Sequence 13, Appl	C 189	14.8	0.3	18	1	PCT-US94-05407-5	Sequence 5, Appl
C 117	16	0.4	24	1	US-08-214-599-13	Sequence 13, Appl	C 190	14.8	0.3	18	1	PCT-US96-11786-42	Sequence 42, Appl
C 118	16	0.4	24	1	US-08-473-015-13	Sequence 13, Appl	C 191	14.8	0.3	18	1	PCT-US96-11786-43	Sequence 43, Appl
C 119	16	0.4	24	1	US-08-465-368-13	Sequence 13, Appl	C 192	14.4	0.3	16	1	US-08-535-249-94	Sequence 94, Appl
C 120	16	0.4	24	1	US-08-477-306-13	Sequence 13, Appl	C 193	14.4	0.3	16	1	US-08-535-249-107	Sequence 107, Appl
C 121	16	0.4	24	1	US-08-700-448-13	Sequence 13, Appl	C 194	14.4	0.3	17	1	US-08-050-073-155	Sequence 155, App
C 122	16	0.4	24	1	US-08-823-386A-13	Sequence 13, Appl	C 195	14.4	0.3	17	1	US-08-390-850-578	Sequence 578, App
C 123	16	0.4	24	1	US-08-899-029-1	Sequence 1, Appl	C 196	14.4	0.3	17	1	US-08-390-850-581	Sequence 581, App
C 124	15.8	0.4	19	1	US-09-696-791-4067	Sequence 4067, Ap	C 197	14.4	0.3	17	1	US-08-373-124A-2153	Sequence 2153, Ap
C 125	15.6	0.4	22	1	US-09-750-401-32	Sequence 32, Appl	C 198	14.4	0.3	17	1	US-08-373-124A-2159	Sequence 2159, Ap
C 126	15.4	0.4	17	1	US-08-390-850-579	Sequence 579, App	C 199	14.4	0.3	17	1	US-08-373-124A-2161	Sequence 2161, Ap
C 127	15.4	0.4	17	1	US-08-390-850-580	Sequence 580, App	C 200	14.4	0.3	17	1	US-08-435-634-578	Sequence 578, App
C 128	15.4	0.4	17	1	US-08-373-124A-2155	Sequence 2155, App	C 201	14.4	0.3	17	1	US-08-435-634-581	Sequence 581, App
C 129	15.4	0.4	17	1	US-08-373-124A-2157	Sequence 2157, Ap	C 202	14.4	0.3	17	1	US-08-435-628-2153	Sequence 2153, Ap
C 130	15.4	0.4	17	1	US-08-435-634-579	Sequence 579, App	C 203	14.4	0.3	17	1	US-08-435-628-2159	Sequence 2159, Ap
C 131	15.4	0.4	17	1	US-08-435-634-580	Sequence 580, App	C 204	14.4	0.3	17	1	US-08-435-628-2161	Sequence 2161, Ap
C 132	15.4	0.4	17	1	US-08-435-628-2155	Sequence 2155, Ap	C 205	14.4	0.3	17	1	US-08-173-489C-92	Sequence 92, Appl
C 133	15.4	0.4	17	1	US-08-435-628-2157	Sequence 2157, Ap	C 206	14.4	0.3	17	1	US-08-173-489C-95	Sequence 95, Appl
C 134	15.4	0.4	18	1	US-08-535-249-112	Sequence 112, App	C 207	14.4	0.3	17	1	US-08-584-040-4006	Sequence 4006, Ap
C 135	15.4	0.4	18	1	US-09-288-679-3	Sequence 3, Appl	C 208	14.4	0.3	17	1	US-08-584-040-7828	Sequence 7828, Ap
C 136	15.4	0.4	18	1	US-09-288-679-5	Sequence 5, Appl	C 209	14.4	0.3	17	1	US-09-371-772B-1773	Sequence 1773, Ap
C 137	15.4	0.4	18	1	US-09-725-265-18	Sequence 18, Appl	C 210	14.4	0.3	17	1	US-09-371-772B-3612	Sequence 3612, Ap
C 138	15.4	0.4	18	1	US-09-556-127-18	Sequence 18, Appl	C 211	14.4	0.3	17	1	US-09-371-772B-6425	Sequence 6425, Ap
C 139	15.4	0.4	19	1	US-09-316-447A-3	Sequence 3, Appl	C 212	14.4	0.3	17	1	US-09-685-664B-1773	Sequence 1773, Ap
C 140	15.4	0.4	19	1	US-09-727-532A-3	Sequence 3, Appl	C 213	14.4	0.3	17	1	US-09-685-664B-3612	Sequence 3612, Ap
C 141	15.4	0.4	19	1	US-09-569-193A-3	Sequence 3, Appl	C 214	14.4	0.3	18	1	US-09-197-360-19	Sequence 19, Appl
C 142	15.4	0.4	19	1	US-09-422-978-4619	Sequence 4619, Ap	C 215	14.4	0.3	18	1	US-09-437-076-2	Sequence 2, Appl
C 143	15.4	0.4	19	1	US-10-057-812A-3	Sequence 3, Appl	C 216	14.4	0.3	18	1	US-08-679-645-1157	Sequence 1157, Ap
C 144	15.4	0.4	19	1	US-09-865-044-3	Sequence 3, Appl	C 217	14.4	0.3	18	1	US-09-637-751A-7	Sequence 7, Appl
C 145	15.4	0.4	19	1	US-09-696-791-3526	Sequence 3526, Ap	C 218	14.4	0.3	18	1	US-09-856-074B-19	Sequence 19, Appl
C 146	15.4	0.4	19	1	US-09-696-791-3529	Sequence 3529, Ap	C 219	14.4	0.3	18	1	US-09-725-265-15	Sequence 15, Appl
C 147	15.4	0.4	20	1	US-08-687-246B-7	Sequence 7, Appl	C 220	14.4	0.3	18	1	US-09-725-265-16	Sequence 16, Appl
C 148	15	0.4	15	1	US-08-087-387-5	Sequence 5, Appl	C 221	14.4	0.3	18	1	US-09-725-265-17	Sequence 17, Appl
C 149	15	0.4	15	1	US-08-455-627-5	Sequence 5, Appl	C 222	14.4	0.3	18	1	US-09-725-265-19	Sequence 19, Appl
C 150	15	0.4	15	1	US-08-461-271-5	Sequence 5, Appl	C 223	14.4	0.3	18	1	US-09-556-127-15	Sequence 15, Appl
C 151	15	0.4	15	1	US-08-713-685A-5	Sequence 5, Appl	C 224	14.4	0.3	18	1	US-09-556-127-16	Sequence 16, Appl
C 152	15	0.4	15	1	US-08-689-856-5	Sequence 5, Appl	C 225	14.4	0.3	18	1	US-09-556-127-17	Sequence 17, Appl
C 153	15	0.4	15	1	US-08-863-639A-8	Sequence 8, Appl	C 226	14.4	0.3	18	1	US-09-556-127-19	Sequence 19, Appl
C 154	15	0.4	15	1	US-08-832-021-17	Sequence 17, Appl	C 227	14.4	0.3	18	1	US-09-904-311-7	Sequence 7, Appl
C 155	15	0.4	15	1	US-08-832-021-22	Sequence 22, Appl	C 228	14.4	0.3	18	1	US-09-904-744-2	Sequence 2, Appl
C 156	15	0.4	15	1	US-09-070-477-5	Sequence 5, Appl	C 229	14	0.3	14	1	US-08-832-021-5	Sequence 5, Appl
C 157	15	0.4	15	1	US-08-787-321-5	Sequence 5, Appl	C 230	14	0.3	14	1	US-08-832-021-9	Sequence 9, Appl
C 158	14.8	0.3	18	1	US-08-145-704-42	Sequence 42, Appl	C 231	14	0.3	14	1	US-08-724-466B-17	Sequence 17, Appl
C 159	14.8	0.3	18	1	US-08-145-704-43	Sequence 43, Appl	C 232	14	0.3	14	1	US-08-724-466B-21	Sequence 21, Appl
C 160	14.8	0.3	18	1	US-08-105-168B-21	Sequence 21, Appl	C 233	14	0.3	14	1	US-08-882-164D-17	Sequence 17, Appl
C 161	14.8	0.3	18	1	US-08-698-948-21	Sequence 21, Appl	C 234	14	0.3	14	1	US-08-882-164D-21	Sequence 21, Appl
C 162	14.8	0.3	18	1	US-08-358-556A-24	Sequence 24, Appl	C 235	14	0.3	14	1	US-08-535-249-57	Sequence 57, Appl
C 163	14.8	0.3	18	1	US-08-863-639A-15	Sequence 15, Appl	C 236	14	0.3	14	1	US-08-535-249-63	Sequence 63, Appl
C 164	14.8	0.3	18	1	US-08-863-639A-16	Sequence 16, Appl	C 237	14	0.3	14	1	US-08-535-249-71	Sequence 71, Appl
C 165	14.8	0.3	18	1	US-08-987-574-42	Sequence 42, Appl	C 238	14	0.3	14	1	US-08-535-249-74	Sequence 74, Appl
C 166	14.8	0.3	18	1	US-08-987-574-43	Sequence 43, Appl	C 239	14	0.3	14	1	US-08-535-249-75	Sequence 75, Appl
C 167	14.8	0.3	18	1	US-08-535-168-42	Sequence 42, Appl	C 240	14	0.3	14	1	US-08-535-249-91	Sequence 91, Appl
C 168	14.8	0.3	18	1	US-08-535-168-43	Sequence 43, Appl	C 241	14	0.3	14	1	US-08-535-249-103	Sequence 103, App
C 169	14.8	0.3	18	1	US-09-475-316A-122	Sequence 122, App	C 242	14	0.3	14	1	US-08-535-249-106	Sequence 106, App
C 170	14.8	0.3	18	1	US-09-437-076-3	Sequence 3, Appl	C 243	14	0.3	14	1	US-08-535-249-122	Sequence 122, App
C 171	14.8	0.3	18	1	US-09-017-974-42	Sequence 42, Appl	C 244	14	0.3	14	1	US-08-535-249-136	Sequence 136, App
C 172	14.8	0.3	18	1	US-09-017-974-43	Sequence 43, Appl	C 245	14	0.3	14	1	US-09-475-947A-310	Sequence 310, App
C 173	14.8	0.3	18	1	US-08-682-255A-42	Sequence 42, Appl	C 246	14	0.3	14	1	US-08-182-968A-299	Sequence 299, App
C 174	14.8	0.3	18	1	US-08-682-255A-43	Sequence 43, Appl	C 247	14	0.3	15	1	US-08-182-968A-300	Sequence 300, App
C 175	14.8	0.3	18	1	US-09-429-130-42	Sequence 42, Appl	C 248	14	0.3	15	1	US-08-292-620A-359	Sequence 359, App
C 176	14.8	0.3	18	1	US-09-429-130-43	Sequence 43, Appl	C 249	14	0.3	15	1	US-08-292-620A-360	Sequence 360, App
C 177	14.8	0.3	18	1	US-08-535-249-72	Sequence 72, Appl	C 250	14	0.3	15	1	US-08-292-620A-364	Sequence 364, App
C 178	14.8	0.3	18	1	US-08-535-249-79	Sequence 79, Appl	C 251	14	0.3	15	1	US-08-292-620A-365	Sequence 365, App
C 179	14.8	0.3	18	1	US-08-535-249-85	Sequence 85, Appl	C 252	14	0.3	15	1	US-08-292-620A-365	Sequence 365, App

c 253	14	0.3	15	1	US-08-774-306A-299	Sequence 299, App	c 326	13.8	0.3	17	1	US-09-371-772B-5582	Sequence 5582, Ap
c 254	14	0.3	15	1	US-08-774-306A-300	Sequence 300, App	c 327	13.8	0.3	17	1	US-09-371-772B-5583	Sequence 5583, Ap
c 255	14	0.3	15	1	US-08-886-456-1	Sequence 1, Appli	c 328	13.8	0.3	17	1	US-09-371-772B-6814	Sequence 6814, Ap
c 256	14	0.3	15	1	US-08-832-021-18	Sequence 18, Appl	c 329	13.8	0.3	17	1	US-09-597-731-7	Sequence 7, Appli
c 257	14	0.3	15	1	US-08-832-021-19	Sequence 19, Appl	c 330	13.8	0.3	17	1	US-09-476-387-756	Sequence 756, App
c 258	14	0.3	15	1	US-08-832-021-19	Sequence 19, Appl	c 331	13.8	0.3	17	1	US-09-401-063-647	Sequence 647, App
c 259	14	0.3	15	1	US-08-832-021-20	Sequence 20, Appl	c 332	13.8	0.3	17	1	US-09-866-108A-243	Sequence 243, App
c 260	14	0.3	15	1	US-08-832-021-21	Sequence 21, Appl	c 333	13.8	0.3	17	1	US-09-866-108A-1065	Sequence 1065, Ap
c 261	14	0.3	15	1	US-08-832-021-21	Sequence 21, Appl	c 334	13.8	0.3	17	1	US-09-866-108A-1066	Sequence 1066, Ap
c 262	14	0.3	15	1	US-08-832-021-23	Sequence 23, Appl	c 335	13.8	0.3	17	1	US-09-866-108A-2222	Sequence 2222, Ap
c 263	14	0.3	15	1	US-08-832-021-24	Sequence 24, Appl	c 336	13.8	0.3	17	1	US-09-866-108A-8557	Sequence 8557, Ap
c 264	14	0.3	15	1	US-09-064-156A-299	Sequence 299, App	c 337	13.8	0.3	17	1	US-09-866-108A-9226	Sequence 9226, Ap
c 265	14	0.3	15	1	US-09-064-156A-300	Sequence 300, App	c 338	13.8	0.3	17	1	US-09-866-108A-10508	Sequence 10508, A
c 266	14	0.3	15	1	US-09-071-845-359	Sequence 359, App	c 339	13.8	0.3	17	1	US-09-866-108A-10509	Sequence 10509, A
c 267	14	0.3	15	1	US-09-071-845-360	Sequence 360, App	c 340	13.8	0.3	17	1	US-09-129-603-4	Sequence 4, Appli
c 268	14	0.3	15	1	US-09-071-845-364	Sequence 364, App	c 341	13.8	0.3	17	1	US-09-685-664B-235	Sequence 235, App
c 269	14	0.3	15	1	US-09-071-845-365	Sequence 365, App	c 342	13.8	0.3	17	1	US-09-685-664B-731	Sequence 731, App
c 270	14	0.3	16	1	US-08-242-664-30	Sequence 30, Appl	c 343	13.8	0.3	17	1	US-09-685-664B-860	Sequence 860, App
c 271	14	0.3	16	1	US-08-484-138-30	Sequence 30, Appl	c 344	13.8	0.3	17	1	US-09-685-664B-1068	Sequence 1068, Ap
c 272	14	0.3	16	1	PCT-US95-06378-30	Sequence 30, Appl	c 345	13.8	0.3	17	1	US-09-685-664B-1069	Sequence 1069, Ap
c 273	14	0.3	17	1	US-09-300-958A-63	Sequence 63, Appl	c 346	13.8	0.3	17	1	US-09-685-664B-1070	Sequence 1070, Ap
c 274	13.8	0.3	17	1	US-09-090-672B-105	Sequence 105, App	c 347	13.8	0.3	17	1	US-09-685-664B-1071	Sequence 1071, Ap
c 275	13.8	0.3	17	1	US-09-300-958A-63	Sequence 63, Appl	c 348	13.8	0.3	17	1	US-09-685-664B-1075	Sequence 1075, Ap
c 276	13.8	0.3	17	1	US-08-281-940-54	Sequence 54, Appl	c 349	13.8	0.3	17	1	US-09-685-664B-1076	Sequence 1076, Ap
c 277	13.8	0.3	17	1	US-08-758-306-1333	Sequence 1333, Ap	c 350	13.8	0.3	17	1	US-09-685-664B-1080	Sequence 1080, Ap
c 278	13.8	0.3	17	1	US-08-710-134-54	Sequence 54, Appl	c 351	13.8	0.3	17	1	US-09-685-664B-1251	Sequence 1251, Ap
c 279	13.8	0.3	17	1	US-08-485-885-54	Sequence 54, Appl	c 352	13.8	0.3	17	1	US-09-685-664B-1772	Sequence 1772, Ap
c 280	13.8	0.3	17	1	US-08-985-162-647	Sequence 647, App	c 353	13.8	0.3	17	1	US-09-685-664B-1781	Sequence 1781, Ap
c 281	13.8	0.3	17	1	US-09-998-099-52	Sequence 52, Appl	c 354	13.8	0.3	17	1	US-09-685-664B-1781	Sequence 2067, Ap
c 282	13.8	0.3	17	1	US-09-135-020-7	Sequence 7, Appli	c 355	13.8	0.3	17	1	US-09-685-664B-2453	Sequence 2453, Ap
c 283	13.8	0.3	17	1	US-09-444-871-7	Sequence 7, Appli	c 356	13.8	0.3	17	1	US-09-685-664B-2800	Sequence 2800, Ap
c 284	13.8	0.3	17	1	US-08-584-040-1690	Sequence 1690, Ap	c 357	13.8	0.3	17	1	US-09-685-664B-3418	Sequence 3418, Ap
c 285	13.8	0.3	17	1	US-08-584-040-2186	Sequence 2186, Ap	c 358	13.8	0.3	17	1	US-09-090-672B-107	Sequence 107, Appl
c 286	13.8	0.3	17	1	US-08-584-040-2315	Sequence 2315, Ap	c 359	13.8	0.3	33	1	US-09-750-401-29	Sequence 29, Appl
c 287	13.8	0.3	17	1	US-08-584-040-2544	Sequence 2544, Ap	c 360	13.6	0.3	16	1	US-08-882-649A-8	Sequence 8, Appli
c 288	13.8	0.3	17	1	US-08-584-040-2545	Sequence 2545, Ap	c 361	13.6	0.3	16	1	US-08-644-827B-10	Sequence 10, Appli
c 289	13.8	0.3	17	1	US-08-584-040-2546	Sequence 2546, Ap	c 362	13.4	0.3	15	1	US-08-363-240A-33	Sequence 33, Appl
c 290	13.8	0.3	17	1	US-08-584-040-2547	Sequence 2547, Ap	c 363	13.4	0.3	15	1	US-08-292-620A-356	Sequence 356, App
c 291	13.8	0.3	17	1	US-08-584-040-2551	Sequence 2551, Ap	c 364	13.4	0.3	15	1	US-08-292-620A-357	Sequence 357, App
c 292	13.8	0.3	17	1	US-08-584-040-2552	Sequence 2552, Ap	c 365	13.4	0.3	15	1	US-08-292-620A-358	Sequence 358, App
c 293	13.8	0.3	17	1	US-08-584-040-2556	Sequence 2556, Ap	c 366	13.4	0.3	15	1	US-08-292-620A-363	Sequence 363, App
c 294	13.8	0.3	17	1	US-08-584-040-2727	Sequence 2727, Ap	c 367	13.4	0.3	15	1	US-08-292-620A-366	Sequence 366, App
c 295	13.8	0.3	17	1	US-08-584-040-4005	Sequence 4005, Ap	c 368	13.4	0.3	15	1	US-08-585-684B-824	Sequence 824, App
c 296	13.8	0.3	17	1	US-08-584-040-4014	Sequence 4014, Ap	c 369	13.4	0.3	15	1	US-08-585-684B-825	Sequence 825, App
c 297	13.8	0.3	17	1	US-08-584-040-4300	Sequence 4300, Ap	c 370	13.4	0.3	15	1	US-08-585-684B-1392	Sequence 1392, Ap
c 298	13.8	0.3	17	1	US-08-584-040-5563	Sequence 5563, Ap	c 371	13.4	0.3	15	1	US-08-879-457-2	Sequence 2, Appli
c 299	13.8	0.3	17	1	US-08-584-040-5963	Sequence 5963, Ap	c 372	13.4	0.3	15	1	US-08-893-204C-2	Sequence 2, Appli
c 300	13.8	0.3	17	1	US-08-584-040-7626	Sequence 7626, Ap	c 373	13.4	0.3	15	1	US-08-832-021-25	Sequence 25, Appli
c 301	13.8	0.3	17	1	US-08-679-645-878	Sequence 878, App	c 374	13.4	0.3	15	1	US-08-832-021-26	Sequence 26, Appli
c 302	13.8	0.3	17	1	US-09-597-735-7	Sequence 7, Appli	c 375	13.4	0.3	15	1	US-08-832-021-29	Sequence 29, Appl
c 303	13.8	0.3	17	1	US-09-444-295-7	Sequence 7, Appli	c 376	13.4	0.3	15	1	US-08-832-021-34	Sequence 34, Appl
c 304	13.8	0.3	17	1	US-09-597-732-7	Sequence 7, Appli	c 377	13.4	0.3	15	1	US-08-832-021-36	Sequence 36, Appl
c 305	13.8	0.3	17	1	US-09-475-947A-118	Sequence 118, App	c 378	13.4	0.3	15	1	US-08-832-021-41	Sequence 41, Appl
c 306	13.8	0.3	17	1	US-09-474-432B-757	Sequence 757, App	c 379	13.4	0.3	15	1	US-08-832-021-43	Sequence 43, Appl
c 307	13.8	0.3	17	1	US-09-371-772B-235	Sequence 235, App	c 380	13.4	0.3	15	1	US-08-832-021-46	Sequence 46, Appl
c 308	13.8	0.3	17	1	US-09-371-772B-731	Sequence 731, App	c 381	13.4	0.3	15	1	US-08-832-021-53	Sequence 53, Appl
c 309	13.8	0.3	17	1	US-09-371-772B-860	Sequence 860, App	c 382	13.4	0.3	15	1	US-08-832-021-58	Sequence 58, Appl
c 310	13.8	0.3	17	1	US-09-371-772B-1068	Sequence 1068, Ap	c 383	13.4	0.3	15	1	US-08-675-119-2	Sequence 2, Appli
c 311	13.8	0.3	17	1	US-09-371-772B-1069	Sequence 1069, Ap	c 384	13.4	0.3	15	1	US-08-851-843A-43	Sequence 43, Appl
c 312	13.8	0.3	17	1	US-09-371-772B-1071	Sequence 1071, Ap	c 385	13.4	0.3	15	1	US-08-851-843A-45	Sequence 45, Appl
c 313	13.8	0.3	17	1	US-09-371-772B-1071	Sequence 1071, Ap	c 386	13.4	0.3	15	1	US-09-071-845-356	Sequence 356, App
c 314	13.8	0.3	17	1	US-09-371-772B-1075	Sequence 1075, Ap	c 387	13.4	0.3	15	1	US-09-071-845-357	Sequence 357, App
c 315	13.8	0.3	17	1	US-09-371-772B-1076	Sequence 1076, Ap	c 388	13.4	0.3	15	1	US-09-071-845-358	Sequence 358, App
c 316	13.8	0.3	17	1	US-09-371-772B-1080	Sequence 1080, Ap	c 389	13.4	0.3	15	1	US-09-071-845-363	Sequence 363, App
c 317	13.8	0.3	17	1	US-09-371-772B-1251	Sequence 1251, Ap	c 390	13.4	0.3	15	1	US-09-071-845-366	Sequence 366, App
c 318	13.8	0.3	17	1	US-09-371-772B-1772	Sequence 1772, Ap	c 391	13.4	0.3	15	1	US-08-974-549A-113	Sequence 113, App
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c 320	13.8	0.3	17	1	US-09-371-772B-2067	Sequence 2067, Ap	c 393	13.4	0.3	15	1	US-09-038-073-825	Sequence 825, App
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c 323	13.8	0.3	17	1	US-09-371-772B-3418	Sequence 3418, Ap	c 396	13.4	0.3	15	1	US-08-854-050-45	Sequence 45, Appl
c 324	13.8	0.3	17	1	US-09-371-772B-5235	Sequence 5235, Ap	c 397	13.4	0.3	15	1	US-09-430-323-43	Sequence 43, Appl
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400	13.4	0.3	15	1	US-09-402-181B-113	Sequence 113, App
401	13.4	0.3	15	1	US-09-721-456-113	Sequence 113, App
402	13.4	0.3	15	1	US-09-766-253-43	Sequence 43, Appl
403	13.4	0.3	15	1	US-09-766-253-45	Sequence 45, Appl
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c 405	13.4	0.3	16	1	US-08-455-627-6	Sequence 6, Appli
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407	13.4	0.3	16	1	US-08-311-760A-383	Sequence 383, App
c 408	13.4	0.3	16	1	US-08-461-271-6	Sequence 6, Appli
c 409	13.4	0.3	16	1	US-08-713-685A-6	Sequence 6, Appli
c 410	13.4	0.3	16	1	US-08-689-856-6	Sequence 6, Appli
c 411	13.4	0.3	16	1	US-08-774-310-375	Sequence 375, App
412	13.4	0.3	16	1	US-08-774-310-383	Sequence 383, App
413	13.4	0.3	16	1	US-08-947-317-4	Sequence 4, Appli
c 414	13.4	0.3	16	1	US-09-070-477-6	Sequence 6, Appli
c 415	13.4	0.3	16	1	US-09-411-628-1	Sequence 1, Appli
c 416	13.4	0.3	16	1	US-08-535-249-109	Sequence 109, App
c 417	13.4	0.3	16	1	US-08-535-249-131	Sequence 131, App
418	13.4	0.3	16	1	US-09-300-958A-57	Sequence 57, Appl
419	13.4	0.3	16	1	US-09-300-958A-85	Sequence 85, Appl
420	13.4	0.3	16	1	US-09-527-972-16	Sequence 16, Appl
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422	13.4	0.3	16	1	US-10-174-794-1	Sequence 1, Appli
423	13.4	0.3	16	1	5262177-6	Patent No. 5262177
424	13.4	0.3	16	1	5262177-6	Patent No. 5262177
c 425	13.4	0.3	25	1	US-09-396-1960-60889	Sequence 60889, A
c 426	13.2	0.3	14	1	US-09-300-958A-65	Sequence 65, Appl
427	13	0.3	14	1	US-08-832-021-5	Sequence 5, Appli
428	13	0.3	14	1	US-08-724-466B-17	Sequence 17, Appl
429	13	0.3	14	1	US-08-882-164D-17	Sequence 17, Appl
c 430	13	0.3	15	1	US-08-863-639A-8	Sequence 8, Appli
431	13	0.3	15	1	US-08-832-021-17	Sequence 17, Appl
432	13	0.3	15	1	US-08-832-021-18	Sequence 18, Appl
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c 434	13	0.3	15	1	US-08-832-021-43	Sequence 43, Appl
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436	12.8	0.3	16	1	US-08-455-627-6	Sequence 6, Appli
437	12.8	0.3	16	1	US-08-461-271-6	Sequence 6, Appli
438	12.8	0.3	16	1	US-08-713-685A-6	Sequence 6, Appli
439	12.8	0.3	16	1	US-08-689-856-6	Sequence 6, Appli
c 440	12.8	0.3	16	1	US-09-070-477-6	Sequence 6, Appli
c 441	12.8	0.3	16	1	US-09-411-628-1	Sequence 1, Appli
c 442	12.8	0.3	16	1	US-09-300-958A-57	Sequence 57, Appl
c 443	12.8	0.3	16	1	US-09-300-958A-85	Sequence 85, Appl
c 444	12.8	0.3	16	1	US-09-527-972-16	Sequence 16, Appl
c 445	12.8	0.3	16	1	US-10-174-794-1	Sequence 1, Appli
446	12.8	0.3	17	1	US-09-090-672B-105	Sequence 105, App
447	12.8	0.3	18	1	US-09-725-265-20	Sequence 20, Appl
448	12.8	0.3	18	1	US-09-556-127-20	Sequence 20, Appl
c 449	12.8	0.3	39	1	US-08-486-057B-6	Sequence 6, Appli
c 450	12.8	0.3	39	1	US-08-789-588-6	Sequence 6, Appli
c 451	12.6	0.3	20	1	US-09-725-265-42	Sequence 42, Appl
c 452	12.6	0.3	20	1	US-09-823-634A-13	Sequence 13, Appl
c 453	12.6	0.3	20	1	US-09-823-634A-14	Sequence 14, Appl
c 454	12.6	0.3	20	1	US-09-823-647B-13	Sequence 13, Appl
c 455	12.6	0.3	20	1	US-09-823-647B-14	Sequence 14, Appl
456	12.6	0.3	20	1	US-09-556-127-42	Sequence 42, Appl
c 457	12.6	0.3	21	1	US-09-009-913-100	Sequence 100, App
c 458	12.6	0.3	39	1	US-08-486-057B-7	Sequence 7, Appli
459	12.6	0.3	39	1	US-08-789-588-7	Sequence 7, Appli
460	12.4	0.3	15	1	US-08-292-620A-359	Sequence 359, App
461	12.4	0.3	15	1	US-08-292-620A-360	Sequence 360, App
462	12.4	0.3	15	1	US-08-292-620A-365	Sequence 365, App
463	12.4	0.3	15	1	US-08-832-021-23	Sequence 23, Appl
464	12.4	0.3	15	1	US-09-071-845-359	Sequence 359, App
465	12.4	0.3	15	1	US-09-071-845-360	Sequence 360, App
466	12.4	0.3	15	1	US-09-071-845-365	Sequence 365, App
467	12.4	0.3	15	1	US-08-292-620A-366	Sequence 366, App
468	12.4	0.3	15	1	US-08-832-021-41	Sequence 41, Appl
469	12.4	0.3	15	1	US-09-071-845-366	Sequence 366, App
470	12.4	0.3	17	1	US-08-584-040-2186	Sequence 2186, App
471	12.4	0.3	17	1	US-09-371-772B-731	Sequence 731, App
472	12.4	0.3	17	1	US-09-685-664B-731	Sequence 731, App
473	12.4	0.3	18	1	US-08-330-000-1	Sequence 1, Appli
474	12.4	0.3	18	1	US-08-965-908-1	Sequence 1, Appli
475	12.4	0.3	18	1	US-09-725-265-17	Sequence 17, Appl
476	12.4	0.3	18	1	US-09-556-127-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-08-486-057B-6

; Sequence 6, Application US/08486057B

; Patent No. 5650494

; GENERAL INFORMATION:

; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.

; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert

; APPLICANT: Meyhack, Bernd

; TITLE OF INVENTION: Process for Refolding Recombinantly Produced TGF-beta-like Proteins

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Henry P. No. 5650494ak

; STREET: 520 White Plains Road, P.O. Box 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,057B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/201,703

FILING DATE: 25-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,309

FILING DATE: 13-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,502

FILING DATE: 03-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8927546.5

FILING DATE: 06-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: No. 5650494ak, Henry P.

REGISTRATION NUMBER: 33200

REFERENCE/DOCKET NUMBER: 4-17861/+Cont3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 277-5110

TELEFAX: (908) 277-4306

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-486-057B-6

Query Match 0.8%; Score 35.8; DB 1; Length 39;

Best Local Similarity 94.9%; Pred. No. 0.63;

Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2124 GCTTTGGATGCTGCTACTGCTTTAGAAATGTCAGGAT 2162

|||||

Db 1 GCTTGGATGGCGCCTATTGCTTTAGAAATGTCAGGAT 39

RESULT 2

US-08-789-588-6

; Sequence 6' Application US/08789588

; Patent No. 5922846

; GENERAL INFORMATION:

; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.

; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert

; APPLICANT: Meyhack, Bernd

; TITLE OF INVENTION: Process for Refolding Recombinantly

; TITLE OF INVENTION: Produced TGF-beta-like Proteins

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Henry P. No. 5922846ak

; STREET: 520 White Plains Road, P.O. Box 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10591-9005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/789,588

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/486,057

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/201,703

; FILING DATE: 25-FEB-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/960,309

; FILING DATE: 13-OCT-1992

; APPLICATION NUMBER: US 07/621,502

; FILING DATE: 03-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 8927546.5

; FILING DATE: 06-DEC-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5922846ak, Henry P.

; REGISTRATION NUMBER: 33200

; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 277-5110

; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-789-588-6

Query Match 0.8%; Score 35.8; DB 1; Length 39;

Best Local Similarity 94.9%; Pred. No. 0.63;

Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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|||||

Db 1 GCTTGGATGCGCCTATTGCTTTAGAAATGTCAGGAT 39

RESULT 3

US-08-486-057B-7/c

; Sequence 7, Application US/08486057B

; Patent No. 5650494

; GENERAL INFORMATION:

; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.

; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert

; APPLICANT: Meyhack, Bernd

; TITLE OF INVENTION: Process for Refolding Recombinantly

; TITLE OF INVENTION: Produced TGF-beta-like Proteins

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Henry P. No. 5650494ak

; STREET: 520 White Plains Road, P.O. Box 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10591-9005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,057B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/201,703

; FILING DATE: 25-FEB-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/960,309

; FILING DATE: 13-OCT-1992

; APPLICATION NUMBER: US 07/621,502

; FILING DATE: 03-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 8927546.5

; FILING DATE: 06-DEC-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5650494ak, Henry P.

; REGISTRATION NUMBER: 33200

; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 277-5110

; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-486-057B-7

Query Match 0.8%; Score 34.2; DB 1; Length 39;

Best Local Similarity 92.3%; Pred. No. 1.2;

Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 39 CTTTCAATATGATGTCAGTCTTGTAATGCGACTAA 1

RESULT 4

US-08-789-588-7/c

; Sequence 7, Application US/08789588

; Patent No. 5922846

; GENERAL INFORMATION:

; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.

; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert

APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-789-588-7

Query Match 0.8%; Score 34.2; DB 1; Length 39;
Best Local Similarity 92.3%; Pred. No. 1.2;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2424 CTTTCAATATGATTGTCAGTCTTTGTAATGAGCTAA 2462
DB 39 CTTTCAATATGATTGTCAGTCTTTGTAATGAGCTAA 1
RESULT 5
US-09-750-401-29
Sequence 29, Application US/09750401
Patent No. 6635422
GENERAL INFORMATION:
APPLICANT: Keene, Jack D.
APPLICANT: Carson, Craig C.
APPLICANT: Tenenbaum, Scott A.
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
TITLE OF INVENTION: complexes
FILE REFERENCE: RBN-001
CURRENT APPLICATION NUMBER: US/09/750,401
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,338

PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 33
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-29
Query Match 0.8%; Score 33; DB 1; Length 33;
Best Local Similarity 33.3%; Pred. No. 1.2;
Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
QY 3264 TTTTTCCTTTTAAATGTAAATGGTTCCTTT 3296
DB 1 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33
RESULT 6
US-09-750-401-31
Sequence 31, Application US/09750401
Patent No. 6635422
GENERAL INFORMATION:
APPLICANT: Keene, Jack D.
APPLICANT: Carson, Craig C.
APPLICANT: Tenenbaum, Scott A.
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
TITLE OF INVENTION: complexes
FILE REFERENCE: RBN-001
CURRENT APPLICATION NUMBER: US/09/750,401
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,338
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 25
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-31
Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 36.0%; Pred. No. 11;
Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY 3693 TTCAATTTTTCATATATATATCTTT 3717
DB 1 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 25
RESULT 7
US-09-396-196G-60887
Sequence 60887, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60887
LENGTH: 25


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; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60887

Query Match      0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GACTTGCACCTACAAATTCATTTT 25

RESULT 8
US-09-396-196G-60888
; Sequence 60888, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60888

Query Match      0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3705 TATATACTATCTCCCTGCTGTAT 3729
      |||
Db 1 TATATACTATCTCCCTGCTGTAT 25

RESULT 9
US-09-396-196G-60889
; Sequence 60889, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889

Query Match      0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3966 TTAAAGATCTCAACTCAGAGTCTT 3990
      |||
Db 1 TTAAAGATCTCAACTCAGAGTCTT 25

; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60890

Query Match      0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4026 TATTATGGACTCTCTTTCGGTTC 4050
      |||
Db 1 TATTATGGACTCTCTTTCGGTTC 25

RESULT 10
US-09-396-196G-60890
; Sequence 60890, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60890
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60890

Query Match      0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4026 TATTATGGACTCTCTTTCGGTTC 4050
      |||
Db 1 TATTATGGACTCTCTTTCGGTTC 25

RESULT 11
US-09-396-196G-60891
; Sequence 60891, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60891
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60891

Query Match      0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTTCGGTTCAAA 4053
      |||
Db 1 TTATGGACTCTCTTTCGGTTCAAA 25

RESULT 12
US-09-396-196G-60892
; Sequence 60892, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
```

102.6
68.1/24

```

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60892

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4038 CTCCTTGCCGTTCAAAAGCAGACAG 4062
Db 1 CTCCTTGCCGTTCAAAAGCAGACAG 25

RESULT 13
US-09-396-196G-60893
; Sequence 60893, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60893

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4158 AAAGTCCAGGCCAGCACTGCTCATT 4182
Db 1 AAAGTCCAGGCCAGCACTGCTCATT 25

RESULT 14
US-09-396-196G-60894
; Sequence 60894, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60896

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4170 AGCACTCGTCATTTTATTTCATAATT 4194
Db 1 AGCACTCGTCATTTTATTTCATAATT 25

RESULT 15
US-09-396-196G-60895
; Sequence 60895, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60895

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4173 ACTCGTCATTTTATTTCATAATTCA 4197
Db 1 ACTCGTCATTTTATTTCATAATTCA 25

RESULT 16
US-09-396-196G-60896
; Sequence 60896, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60896

```

```
Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4188 CATAATTCATCCATTATTTCCCTG 4212
Db 1 CATAATTCATCCATTATTTCCCTG 25

RESULT 17
US-09-396-196G-60897
; Sequence 60897, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60897
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60897

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4194 TTCATCCATTATTTCCCTGATTTC 4218
Db 1 TTCATCCATTATTTCCCTGATTTC 25

RESULT 18
US-09-396-196G-60898
; Sequence 60898, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60898

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4200 CATTATTTCCCTGATTTCATTGAAA 4224
Db 1 CATTATTTCCCTGATTTCATTGAA 25

RESULT 19
US-09-396-196G-60899
; Sequence 60899, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60899
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60899

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3708 ATACTATCTTCCTGCCTGCTGATTTT 3732
Db 1 ATACTATCTTCCTGCCTGCTGATTTT 25

RESULT 20
US-09-396-196G-60900
; Sequence 60900, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60900
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60900

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3750 TGACATGAGCTACCTGGGTCCATTC 3774
Db 1 TGACATGAGCTACCTGGGTCCATTC 25

RESULT 21
US-09-396-196G-60901
; Sequence 60901, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
```

```

; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60901

```

```

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3753 CATGAGCTACCTGGTCCATTCCTC 3777
Db 1 CATGAGCTACCTGGTCCATTCCTC 25

```

```

RESULT 22
US-09-396-196G-60902
; Sequence 60902, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60902

```

```

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 3834 AGGTTTGAGCTCCACAGTGTTCAG 3858
Db 1 AGGTTTGAGCTCCACAGTGTTCAG 25

```

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RESULT 23
US-09-396-196G-60903
; Sequence 60903, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60903

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60903

```

```

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3840 GAGTCCACAGTGTTCAGCCTTTT 3864
Db 1 GAGTCCACAGTGTTCAGCCTTTT 25

```

```

RESULT 24
US-09-396-196G-60904
; Sequence 60904, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60904
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60904

```

```

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3858 GCCTTTTCGCTCAGTGTGAGTCA 3882
Db 1 GCCTTTTCGCTCAGTGTGAGTCA 25

```

```

RESULT 25
US-09-396-196G-60905
; Sequence 60905, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60905
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60905

```

```

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 3861 TTTTCTGCGTCACTGTGAGTCATGT 3885
Db 1 TTTTCTGCGTCACTGTGAGTCATGT 25

RESULT 26
US-09-396-196G-60906
; Sequence 60906, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60906

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3864 TCTGCGTCACTGTGAGTCATGTGGC 3888
Db 1 TCTGCGTCACTGTGAGTCATGTGGC 25

RESULT 27
US-09-750-401-32
; Sequence 32, Application US/09750401
; Patent No. 6635422
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: complexes
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-32

Query Match 0.5%; Score 22; DB 1; Length 22;
Best Local Similarity 22.7%; Pred. No. 24;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTTAATGGTTTTTT 4099
Db 1 UUUUUCUUAAUUGUUUUUU 22

RESULT 28
US-09-380-662-8
```

```
; Sequence 8, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-380-662-8

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 CATCTGTCCTCGGTGGCGCT 1273
Db 1 CATCTGTCCTCGGTGGCGCT 20

RESULT 29
US-09-661-753-48/c
; Sequence 48, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-48

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAAACTGCCGCGC 53
Db 20 GAGCTGCTGAAACTGCCGCGC 1

RESULT 30
US-09-661-753-49/c
; Sequence 49, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
```

; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-49

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 AAGCTAGGGAAGGTGGAG 278
Db 20 AAGCTAGGGAAGGTGGAG 1

RESULT 31
US-09-661-753-50/c
; Sequence 50, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-50

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 TGGCCGCGCTGGAGCAAGAA 381
Db 20 TGGCCGCGCTGGAGCAAGAA 1

RESULT 32
US-09-661-753-51/c
; Sequence 51, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-51

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GGGATCCTCGCGCGCTGCTC 512
Db 20 GGGATCCTCGCGCGCTGCTC 1

RESULT 33
US-09-661-753-52/c
; Sequence 52, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-52

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 ACACGTGTGGAAGGCGGCGC 690
Db 20 ACACGTGTGGAAGGCGGCGC 1

RESULT 34
US-09-661-753-53/c
; Sequence 53, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-53

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 830 TCAGATCAGCCACTCCGCAC 849
Db 20 TCAGATCAGCCACTCCGCAC 1

RESULT 35
US-09-661-753-54/c

```
/ Sequence 54, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 54
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-54

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1016 TTGGGAACGCGTGCAATTT 1035
Db 20 TTGGGAACGCGTGCAATTT 1

RESULT 36
US-09-661-753-55/c
/ Sequence 55, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 55
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-55

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 GCTCTGCACTCGTCCCGG 1266
Db 20 GCTCTGCACTCGTCCCGG 1

RESULT 37
US-09-661-753-56/c
/ Sequence 56, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 56
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-56/c

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 GCTCTGCACTCGTCCCGG 1266
Db 20 GCTCTGCACTCGTCCCGG 1

RESULT 38
US-09-661-753-57/c
/ Sequence 57, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 57
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-57

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 GTCTTCGCTTGCAAAACCC 1687
Db 20 GTCTTCGCTTGCAAAACCC 1

RESULT 39
US-09-661-753-58/c
/ Sequence 58, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 58
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-58

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 GTCTTCGCTTGCAAAACCC 1687
Db 20 GTCTTCGCTTGCAAAACCC 1
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1754 TCCACCCAGCGCTACATCG 1773
 DB 20 TCCACCCAGCGCTACATCG 1

RESULT 40
 US-09-661-753-59/c
 ; Sequence 59, Application US/09661753
 ; Patent No. 6436909
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: Susan F. Murray
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
 ; FILE REFERENCE: ISPH-0498
 ; CURRENT APPLICATION NUMBER: US/09/661,753
 ; CURRENT FILING DATE: 2000-09-14
 ; EARLIER APPLICATION NUMBER: 60/154,546
 ; EARLIER FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 68
 ; SEQ ID NO 59
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-661-753-59

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2032 AAAAAACAGTGGGAGACC 2051
 DB 20 AAAAAACAGTGGGAGACC 1

RESULT 41
 US-09-661-753-60/c
 ; Sequence 60, Application US/09661753
 ; Patent No. 6436909
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: Susan F. Murray
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
 ; FILE REFERENCE: ISPH-0498
 ; CURRENT APPLICATION NUMBER: US/09/661,753
 ; CURRENT FILING DATE: 2000-09-14
 ; EARLIER APPLICATION NUMBER: 60/154,546
 ; EARLIER FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 68
 ; SEQ ID NO 60
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-661-753-60

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2321 CACCATAATCCGAGCTT 2340
 DB 20 CACCATAATCCGAGCTT 1

RESULT 42
 US-09-661-753-61/c
 ; Sequence 61, Application US/09661753
 ; Patent No. 6436909

; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: Susan F. Murray
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
 ; FILE REFERENCE: ISPH-0498
 ; CURRENT APPLICATION NUMBER: US/09/661,753
 ; CURRENT FILING DATE: 2000-09-14
 ; EARLIER APPLICATION NUMBER: 60/154,546
 ; EARLIER FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 68
 ; SEQ ID NO 61
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-661-753-61

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2478 CAGGACGAAAAATCACGGT 2497
 DB 20 CAGGACGAAAAATCACGGT 1

RESULT 43
 US-09-661-753-62/c
 ; Sequence 62, Application US/09661753
 ; Patent No. 6436909
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: Susan F. Murray
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
 ; FILE REFERENCE: ISPH-0498
 ; CURRENT APPLICATION NUMBER: US/09/661,753
 ; CURRENT FILING DATE: 2000-09-14
 ; EARLIER APPLICATION NUMBER: 60/154,546
 ; EARLIER FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 68
 ; SEQ ID NO 62
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-661-753-62

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2854 ACGTATTGTTCCAGCCGC 2873
 DB 20 ACGTATTGTTCCAGCCGC 1

RESULT 44
 US-09-661-753-63/c
 ; Sequence 63, Application US/09661753
 ; Patent No. 6436909
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: Susan F. Murray
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
 ; FILE REFERENCE: ISPH-0498
 ; CURRENT APPLICATION NUMBER: US/09/661,753
 ; CURRENT FILING DATE: 2000-09-14
 ; EARLIER APPLICATION NUMBER: 60/154,546
 ; EARLIER FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 68
 ; SEQ ID NO 63


```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-63

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3075 GAACTCAATAAGCCAGGGG 3094
Db 20 GAACTCAATAAGCCAGGGG 1

RESULT 45
US-09-661-753-64/c
; Sequence 64, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-64

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3297 GCCAGTTTAAGCAAGCCGGT 3316
Db 20 GCCAGTTTAAGCAAGCCGGT 1

RESULT 46
US-09-661-753-65/c
; Sequence 65, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-65

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3352 TTTTGACCGTGAAGTGGCTG 3371
Db 20 TTTTGACCGTGAAGTGGCTG 1

RESULT 47
US-09-661-753-66/c
; Sequence 66, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-66

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3753 CATGAGCTACCTGGGTCCAT 3772
Db 20 CATGAGCTACCTGGGTCCAT 1

RESULT 48
US-09-661-753-67/c
; Sequence 67, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-67

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3874 TGTGAGTCATGTGGCGGGTG 3893
Db 20 TGTGAGTCATGTGGCGGGTG 1

RESULT 49
US-09-661-753-68/c
; Sequence 68, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
```

; APPLICANT: Susan F. Murray
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
 ; FILE REFERENCE: ISPH-0498
 ; CURRENT APPLICATION NUMBER: US/09/661,753
 ; CURRENT FILING DATE: 2000-09-14
 ; EARLIER APPLICATION NUMBER: 60/154,546
 ; EARLIER FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 68
 ; SEQ ID NO 68
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-661-753-68

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4097 TTTGGTCTCATGGGTGTA 4116
 Db 20 TTTGGTCTCATGGGTGTA 1

RESULT 50
 US-08-478-470-13
 ; Sequence 13, Application US/08478470
 ; Patent No. 5591607
 ; GENERAL INFORMATION:
 ; APPLICANT: GRYAZNOV, SERGEI
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE
 ; TITLE OF INVENTION: N3'-P5' PHOSPHORAMIDATES:
 ; TITLE OF INVENTION: HYBRIDIZATION AND NUCLEASE
 ; TITLE OF INVENTION: RESISTANCE PROPERTIES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro
 ; ADDRESSEE: Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; STREET: 3000 El Camino Real
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306

; COMPUTER READABLE FORM: disk
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,470
 ; FILING DATE: June 6, 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: John D. Mendlein
 ; REGISTRATION NUMBER: 38,770
 ; REFERENCE/DOCKET NUMBER: LYNX-005/020US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 843-5020
 ; TELEFAX: (415) 857-0663
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO

; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: DNA Target, Experiment 7,
 ; INDIVIDUAL ISOLATE: Fig. 2

US-08-478-470-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 88;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTTTTT 2754
 Db 1 AAAAGAAAAACCCCTTTTTTTT 24

RESULT 51
 US-08-214-599-13
 ; Sequence 13, Application US/08214599
 ; Patent No. 5599922
 ; GENERAL INFORMATION:
 ; APPLICANT: Gryaznov, Sergei
 ; TITLE OF INVENTION: Oligonucleotide N3'-P5'
 ; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
 ; TITLE OF INVENTION: Properties
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/214,599
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 5525-0012
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO

; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
 US-08-214-599-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 88;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTTTTT 2754
 Db 1 AAAAGAAAAACCCCTTTTTTTT 24

RESULT 52
 US-08-473-015-13
 ; Sequence 13, Application US/08473015
 ; Patent No. 5631135
 ; GENERAL INFORMATION:
 ; APPLICANT: Gryaznov, Sergei
 ; TITLE OF INVENTION: Oligonucleotide N3'-P5'

```
/ TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
/ TITLE OF INVENTION: Properties
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/473,015
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/214,599 - 584922
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 5525-0012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
/ US-08-473-015-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAAAAAAACCCCTTTTITTTT 24

RESULT 53
US-08-465-368-13
/ Sequence 13, Application US/08465368
/ Patent No. 5726297
/ GENERAL INFORMATION:
/ APPLICANT: Gryaznov, Sergei
/ APPLICANT: Schultz, Ronald G.
/ APPLICANT: Chen, Jer-kang
/ TITLE OF INVENTION: OLIGODXRYBONUCLEOTIDE
/ TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/465,368
/ FILING DATE: 05-JUN-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/210,505
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 5525-0013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
/ US-08-465-368-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAAAAAAACCCCTTTTITTTT 24

RESULT 54
US-08-477-306-13
/ Sequence 13, Application US/08477306
/ Patent No. 5837835
/ GENERAL INFORMATION:
/ APPLICANT: Gryaznov, Sergei
/ TITLE OF INVENTION: Oligonucleotide N3'-P5'
/ TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,306
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/214,599
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 5525-0012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
```

TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
 US-08-477-306-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 88;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTITTTT 2754
 DB 1 AAAAGAAAAACCCCTTTTITTTT 24

RESULT 55
 US-08-700-448-13
 Sequence 13, Application US/08700448
 Patent No. 5965720

GENERAL INFORMATION:
 APPLICANT: Gryaznov, Sergei et al.
 TITLE OF INVENTION: Oligonucleotide N3'-p5',
 TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/700,448
 FILING DATE: 01/10/97
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent M. Powers
 REGISTRATION NUMBER: 36,246
 REFERENCE/DOCKET NUMBER: 5525-0012.10

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0960
 TELEFAX: (650) 324-0960
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
 US-08-700-448-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 88;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTITTTT 2754
 DB 1 AAAAGAAAAACCCCTTTTITTTT 24

RESULT 56

US-08-923-386A-13
 Sequence 13, Application US/08923386A
 Patent No. 6169170
 GENERAL INFORMATION:
 APPLICANT: Gryaznov, Sergei
 TITLE OF INVENTION: Oligonucleotide N3'-p5',
 TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/923,386A
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 5525-0012

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 3
 US-08-923-386A-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 88;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTITTTT 2754
 DB 1 AAAAGAAAAACCCCTTTTITTTT 24

RESULT 57

US-09-655-804B-67
 Sequence 67, Application US/09655804B
 Patent No. 6548251
 GENERAL INFORMATION:
 APPLICANT: KOZYAVKIN, Sergei
 APPLICANT: MALYKH, Andrei
 APPLICANT: POLOUCHINE, Nikolai
 APPLICANT: SLESAREV, Alexei
 TITLE OF INVENTION: INHIBITION OF MOLECULAR AND BIOLOGICAL PROCESSES USING MODIFIED
 TITLE OF INVENTION: OLIGONUCLEOTIDES
 FILE REFERENCE: 107070
 CURRENT APPLICATION NUMBER: US/09/655,804B

```

RESULT 61
US-08-458-367-18
  Sequence 18, Application US/08458367
  Patent No. 5783433
  GENERAL INFORMATION:
  APPLICANT: Frenz, John
  APPLICANT: Shire, Steven J.
  APPLICANT: Sliwowski, Mary B.
  TITLE OF INVENTION: PURIFIED FORMS OF DNase
  NUMBER OF SEQUENCES: 18
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Genentech, Inc.
  STREET: 460 Point San Bruno Blvd
  CITY: South San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94080
  COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: WinPatIn (Genentech)

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;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/458,367
;/ FILING DATE: 02-Jun-1995
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/409631
;/ FILING DATE: 22-Mar-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/348284
;/ FILING DATE: 30-No. 5783433-1994
;/ PRIOR APPLICATION DATA: 08/116186
;/ APPLICATION NUMBER: 08/116186
;/ FILING DATE: 02-Sep-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 07/895300
;/ FILING DATE: 08-Jun-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Johnston, Sean A.
;/ REGISTRATION NUMBER: 35,910
;/ REFERENCE/DOCKET NUMBER: P0747C4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415/225-3562
;/ TELEFAX: 415/952-9881
;/ TELEX: 910/371-7168
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 22 base pairs
;/ TYPE: Nucleic Acid
;/ STRANDEDNESS: Single
;/ TOPOLOGY: Linear
;/ US-08-458-367-18

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGCGC 636
Db 1 GCGCGCGCGCGCGCGCGCGC 22

RESULT 62
US-08-458-367-18/c
;/ Sequence 18, Application US/08458367
;/ Patent No. 5783433
;/ GENERAL INFORMATION:
;/ APPLICANT: Frenz, John
;/ APPLICANT: Shire, Steven J.
;/ APPLICANT: Sliwowski, Mary B.
;/ TITLE OF INVENTION: PURIFIED FORMS OF DNase
;/ NUMBER OF SEQUENCES: 18
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Genentech, Inc.
;/ STREET: 460 Point San Bruno Blvd
;/ CITY: South San Francisco
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94080
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: WinPatIn (Genentech)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/458,367
;/ FILING DATE: 02-Jun-1995
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/409631
;/ FILING DATE: 22-Mar-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/348284
;/ FILING DATE: 30-No. 5783433-1994

;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/116186
;/ FILING DATE: 02-Sep-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 07/895300
;/ FILING DATE: 08-Jun-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Johnston, Sean A.
;/ REGISTRATION NUMBER: 35,910
;/ REFERENCE/DOCKET NUMBER: P0747C4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415/225-3562
;/ TELEFAX: 415/952-9881
;/ TELEX: 910/371-7168
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 22 base pairs
;/ TYPE: Nucleic Acid
;/ STRANDEDNESS: Single
;/ TOPOLOGY: Linear
;/ US-08-458-367-18

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGCGC 636
Db 22 GCGCGCGCGCGCGCGCGCGC 1

RESULT 63
US-08-482-577B-34
;/ Sequence 34, Application US/08482577B
;/ Patent No. 5807713
;/ GENERAL INFORMATION:
;/ APPLICANT: HOTTEN, GERTRUD
;/ APPLICANT: NEIDHARDT, HELGE
;/ APPLICANT: BECHTOLD, ROLF
;/ APPLICANT: POHL, JENS
;/ TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
;/ TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
;/ NUMBER OF SEQUENCES: 49
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY, AND ORAM
;/ STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
;/ CITY: WASHINGTON
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20005
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/482,577B
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: KLEGENER, SHARON
;/ REGISTRATION NUMBER: 36,335
;/ REFERENCE/DOCKET NUMBER: P564-5010
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202/638-5000
;/ TELEFAX: 202/638-4810
;/ INFORMATION FOR SEQ ID NO: 34:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 22 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear

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; MOLECULE TYPE: DNA
US-08-482-577B-34

Query Match          0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
    ||||| ||||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

RESULT 64
US-08-288-508C-25
; Sequence 25, Application US/08288508C
; Patent No. 5994094
; GENERAL INFORMATION:
; APPLICANT: H tten, Gertrud
; APPLICANT: Neidhardt, Helge
; APPLICANT: Paulista, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
; TITLE OF INVENTION: THE TGF- FAMILY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikolaio, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,508C
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 26 829.3
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 18 222.8
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 20 157.5
; FILING DATE: 09-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: P-41,092
; REFERENCE/DOCKET NUMBER: P564-4019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-288-508C-25

Query Match          0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
    ||||| ||||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

US-08-289-222E-38
; Sequence 38, Application US/08289222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; TITLE OF INVENTION: FAMILY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARMELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-289-222E-38

Query Match          0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
    ||||| ||||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

RESULT 66
US-09-218-176-17
; Sequence 17, Application US/09218176
; Patent No. 6171584
; GENERAL INFORMATION:
; APPLICANT: H ITTEN, Gertrud
; APPLICANT: NEIDHARDT, Helge
```

```
; APPLICANT: BECHTOLD, Rolf
; APPLICANT: POHL, Jens
; APPLICANT: PAULISTA, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
; TITLE OF INVENTION: TGF- FAMILY
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., G Street Lobby,
; STREET: Suite 330
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/218,176
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03065
; FILING DATE: 12-JUL-1996
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 2-FEB-1993
; APPLICATION NUMBER: US 08/482,577
; FILING DATE: 7-JUN-1995
; APPLICATION NUMBER: EP 92 102 324.8
; FILING DATE: 12-FEB-1992
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 01-JUL-1994
; APPLICATION NUMBER: DE 195 11 243.1
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-6010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-218-176-17
;
; Query Match 0.4%; Score 18.8; DB 1; Length 22;
; Best Local Similarity 90.9%; Pred. No. 81;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2200 GGGATCTTGGATGGAAATGGAT 2221
;
; DB 1 GGGATCTAGGTGGAAATGGAT 22
;
; RESULT 67
; US-09-054-526B-38
; Sequence 38, Application US/09054526B
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; Patent No. 6197550
; GENERAL INFORMATION:
; APPLICANT: H TTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; STREET: SUITE 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,526B
; FILING DATE: 03-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-8005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-054-526B-38
;
; Query Match 0.4%; Score 18.8; DB 1; Length 22;
; Best Local Similarity 90.9%; Pred. No. 81;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2200 GGGATCTTGGATGGAAATGGAT 2221
;
; DB 1 GGGATCTAGGTGGAAATGGAT 22
;
; RESULT 68
; US-09-386-450D-25
; Sequence 25, Application US/09386450D
; Patent No. 6764994
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Neidhardt, Helge
; APPLICANT: Paulista, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TGF-? Family
; FILE REFERENCE: 100564-09022
; CURRENT APPLICATION NUMBER: US/09/386,450D
```



```
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/288,508
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: DE P 43 26 829.3
; PRIOR FILING DATE: 1993-08-10
; PRIOR APPLICATION NUMBER: DE P 44 18 222.8
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: DE P 44 20 157.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: portion of TGF-beta-2 corresponding to primer OD
US-09-386-450D-25

Query Match          0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAATGGAT 2221
Db 1 GGGATCTAGGTTGGAATGGAT 22

RESULT 69
US-09-823-634A-15
; Sequence 15, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-634A-15

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGAGAAAAA 2599
Db 1 AAAAAAAAAATTGAGAAAAA 20

RESULT 70
US-09-823-647B-15
; Sequence 15, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
```

```
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-647B-15

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGAGAAAAA 2599
Db 1 AAAAAAAAAATTGAGAAAAA 20

RESULT 71
US-09-380-662-9/c
; Sequence 9, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Oligo sapiens
US-09-380-662-9

Query Match          0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 CCCTACTTCAGAAATCGTC 1607
Db 18 CCCTACTTCAGAAATCGTC 1

RESULT 72
US-08-535-249-67/c
; Sequence 67, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immune-suppressive effect of transforming-growth-factor beta (1
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
```


Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTCTTTTAAAGGAAAAA 2765
Db 2 TTTTCTTTTAAAGGAAAAA 21

RESULT 75

US-09-657-472-1948/c
; Sequence 1948, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1948
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1948

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 588 CCCCGGGCTCCAGGCTCG 608
Db 21 CCCCGGGCTCCAGGCTCG 1

RESULT 76

US-09-687-246B-7/c
; Sequence 7, Application US/09687246B
; Patent No. 6709818
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins School of Medicine
; APPLICANT: Nelson, William
; APPLICANT: Tchou, Julia
; APPLICANT: Bakker, Jila
; APPLICANT: Lin, Xiaohui
; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS
; FILE REFERENCE: JHU1660-1
; CURRENT APPLICATION NUMBER: US/09/687,246B
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,168
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer N-F1
US-09-687-246B-7

Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTTAAAAAATAATT 2590
Db 19 TTTAAAAAATAATT 3

RESULT 77

US-08-482-182-68
; Sequence 68, Application US/08482182
; Patent No. 5861273
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, DESMOND
; APPLICANT: OLSON, PAMELA S.
; TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: GENES IN BACTERIAL CELLS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,182
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 22095-20281.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-482-182-68

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2212 GGAATGGATCATGAACCC 2231
Db 1 GGAATGGATCATGAACCC 20

RESULT 78

US-08-863-639A-51
; Sequence 51, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak

```

; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-51

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 79
US-08-863-639A-51/c
; Sequence 51, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321

```

```

; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-51

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 80
US-09-030-701-59
; Sequence 59, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; PRIOR FILING DATE: 1998-02-25
; PRIOR FILING DATE: 60/039,405
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; US-09-030-701-59

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 81
US-09-030-701-59/c
; Sequence 59, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; PRIOR FILING DATE: 1998-02-25
; PRIOR FILING DATE: 60/039,405
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```
;
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-59

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 82
US-09-082-649B-22
; Sequence 22, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-22

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 83
US-09-082-649B-22/c
; Sequence 22, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA

;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-22

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 84
US-09-082-649B-76
; Sequence 76, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-76

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGACGCGCG 634
Db 1 GCGCGCGCGCGCGCGCGCG 20

RESULT 85
US-09-082-649B-76/c
; Sequence 76, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
```

;
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-76
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCAGCGCGC 634
Db 20 GCGCGCGCGCGCGCGCGC 1

RESULT 86
US-08-535-249-99/c
; Sequence 99, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersien, Georg-Ferdinand
; APPLICANT: Bysch, Wolfgang
; APPLICANT: Schlengersien, Karl-Hermann
; APPLICANT: Schlengersien, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-99
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAGCG 1947
Db 1928 CATCATCCCGAATAAAGCG 1947
|||||

Db 20 CATCATCCCAATAAAAGTG 1

RESULT 87
US-09-725-265-42/c
; Sequence 42, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-42
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATATATTT 1171
Db 20 TTTTATATATATATAT 1

RESULT 88
US-09-823-634A-13
; Sequence 13, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTCGAGAAAAA 2599
Db 1 AAAAAAATTCGAGAAAAA 20
|||||

RESULT 89
US-09-823-634A-14
; Sequence 14, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
|||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 92
US-09-556-127-42/c
; Sequence 42, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-42

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATATATTT 1171
|||||
Db 20 TTTTATATATATATATAT 1

RESULT 93
US-09-965-101-22
; Sequence 22, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim

US-09-823-634A-14
; Sequence 14, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
|||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 90
US-09-823-647B-13
; Sequence 13, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
|||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 91
US-09-823-647B-14
; Sequence 14, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan

```

; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US 09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-22

```

```

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCGCG 20

```

```

RESULT 94
US-09-965-101-22/c
; Sequence 22, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-22

```

```

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCGCG 1

```

```

RESULT 95
US-09-965-101-76
; Sequence 76, Application US/09965101

```

```

; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-76

```

```

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 615 GCGCGCGCGCACGCGCGC 634
Db 1 GCGCGCGCGCGCGCGCGCG 20

```

```

RESULT 96
US-09-965-101-76/c
; Sequence 76, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-76

```

```

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 615 GCGCGCGCGCACGCGCGC 634
Db 20 GCGCGCGCGCGCGCGCGCG 1

```



```
; APPLICANT: POLOUCHINE, Nikolai
; APPLICANT: SLESAREV, Alexei
; TITLE OF INVENTION: INHIBITION OF MOLECULAR AND BIOLOGICAL PROCESSES USING MODIFIED
; FILE OF INVENTION: OLIGONUCLEOTIDES.
; FILE REFERENCE: 107070
; CURRENT APPLICATION NUMBER: US/09/655,804B
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-655-804B-67

Query Match          0.4%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.8%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2732 AAAAGAAACATCTTTTTTTTTT 2754
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 24 AAAAAAAAAAGTGTGTGTGTGT 2

RESULT 100
US-08-535-249-76/c
; Sequence 76, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdan, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
```

```

;
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-76

Query Match          0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGAAATCGT 1606
Db 18 ACCCTACTTCAGAAATGTT 1

RESULT 101
US-08-535-249-133/c
; Sequence 133, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-133

Query Match          0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATTCAGCTAAA 2463
Db 18 CTTGCAATTCAGCTAAA 1

chong-10-633-163-47.rni

RESULT 102
US-09-696-791-3527/c
; Sequence 3527, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3527
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3527

Query Match          0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAAACAAC 941
Db 19 CCAGGAGAAAAAACAAC 2

RESULT 103
US-09-696-791-3528/c
; Sequence 3528, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3528
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3528

Query Match          0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAAACAAC 941
Db 18 CCAGGAGAAAAAACAAC 1

RESULT 104
US-09-702-251-10
; Sequence 10, Application US/09702251
; Patent No. 6372492
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0199
```

```
; CURRENT APPLICATION NUMBER: US/09/702,251
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-251-10

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3393 TCCTTTGCTCTGGTATAT 3410
Db 2 TCCTTCGCTCTGGTATAT 19

RESULT 105
US-09-198-452A-2628
; Sequence 2628, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2628
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2628

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1055 GCCAGGACGCTTTTCTTA 1072
Db 2 GCCAGGACGCTTTTCTTA 19

RESULT 106
US-09-380-662-16/c
; Sequence 16, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-380-662-16

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1217 CATGCACTACTGTGTG 1232
Db 1 CATGCACTACTGTGTG 16

RESULT 107
US-09-380-662-17
; Sequence 17, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-380-662-17

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1217 CATGCACTACTGTGTG 1232
Db 1 CATGCACTACTGTGTG 16

RESULT 108
US-08-535-249-105/c
; Sequence 105, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
```

```
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1217 CATGCACTACTGTGTG 1232
Db 16 CATGCACTACTGTGTG 1

RESULT 107
US-09-380-662-17
; Sequence 17, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-380-662-17

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1217 CATGCACTACTGTGTG 1232
Db 1 CATGCACTACTGTGTG 16

RESULT 108
US-08-535-249-105/c
; Sequence 105, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELE: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-105

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2020 AGTCCACTAGGAAAA 2035
Db      16 AGTCCACTAGGAAAA 1

RESULT 109
US-08-535-249-113/c
; Sequence 113, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELE: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-113

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2153 TGTGCAGGATAATTGC 2168
Db      16 TGTGCAGGATAATTGC 1

RESULT 110
US-09-601-144-2
; Sequence 2, Application US/09601144
; Patent No. 6566514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDOXIN
; TITLE OF INVENTION: AND THIOREDOXIN REDUCTASE GENES AND METHODS OF USING
; TITLE OF INVENTION: SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 683-112US-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Human
US-09-601-144-2

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2209 GATGGAATGGATCCA 2224
Db      1 GATGGAATGGATCCA 16

RESULT 111
US-08-330-000-1/c
; Sequence 1, Application US/08330000
; Patent No. 5686242
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; APPLICANT: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5686242ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,000
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 755,485
; FILING DATE: September 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07489
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca Lynne
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1723
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-330-000-1

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATC 2818
Db 17 AAAAAAAAAAACATC 2

RESULT 112
US-08-965-908-1/c
; Sequence 1, Application US/08965908
; Patent No. 6022691
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; ADDRESS: Lima, Walter F.
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,908
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330,000
; FILING DATE:
; APPLICATION NUMBER: 755,485
; FILING DATE: September 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07489
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca Lynne
; REGISTRATION NUMBER: 35,152

```

```

; REFERENCE/DOCKET NUMBER: ISIS-1723
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-965-908-1

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATC 2818
Db 17 AAAAAAAAAAACATC 2

RESULT 113
US-09-026-601-25
; Sequence 25, Application US/09026601
; Patent No. 6358680
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: Detection of Wheat and Barley Fungal
; TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6358680artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6358680th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer JB659"
; US-09-026-601-25

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGGACGC 3205
Db 1 GAAGCTTCATGGACGC 16

```

RESULT 114

US-08-842-079-4
; Sequence 4, Application US/08842079
; Patent No. 6133434
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/08/842,079
; CURRENT FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-08-842-079-4

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCGCGGGAAG 2117

Db 1 GTCCAGCGCGGGAAG 16

RESULT 115

US-09-638-857-4
; Sequence 4, Application US/09638857
; Patent No. 6509163
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/09/638,857
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 08/842,079
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-638-857-4

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCGCGGGAAG 2117

Db 1 GTCCAGCGCGGGAAG 16

RESULT 116

US-08-478-470-13/c
; Sequence 13, Application US/08478470
; Patent No. 5591607
; GENERAL INFORMATION:
; APPLICANT: GRYAZNOV, SERGEI
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: N3',P5', PHOSPHORAMIDATES:
; TITLE OF INVENTION: HYBRIDIZATION AND NUCLEASE

; TITLE OF INVENTION: RESISTANCE PROPERTIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro
; ADDRESSEE: Huddleson & Tatum
; STREET: 5 Palo Alto Square
; STREET: 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,470
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: John D. Mendlein
; REGISTRATION NUMBER: 38,770
; REFERENCE/DOCKET NUMBER: LYNX-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5020
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7,
; INDIVIDUAL ISOLATE: Fig. 2
US-08-478-470-13

Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAGAAACATCTTTTTTTT 2754

Db 24 AAAAAAGAGGGTTTTTTTTT 1

RESULT 117

US-08-214-599-13/c
; Sequence 13, Application US/08214599
; Patent No. 5599922
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3',P5',
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
US-08-473-015-13

Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels

QY 2731 AAAAAAGAAACATCTTTTITTTT 2754
    ||||| ||||| ||||| |||||
Db 24 AAAAAAAAAAGGGGTTTTTTTTTT 1

RESULT 119
US-08-465-368-13/c
; Sequence 13, Application US/08465368
; Patent No. 5726297
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Schultz, Ronald G.
; APPLICANT: Chen, Jer-kang
; TITLE OF INVENTION: OLIGODEXYRIBONUCLEOTIDE
; TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,368
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/210,505
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
US-08-465-368-13

Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels

QY 2731 AAAAAAGAAACATCTTTTITTTT 2754

```

Db 24 AAAAAAAAAAGGGGTTTTTTTTTT 1

RESULT 120
US-08-477-306-13/c
; Sequence 13, Application US/08477306
; Patent No. 5837835
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,306
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
US-08-477-306-13

Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAACAATCTTTTTTTT 2754
Db 24 AAAAAAAAAAGGGGTTTTTTTTTT 1

RESULT 121
US-08-700-448-13/c
; Sequence 13, Application US/08700448
; Patent No. 5965720
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei et al.
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,448
; FILING DATE: 01/10/97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent M. Powers
; REGISTRATION NUMBER: 36,246
; REFERENCE/DOCKET NUMBER: 5525-0012.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
US-08-700-448-13

Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAACAATCTTTTTTTT 2754
Db 24 AAAAAAAAAAGGGGTTTTTTTTTT 1

RESULT 122
US-08-923-386A-13/c
; Sequence 13, Application US/08923386A
; Patent No. 6163170
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,386A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 5525-0012
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid

STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 3

US-08-923-386A-13
US-08-923-386A-13

Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAGAAACATCTTTTTTTT 2754

Db 24 AAAAAAAAAAGGGTTTTTTTTT 1

RESULT 123

US-08-899-029-1/c
Sequence 1, Application US/08899029
Patent No. 6143531

GENERAL INFORMATION:

APPLICANT: HUSE, WILLIAM D.

TITLE OF INVENTION: IMPROVED METHOD OF DOUBLE
TITLE OF INVENTION: STRANDED DNA SYNTHESIS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds, LLP

STREET: 1155 Avenue of the Americas

CITY: New York,

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,029

FILING DATE: 22-JUL-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/116,049

FILING DATE: 02-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Abrams, Samuel B

REGISTRATION NUMBER: 30,605

REFERENCE/DOCKET NUMBER: 8142-125-999

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

US-08-899-029-1

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATTGGAG 2594

Db 19 AAAAAAAAAAAACTCGAG 1

RESULT 124

US-09-696-791-4067/c

Sequence 32, Application US/09696791

Patent No. 6770633

GENERAL INFORMATION:

APPLICANT: Robbins, Joan M.

APPLICANT: Tritz, Richard

TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EYE DISEASES

FILE REFERENCE: 480124.407

CURRENT APPLICATION NUMBER: US/09/696,791

CURRENT FILING DATE: 2000-10-25

NUMBER OF SEQ ID NOS: 4523

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4067

LENGTH: 19

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: PCNA HH ribozyme binding site

US-09-696-791-4067

Query Match 0.4%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3591 TTGGACTTTTTTTTAA 3609

Db 19 TTGGACTTTATCTTTAA 1

RESULT 125

US-09-750-401-32/c

Sequence 32, Application US/09750401

Patent No. 6635422

GENERAL INFORMATION:

APPLICANT: Keene, Jack D.

APPLICANT: Carson, Craig C.

APPLICANT: Tenenbaum, Scott A.

TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein

TITLE OF INVENTION: complexes

FILE REFERENCE: RBN-001

CURRENT APPLICATION NUMBER: US/09/750,401

CURRENT FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,338

PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn version 3.1

SEQ ID NO 32

LENGTH: 22

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: 3'-UTR sequence of TGF beta 2

US-09-750-401-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAA 2599

Db 22 AAAAAAACCAATTAAGAAAA 1

RESULT 126

US-08-390-850-579

```
; Sequence 579, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-390-850-579

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 1.4e+02;
Matches 7; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTTCTTTTAAAGGA 1048
Db 1 UUUCAUUUUUAAAGGA 17

RESULT 127
US-08-390-850-580
; Sequence 580, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-390-850-580

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.4e+02;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTTTCTTTTAAAGGA 1049
Db 1 UUUCAUUUUUAAAGGA 17

RESULT 128
US-08-373-124A-2155
; Sequence 2155, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
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/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/373,124A
/ FILING DATE: January 13, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2155:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-373-124A-2155

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 23.5%; Pred. No. 1.4e+02;
Matches 4; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATA 1168
:::||||:|:
Db 1 UUUUUUUUAUAUA 17

RESULT 129
US-08-373-124A-2157
/ Sequence 2157, Application US/08373124A
/ Patent No. 5646042
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: McSwiggen, James
/ APPLICANT: Jarvis, Thale
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/373,124A
/ FILING DATE: January 13, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994

/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2157:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-373-124A-2157

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 23.5%; Pred. No. 1.4e+02;
Matches 4; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCTTTTATATATA 1169
:::||||:|:
Db 1 UUUUUUUUAUAUA 17

RESULT 130
US-08-435-634-579
/ Sequence 579, Application US/08435634
/ Patent No. 5731295
/ GENERAL INFORMATION:
/ APPLICANT: Draper, Kenneth G.
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Gustofson, John
/ APPLICANT: Stinchcomb, Dan T.
/ TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
/ TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
/ NUMBER OF SEQUENCES: 1151
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,634
/ FILING DATE: 05-MAY-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/390,850
/ FILING DATE: February 17, 1995
/ APPLICATION NUMBER: 08/354,920
/ FILING DATE: December 13, 1994
/ APPLICATION NUMBER: 08/152,487
/ FILING DATE: No. 5731295ember 12, 1993
/ APPLICATION NUMBER: 07/989,848
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard

```
;
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-634-579

Query Match          0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 1.4e+02;
Matches 7; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTCTTTTAAAGGA 1048
Db 1 UUUCAUUUUUAAAGGA 17

RESULT 131
US-08-435-634-580
; Sequence 580, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-634-580
```

```
;
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-634-580

Query Match          0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.4e+02;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTTCTTTTAAAGGA 1049
Db 1 UUUCAUUUUUAAAGGA 17

RESULT 132
US-08-435-628-2155
; Sequence 2155, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-2155
```


; APPLICANT: Cole, Douglas
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric Compounds
; FILE REFERENCE: ISIS3380
; CURRENT APPLICATION NUMBER: US/09/288,679
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Phosphorothioate backbone
US-09-288-679-3

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATGGAG 2594
Db 18 AAAAAAAAAAATGGGG 2

RESULT 136
US-09-288-679-5/c
; Sequence 5, Application US/09288679
; Patent No. 6465628
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; APPLICANT: Manoharan, Muthia
; APPLICANT: Capaldi, Daniel
; APPLICANT: Krotz, Achim
; APPLICANT: Cole, Douglas
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric Compounds
; FILE REFERENCE: ISIS3380
; CURRENT APPLICATION NUMBER: US/09/288,679
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. 6465628el Sequence
US-09-288-679-5

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATGGAG 2594
Db 18 AAAAAAAAAAATGGGG 2

RESULT 137
US-09-725-265-18/c
; Sequence 18, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU

; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-18

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1

RESULT 138
US-09-556-127-18/c
; Sequence 18, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-18

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1

RESULT 139
US-09-316-447A-3
; Sequence 3, Application US/09316447A

```
/ Patent No. 6287774
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Assay Methods and Systems
/ FILE REFERENCE: 09316447
/ CURRENT APPLICATION NUMBER: US/09/316,447A
/ CURRENT FILING DATE: 1999-02-21
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-316-447A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2123 CGCTTTGGATGCTGCCT 2139
      ||||| ||||| ||||| |||||
Db      1 CGCTGTGGATGCTGCCT 17

RESULT 140
US-09-727-532A-3
/ Sequence 3, Application US/09727532A
/ Patent No. 6436646
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Kinase Assays Using Polycations
/ FILE REFERENCE: 100/07930
/ CURRENT APPLICATION NUMBER: US/09/727,532A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/316,447
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: US 60/156,366
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/139,562
/ PRIOR FILING DATE: 1999-06-16
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PNA probe
US-09-727-532A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2123 CGCTTTGGATGCTGCCT 2139
      ||||| ||||| ||||| |||||
Db      1 CGCTGTGGATGCTGCCT 17

RESULT 141
US-09-569-193A-3
/ Sequence 3, Application US/09569193A
/ Patent No. 6472141
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Kinase Assays Using Polycations
/ FILE REFERENCE: 100/07930
/ CURRENT APPLICATION NUMBER: US/09/569,193A
/ CURRENT FILING DATE: 2000-05-11
/ PRIOR APPLICATION NUMBER: US 09/316,447

/ Patent No. 6287774
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Assay Methods and Systems
/ FILE REFERENCE: 09316447
/ CURRENT APPLICATION NUMBER: US/09/316,447A
/ CURRENT FILING DATE: 1999-02-21
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-316-447A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2123 CGCTTTGGATGCTGCCT 2139
      ||||| ||||| ||||| |||||
Db      1 CGCTGTGGATGCTGCCT 17

RESULT 142
US-09-422-978-4619
/ Sequence 4619, Application US/09422978
/ Patent No. 6537751
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
/ FILE REFERENCE: GENSET.020CP1
/ CURRENT APPLICATION NUMBER: US/09/422,978
/ CURRENT FILING DATE: 1999-10-20
/ EARLIER APPLICATION NUMBER: US 09/298,850
/ EARLIER FILING DATE: 1999-04-21
/ EARLIER APPLICATION NUMBER: US 60/109,732
/ EARLIER FILING DATE: 1998-11-23
/ EARLIER APPLICATION NUMBER: US 60/082,614
/ EARLIER FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 11796
/ SEQ ID NO 4619
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: 1..19
/ OTHER INFORMATION: upstream amplification primer 99-16399 for SEQ 685,
US-09-422-978-4619

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3126 GTTGTATAGGACTAAG 3142
      ||||| ||||| ||||| |||||
Db      2 GTTGTATAGGACTAAG 18

RESULT 143
US-10-057-812A-3
/ Sequence 3, Application US/10057812A
/ Patent No. 6689565
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Kinase Assays Using Polycations
/ FILE REFERENCE: 100/07930
/ CURRENT APPLICATION NUMBER: US/10/057,812A
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: US/09/569,193
```

```

; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 09/316,447
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/156,366
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/139,562
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-057-812A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGATGCTGCCT 17

RESULT 144
US-09-865-044-3
; Sequence 3, Application US/09865044
; Patent No. 6699655
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Assay Methods and Systems
; FILE REFERENCE: 09316447
; CURRENT APPLICATION NUMBER: US/09/865,044
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/316,447
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-865-044-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGATGCTGCCT 17

RESULT 145
US-09-696-791-3526/c
; Sequence 3526, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3526
```

```

; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3526

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CAGGAGAAAAAACAAC 941
Db 19 CAGGAGAAAAAACAAC 3

RESULT 146
US-09-696-791-3529/c
; Sequence 3529, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3529
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3529

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAAACA 940
Db 17 CCAGGAGAAAAAACA 1

RESULT 147
US-09-687-246B-7
; Sequence 7, Application US/09687246B
; Patent No. 6709818
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins School of Medicine
; APPLICANT: Nelson, William
; APPLICANT: Tchou, Julia
; APPLICANT: Bakker, Jila
; APPLICANT: Lin, Xiaohui
; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS
; FILE REFERENCE: JHU1660-1
; CURRENT APPLICATION NUMBER: US/09/687,246B
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,168
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer N-F1
US-09-687-246B-7
```



```
Query Match      0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTAAAG 2758
Db 4 ATTTTAAAG 20

RESULT 148
US-08-087-387-5/c
; Sequence 5, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applic
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,387
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-087-387-5

Query Match      0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 149
US-08-455-627-5/c
; Sequence 5, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
```

```
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-455-627-5

Query Match      0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 150
US-08-461-271-5/c
; Sequence 5, Application US/08461271
; Patent No. 5741643
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,271
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 5:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-461-271-5

Query Match          0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 151
US-08-713-685A-5/c
; Sequence 5, Application US/08713685A
; Patent No. 5817795
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,685A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-713-685A-5

Query Match          0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 152
US-08-689-856-5/c
; Sequence 5, Application US/08689856
```

```
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-689-856-5

Query Match          0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 153
US-08-863-639A-8
; Sequence 8, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C.T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-8
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTTAAAAA 2587
Db 1 TTTTAAAAA 15

RESULT 154
US-08-832-021-17/c
; Sequence 17, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-17

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTTAAAAA 2587
Db 15 TTTTAAAAA 1

RESULT 155
US-08-832-021-22/c
; Sequence 22, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
```

```
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-22

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 156
US-09-070-477-5/c
; Sequence 5, Application US/09070477
; Patent No. 6048974
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94040
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,685
; FILING DATE:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-070-477-5

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 157
US-08-787-321-5/c
; Sequence 5, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; oligonucleotide
US-08-787-321-5

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 158
US-08-145-704-42
; Sequence 42, Application US/08145704
; Patent No. 5567604
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Joshua O. Ojwang
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,704
; FILING DATE: 28-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

QY 973 CCCCCCCCCCCCCCCC 990
Db 1 CCCCCCCCCCCCCCCC 18

RESULT 159
US-08-145-704-43
; Sequence 43, Application US/08145704
; Patent No. 5567604
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Joshua O. Ojwang
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,704
; FILING DATE: 28-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety attached to 3'
; OTHER INFORMATION: end"
US-08-145-704-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety attached to 3'
US-08-145-704-43
OTHER INFORMATION: end and phosphorothioate backbone"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 973 CCCCCCCCCCGCCCC 990
Db 1 CCCCCCCCCCCCCCCCC 18
RESULT 160
US-08-105-168B-21/c
Sequence 21, Application US/08105168B
Patent No. 5589585
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: August 12, 1993
APPLICATION NUMBER: US/08/105,168B
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 640-657
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-105-168B-21

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 359 CCTTGGCCGCTTGAGCA 376
Db 18 CCTTGGCCGACTTGAGCA 1
RESULT 161
US-08-698-948-21/c
Sequence 21, Application US/08698948
Patent No. 5849901
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,948
FILING DATE: August 16, 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,168
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 640-657
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-698-948-21
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 359 CCTTGGCCGCTGGAGCA 376
Db 18 CCTTGGCCGCTGGAGCA 1

RESULT 162
US-08-358-556A-24
; Sequence 24, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelet, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; NAME/KEY: CDS
; LOCATION: 1..18
; US-08-358-556A-24

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCCGCC 990
Db 1 CCCCCCCCCCGCCGCC 18

RESULT 163
US-08-863-639A-15
; Sequence 15, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.

```

```

; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-15

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2666 ACAGCAACCAACCAACA 2683
Db 1 ACAACAACCAACCAACA 18

RESULT 164
US-08-863-639A-16
; Sequence 16, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435

```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-639A-16

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2667 CAGCAACAACAACACAA 2684
Db 1 CAACAACAACAACA 18

RESULT 165
US-08-987-574-42
; Sequence 42, Application US/08987574
; Patent No. 6150339
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendeigui, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04529
; FILING DATE: 28-OCT-1993
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end"
; US-08-987-574-42

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCGCCCCC 990
Db 1 CCCCCCCCCCGCCCCC 18

RESULT 166
US-08-987-574-43
; Sequence 43, Application US/08987574
; Patent No. 6150339
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendeigui, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04529
; FILING DATE: 28-OCT-1993
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end and phosphorothioate
; OTHER INFORMATION: backbone"
; US-08-987-574-43
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Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCGCCC 990
 Db 1 CCCCCCCCCCCCCCCC 18

RESULT 167
 US-08-535-168-42
 ; Sequence 42, Application US/08535168
 ; Patent No. 6184369
 ; GENERAL INFORMATION:
 ; APPLICANT: Rando, Robert F.
 ; APPLICANT: Fennwald, Susan
 ; APPLICANT: Zendequi, Joseph G.
 ; APPLICANT: Ojwang, Joshua O.
 ; APPLICANT: Hogan, Michael E.
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
 ; TITLE OF INVENTION: Oligonucleotides
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/535,168
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/04529
 ; FILING DATE: 28-OCT-1993
 ; APPLICATION NUMBER: US 08/053,027
 ; FILING DATE: 23-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5574-CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5151
 ; TELEFAX: 713/651-5246
 ; TELEX: 762829
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 18
 ; OTHER INFORMATION: /note= "Amine moiety
 ; OTHER INFORMATION: attached to 3' end"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCGCCC 990
 Db 1 CCCCCCCCCCCCCCCC 18

RESULT 168
 US-08-535-168-43
 ; Sequence 43, Application US/08535168
 ; Patent No. 6184369
 ; GENERAL INFORMATION:
 ; APPLICANT: Rando, Robert F.
 ; APPLICANT: Fennwald, Susan
 ; APPLICANT: Zendequi, Joseph G.
 ; APPLICANT: Ojwang, Joshua O.
 ; APPLICANT: Hogan, Michael E.
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
 ; TITLE OF INVENTION: Oligonucleotides
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/535,168
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/04529
 ; FILING DATE: 28-OCT-1993
 ; APPLICATION NUMBER: US 08/053,027
 ; FILING DATE: 23-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5574-CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5151
 ; TELEFAX: 713/651-5246
 ; TELEX: 762829
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 18
 ; OTHER INFORMATION: /note= "Amine moiety
 ; OTHER INFORMATION: attached to 3' end and phosphorothioate
 ; OTHER INFORMATION: backbone"
 ; US-08-535-168-43

Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCGCCC 990
 Db 1 CCCCCCCCCCCCCCCC 18

RESULT 169
 US-09-475-316A-122/c
 ; Sequence 122, Application US/09475316A
 ; Patent No. 6210942
 ; GENERAL INFORMATION:

APPLICANT: Lewis, No. 6210942man G.
APPLICANT: Davin, Laurence B.
APPLICANT: Dinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Gang, David R.
APPLICANT: Sarkanen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
FILE REFERENCE: WSUR-1-13793
CURRENT APPLICATION NUMBER: US/09/475,316A
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/307,653
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/US97/20391
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/054,380
PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION NUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 122
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide
NAME/KEY: misc_feature
LOCATION: (1)..(18)
OTHER INFORMATION: Linker primer
US-09-475-316A-122

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAAAAAATTGGAG 2594
DB 18 AAAAAAAAAAACTCGAG 1

RESULT 170
US-09-437-076-3/c
Sequence 3, Application US/09437076
Patent No. 6261779
GENERAL INFORMATION:
APPLICANT: Barber-Guillem, Emilio
APPLICANT: Nelson, M. Bud
APPLICANT: Castro, Stephanie
TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
CURRENT APPLICATION NUMBER: US/09/437,076
CURRENT FILING DATE: 1999-11-09
EARLIER FILING DATE:
EARLIER APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Word for Windows
SEQ ID NO 3
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: synthesized
US-09-437-076-3

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCCCCCCCC 990

Db 18 CCCCCCCCCCCCCCCCC 1
RESULT 171
US-09-017-974-42
Sequence 42, Application US/09017974
Patent No. 6288042
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Wallace, Thomas L.
APPLICANT: Cossum, Paul A.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Tetrad Forming Oligonucleotides
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSES: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1800
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,974
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,374
FILING DATE: 04-FEB-97
APPLICATION NUMBER:
FILING DATE: 09-DEC-97
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06223
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end"
US-09-017-974-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCCCCCCCC 990
DB 1 CCCCCCCCCCCCCCCCC 18

RESULT 172
US-09-017-974-43
Sequence 43, Application US/09017974
Patent No. 6288042
GENERAL INFORMATION:

APPLICANT: Rando, Robert F.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Wallace, Thomas L.
APPLICANT: Cossum, Paul A.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Tetrad Forming Oligonucleotides
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1800
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,974
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,374
FILING DATE: 04-FEB-97
APPLICATION NUMBER:
FILING DATE: 09-DEC-97
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06223
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end and phosphorothioate
OTHER INFORMATION: backbone"
US-09-017-974-43

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 173
US-08-682-255A-42
Sequence 42, Application US/08682255A
Patent No. 6323185
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendequi, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyles
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,255A
FILING DATE: 17-JULY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,168
FILING DATE: 23-OCT-95
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/015,714
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 23-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end"
US-08-682-255A-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 174
US-08-682-255A-43
Sequence 43, Application US/08682255A
Patent No. 6323185
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendequi, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyles
APPLICANT: Mazumder, Abhijit

```

; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/015,714
; FILING DATE: 17-APRIL-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 23-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end and phosphorothioate
; OTHER INFORMATION: backbone"
; US-08-682-255A-43

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCGCCCC 990
Db 1 CCCCCCCCCCGCGCCCC 18

RESULT 175
US-09-429-130-42
; Sequence 42, Application US/09429130
; Patent No. 6355785
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; Fennewald, Susan
; Zendegui, Joseph G.
; Ojwang, Joshua O.
; Hogan, Michael E.

```

```

; Pommier, Yves
; Mazumder, Abhijit
; 60/015,714
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/429,130
; FILING DATE: 28-Oct-1999
; CLASSIFICATION: <Unknown>
; 19-JULY-95
; 25-MARCH-96
; 19-MARCH-96
; 17-APRIL-96
; 23-APRIL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/682,255
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end"
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
; US-09-429-130-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCGCCCC 990
Db 1 CCCCCCCCCCGCGCCCC 18

RESULT 176
US-09-429-130-43
; Sequence 43, Application US/09429130
; Patent No. 6355785

```

GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
Zendegui, Joseph G.
Ojwang, Joshua O.
Hogan, Michael E.
Pommier, Eyles
Mazumder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tavon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96
17-APRIL-96
23-APRIL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc.feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
attached to 3' end and phosphorothioate
backbone"
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-429-130-43
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 973 CCCCCCCCCCGCCCC 990
|||||

Db 1 CCCCCCCCCCCCCCCCC 18
RESULT 177
US-08-535-249-72/c
Sequence 72, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
immuno-suppressive effect of transforming-growth-factor beta (7)
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-72
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1527 TATAAATCGACATGCCG 1544
|||||
Db 18 TACAAATAGACATGCCG 1
|||||
RESULT 178
US-08-535-249-79/c
Sequence 79, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar

```

; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
;   transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-79

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1636 ATGCTTCGAATCTGGTGA 1653
Db 18 ATGCTTCCAATTGGTGA 1
||||| ||| |||||

RESULT 179
US-08-535-249-85/c
; Sequence 85, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
;   transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA: EP 93 107 849.0
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-79

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```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-85

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1711 GGATTGCACTGATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1
||||| ||| |||||

RESULT 180
US-08-535-249-96/c
; Sequence 96, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
;   transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-85

```

```
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-96

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1880 AATAAGTTTACACTGCGC 1897
Db 18 AATAAGCTTACACTGTCC 1

RESULT 181
US-08-535-249-115/c
; Sequence 115, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; ADDRESS: 400 Seventh St. N.W.
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-96
```

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; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-115

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2175 CGCCCTCTTTACATTGAT 2192
Db 18 CGTCCACTTTACATTGAT 1

RESULT 182
US-08-535-249-128/c
; Sequence 128, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; ADDRESS: 400 Seventh St. N.W.
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-128

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2375 ACCACTGACCATTTCTCTA 2392
```

Db ||| || ||||| ||||| |||||
18 ACCTCTAACCATTTCTCTA 1

RESULT 183

US-08-535-249-132/c
; Sequence 132, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514

; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350

; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-132

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2439 GTCAAGTCTTTGTAATGC 2456

Db ||| ||||| ||||| |||||
18 GTAAAGTCTTGCAATGC 1

RESULT 184

US-09-725-265-20/c
; Sequence 20, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI

; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTTAC 1179

Db ||| ||||| ||||| |||||
18 ATATATATTTTCTTTC 1

RESULT 185

US-09-704-640-122/c
; Sequence 122, Application US/09704640
; Patent No. 6635459
; GENERAL INFORMATION:

; APPLICANT: Lewis, No. 6635459man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.

; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,
; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEIN AND METHODS OF USE

; FILE REFERENCE: WSUR-1-16492
; CURRENT APPLICATION NUMBER: US/09/704,640
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/475,316
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(18)
; OTHER INFORMATION: Linker primer
US-09-704-640-122

Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0;

QY 2577 AAAAAAAAAAATGGAG 2594

Db 18 AAAAAAAAAAACTCGAG 1

RESULT 186
 US-09-556-127-20/c
 ; Sequence 20, Application US/09556127
 ; Patent No. 669661
 ; GENERAL INFORMATION:
 ; APPLICANT: KURANE, RYUICHIRO
 ; APPLICANT: KANAGAWA, TAKAHIRO
 ; APPLICANT: KAMAGATA, YOICHI
 ; APPLICANT: YAMADA, KAZUTAKA
 ; APPLICANT: YOKOMAKU, TOYOKAZU
 ; APPLICANT: KOYAMA, OSAMU
 ; APPLICANT: FURUSHO, KENTA
 ; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
 ; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
 ; FILE REFERENCE: 0163-0758-0X
 ; CURRENT APPLICATION NUMBER: US/09/556,127
 ; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: JP 1999-111601
 ; PRIOR FILING DATE: 1999-04-20
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL SEQUENCE
 ; FEATURE:
 ; OTHER INFORMATION: SYNTHETIC DNA
 US-09-556-127-20

Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0;

QY 1162 ATATATATTTTCTTAC 1179

Db 18 ATATATATTTTCTTAC 1

RESULT 187
 US-10-352-704-24
 ; Sequence 24, Application US/10352704
 ; Patent No. 682539
 ; GENERAL INFORMATION:
 ; APPLICANT: Chatelain, Francois
 ; APPLICANT: Kumarev, Viktor
 ; TITLE OF INVENTION: Process for Preparing Polynucleotides on
 ; a Solid Support and Apparatus Permitting its
 ; Implementation
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jacobson, Price, Holman & Stern
 ; STREET: 400 Seventh St. N.W.
 ; CITY: Washington D.C.
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/352,704
 FILING DATE: 28-Jan-2003
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/358,556A
 FILING DATE: 14-DEC-1994
 APPLICATION NUMBER: FR 9315164
 FILING DATE: 16-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Player, William E.
 REGISTRATION NUMBER: 31,409
 REFERENCE/DOCKET NUMBER: 10577/P58418
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)638-6666
 TELEFAX: (202) 393-5350
 TELEX: RCA 248593 IDEA UR
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..18
 SEQUENCE DESCRIPTION: SEQ ID NO: 24:
 US-10-352-704-24

Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0;

QY 973 CCCCCCCCCCGCCCC 990

Db 1 CCCCCCCCCCGCCCC 18

RESULT 188
 US-09-904-744-3/c
 ; Sequence 3, Application US/09904744
 ; Patent No. 6828142
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbera-Guillem, Emilio
 ; APPLICANT: Nelson, M. Bud
 ; APPLICANT: Castro, Stephanie
 ; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
 ; FILE REFERENCE: B-73
 ; CURRENT APPLICATION NUMBER: US/09/904,744
 ; CURRENT FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: 09/437076
 ; PRIOR FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: 60/107828
 ; PRIOR FILING DATE: 1998-11-10
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthesized
 US-09-904-744-3
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0;

QY 973 CCCCCCCCCCGCCCC 990


```
Db      18 CCCCCCCCCCCCCCCCC 1
||||||| ||| |||
RESULT 189
PCT-US94-05407-5/c
; Sequence 5, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-5

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      254 AGGAGAAGCTAGGAGG 271
Db      18 AGGAGAAGATAGGGAGG 1
||||||| ||| |||
RESULT 190
PCT-US96-11786-42
; Sequence 42, Application PC/TUS9611786
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Yves
; APPLICANT: Mazumder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11786
; PRIOR APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 19-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end"
PCT-US96-11786-42

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      973 CCCCCCCCCCGCCCC 990
Db      1 CCCCCCCCCCCCCCCCC 18
||||||| ||| |||
RESULT 191
PCT-US96-11786-43
; Sequence 43, Application PC/TUS9611786
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Yves
; APPLICANT: Mazumder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11786
; FILING DATE: 17-JULY-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96
```

```

; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-94

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. NO. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1851 CACCACAAGACAGGA 1866
Db 16 CACCATAAAGACAGGA 1

RESULT 193
US-08-535-249-107/c
; Sequence 107, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-fact
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-107

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. NO. 1.7e+02;

```

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTGTG 2075
|||||
Db 16 CCTGCTAATGTATTG 1

RESULT 194

US-08-050-073-155
; Sequence 155, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2974
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA

US-08-050-073-155

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 365 CCGCTGGAGCAAGAA 380
|||
Db 1 CCTCCTGGAGCAAGAA 16

RESULT 195

US-08-390-850-578
; Sequence 578, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT

; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 578:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-390-850-578

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 2e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTCTTTTAAAGG 1047
:::|:::|
Db 2 UUUUCAUUUUAAGG 17

RESULT 196

US-08-390-850-581
; Sequence 581, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT

TITLE OF INVENTION: OF ARTHRITIC CONDITIONS

; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:

/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/390,850
/ FILING DATE: February 17, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/354,920
/ FILING DATE: December 13, 1994
/ APPLICATION NUMBER: 08/152,487
/ FILING DATE: No. 5612215ember 12, 1993
/ APPLICATION NUMBER: 07/989,848
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 211/084
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 581:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-390-850-581

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1034 TTCTTTTAAAGGAA 1049
Db 1 UUCAUUUUUAAGGAA 16

RESULT 197
US-08-373-124A-2153
/ Sequence 2153, Application US/08373124A
/ Patent No. 5646042
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: McSwiggen, James
/ APPLICANT: Jarvis, Thale
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/373,124A
/ FILING DATE: January 13, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994

/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2153:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-373-124A-2153

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 2e+02;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATAT 1167
Db 2 UUUUUUUUUUAU 17

RESULT 198
US-08-373-124A-2159
/ Sequence 2159, Application US/08373124A
/ Patent No. 5646042
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: McSwiggen, James
/ APPLICANT: Jarvis, Thale
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/373,124A
/ FILING DATE: January 13, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327

Qy 1032 TTTTCTTTTAAAGG 1047
 :::| ::::|::|
 Db 2 UUUUCAUUUUUAAAGG 17

RESULT 201
US-08-435-634-581
? Sequence 581, Application US/08435634
? Patent No. 5731295
? GENERAL INFORMATION:
? APPLICANT: Draper, Kenneth G.
? APPLICANT: Pavco, Pamela
? APPLICANT: McSwiggen, James
? APPLICANT: Gustofson, John
? APPLICANT: Stinchcomb, Dan T.
? TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
? OF ARTHRITIC CONDITIONS
? NUMBER OF SEQUENCES: 1151
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
? STREET: Suite 4700
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 8; Conservative 7; Mismatches 1; Indels

Qy	1034	TTCTTTT	TAAAGGAA	1049
		::	:::::	
D _b	1	UUCAUUUU	UAAAGGAA	16

RESULT 202
US-08-435-628-2153
; Sequence 2153, Application US/08435628

```

: Patent No. 5817796
:
: GENERAL INFORMATION:
:
: APPLICANT: Stinchcomb, Dan T.
:
: APPLICANT: Draper, Kenneth
:
: APPLICANT: McSwiggen, James
:
: APPLICANT: Jarvis, Thale
:
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
:
: TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
:
: TITLE OF INVENTION: CANCER USING RIBOZYMES
:
: NUMBER OF SEQUENCES: 2627
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Lyon & Lyon
:
: STREET: 633 West Fifth Street
:
: STREET: Suite 4700
:
: CITY: Los Angeles
:
: STATE: California
:
: COUNTRY: U.S.A.
:

```

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 2e+02;
Matches 3; Conservative 12; Mismatches 1; Indels

Qy 1152 TTCTTTTATATAT 1167
:: ::::|::|::
pb 2 UUUUUUUUUUU 17

RESULT 203
US-08-435-628-2159
Sequence 2159, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Slinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale

```
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,628
/ FILING DATE: 05-MAY-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/373,124
/ FILING DATE: January 13, 1995
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2159:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-435-628-2159

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 2e+02;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

Qy 1154 TCTTTTATATATAT 1169
Db 1 UAUUUUAUAUAU 16

RESULT 204
US-08-435-628-2161
; Sequence 2161, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

```
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,628
/ FILING DATE: 05-MAY-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/373,124
/ FILING DATE: January 13, 1995
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2161:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-435-628-2161

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 2e+02;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

Qy 1156 TTTTATATATATTT 1171
Db 1 UUUUUUAUAUAU 16

RESULT 205
US-08-173-489C-92
; Sequence 92, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
```

```
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from superoxide
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 92 :FROM 1 TO 17
; US-08-173-489C-92

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2930 CCCCCGCTTCTCTCC 2945
Db 1 CCCCCGCTTCTCTCC 16

RESULT 206
US-08-173-489C-95
; Sequence 95, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: superoxide dismutase gene (accession #
; DESCRIPTION: J02947) nucleotides 1212 to 1228
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: chromosome 21
; MAP POSITION: 21q22.1
; PUBLICATION INFORMATION:
; AUTHORS: Hjalmarsson, K, Marklund, S L,
; AUTHORS: Engstroem, A, Edlund, T.
; TITLE: Isolation and sequence of
; TITLE: complementary dna encoding human extracellular-
; TITLE: superoxide dismutase
; JOURNAL: Proceedings of the National Academy of
; JOURNAL: Sciences, USA
; VOLUME: 84
; PAGES: 6340-6344
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 95 :FROM 1 TO 17
; US-08-173-489C-95

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 975 CCCCCCACCCTCCCTCCC 990
Db 2 CCCCCCACCCTCCCTCCC 17

RESULT 207
US-08-584-040-4006
; Sequence 4006, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
```



```
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 4006:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-4006

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 2 UCUCUCCUCCACGUGAC 17

RESULT 208
US-08-584-040-7828/c
; Sequence 7828, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
```

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/ INFORMATION FOR SEQ ID NO: 7828:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-7828

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACAACAACCA 2681
Db 17 ACAGCAACAACAACA 2

RESULT 209
US-09-371-772B-1773
; Sequence 1773, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-371-772B-1773

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 2 UCUCUCCUCCACGUGAC 17

RESULT 210
US-09-371-772B-3612/c
; Sequence 3612, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
```

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3612
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3612

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACAAACCA 2681
Db 17 ACAGCAACAAACAA 2

RESULT 211
US-09-371-772B-6425
; Sequence 6425, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MH800.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6425
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6425

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 1 UCUCUCCAGGUGAC 16

RESULT 212
US-09-685-664B-1773
; Sequence 1773, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MH800-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
```

```
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1773

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 92.5%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 2 UCUCUCCAGGUGAC 17

RESULT 213
US-09-685-664B-3612/c
; Sequence 3612, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MH800-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3612
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3612

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACAAACCA 2681
Db 17 ACAGCAACAAACAA 2

RESULT 214
US-09-197-360-19
; Sequence 19, Application US/09197360
; Patent No. 5962673
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0018
; CURRENT APPLICATION NUMBER: US/09/197,360
; CURRENT FILING DATE: 1998-11-28
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

US-09-197-360-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3727 TATTTATGTATTGTC 3742
|||||
Db 1 TATTTATGTATTATC 16

RESULT 215

US-09-437-076-2/c
; Sequence 2, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
; APPLICANT: Barber-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; CURRENT APPLICATION NUMBER: US/09/437,076
; CURRENT FILING DATE: 1999-11-09
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Word for Windows
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-437-076-2

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACCAACC 946
|||||
Db 17 AAAAAAAAAAAAAAAAACC 2

RESULT 216

US-08-679-645-1157
; Sequence 1157, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA: US/08/679,645
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-1157

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 586 CTCCTCCGCGCTCGCC 601
|:|||||:|:|
Db 2 CUCCTCCGCGCTCGCC 17

RESULT 217

US-09-637-751A-7/c
; Sequence 7, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Peng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6383754
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/637,751A
; CURRENT FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-7

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2816
|||||
Db 18 TGAATAAAAAAAAAA 3

RESULT 218

US-09-856-074B-19
; Sequence 19, Application US/09856074B
; Patent No. 6395545
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-ALPHA EXPRESSION
; FILE REFERENCE: RTSP-0117
; CURRENT APPLICATION NUMBER: US/09/856,074B
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US/09/197,360
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US/09/856,074
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-856-074B-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3727 TATTTTATGTATGTC 3742
|||||
DB 1 TATTTTATGTATTATC 16

RESULT 219
US-09-725-265-15/c
; Sequence 15, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-15

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
|||||
DB 18 ATATATATTTTCTT 3

RESULT 220
US-09-725-265-16/c
; Sequence 16, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-16

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
|||||
DB 18 ATATATATTTTCTT 3

RESULT 221
US-09-725-265-17/c
; Sequence 17, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17

```
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 222
US-09-725-265-19/c
; Sequence 19, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199933USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-19

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 223
US-09-556-127-15/c
; Sequence 15, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-15

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 224
US-09-556-127-16/c
; Sequence 16, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-16

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 225
US-09-556-127-17/c
; Sequence 17, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
```

; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
|||||
Db 18 ATATATATTTTCTT 3

RESULT 226
US-09-556-127-19/c
; Sequence 19, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOKAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
|||||
Db 18 ATATATATTTTCTT 3

RESULT 227
US-09-994-311-7/c
; Sequence 7, Application US/09994311
; Patent No. 6773886
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew B.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Peng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6773886
; FILE REFERENCE: AGL 100

; CURRENT APPLICATION NUMBER: US/09/994,311
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-7

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACA 2816
|||||
Db 18 TGAATAAAAAAAAAACA 3

RESULT 228
US-09-904-744-2/c
; Sequence 2, Application US/09904744
; Patent No. 6828142
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; TITLE OF INVENTION: dendrimers in a signal amplification system
; FILE REFERENCE: B-73
; CURRENT APPLICATION NUMBER: US/09/904,744
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/437076
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/107828
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-09-904-744-2

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACCAACC 946
|||||
Db 17 AAAAAAAAAACCAACC 2

RESULT 229
US-08-832-021-5/c
; Sequence 5, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-5

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAGAAAAA 2587
|||||

Db 14 TTAAGAAAAA 1

RESULT 230

US-08-832-021-9/c
; Sequence 9, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-9

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAAGAAAAA 2814
|||||

Db 14 TGAAGAAAAA 1

RESULT 231

US-08-724-466B-17/c
; Sequence 17, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.;
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-17

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAGAAAAA 2587
|||||

Db 14 TTAAGAAAAA 1

RESULT 232

US-08-724-466B-21/c
; Sequence 21, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.;
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-21

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814
Db 14 TGAIAAAAAAAAAA 1

RESULT 233
US-08-882-164D-17/c
; Sequence 17, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-17

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAIAAAAAAAAAA 2587
Db 14 TTAIAAAAAAAAAA 1

RESULT 234
US-08-882-164D-21/c
; Sequence 21, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario

; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-21

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814
Db 14 TGAIAAAAAAAAAA 1

RESULT 235
US-08-535-249-57/c
; Sequence 57, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; immunosuppressive effect of transforming-growth-factor beta (1
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993


```
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-57

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACACTGTGTG 1232
Db 14 TGCACACTGTGTG 1

RESULT 236
US-08-535-249-63/c
; Sequence 63, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/535,249
; PRIORITY DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: EP 93 107 089.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-57
```

```
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-63

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357
Db 14 CAGATCCTGAGCAA 1

RESULT 237
US-08-535-249-71/c
; Sequence 71, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/535,249
; PRIORITY DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: EP 93 107 089.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-71

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520
Db 14 AGTACTACGCCAAG 1520
```

Db 14 AGTACTACGCAAG 1

RESULT 238

US-08-535-249-74/c

; Sequence 74, Application US/08535249

; Patent No. 6455689

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann

; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/535,249

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)638-6666

; TELEFAX: (202) 393-5350

; TELEX: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

; US-08-535-249-74

Query Match

Best Local Similarity 0.3%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1561 AAAATGCCATCCCG 1574

|||||

Db 14 AAAATGCCATCCCG 1

RESULT 239

US-08-535-249-75/c

; Sequence 75, Application US/08535249

; Patent No. 6455689

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann

; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-75

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTTCTACAG 1588
|||||
Db 14 CCCACTTTCTACAG 1

RESULT 240
US-08-535-249-91/c
; Sequence 91, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-91

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1807 AATGGCTCTCCTTC 1820
DB 14 AATGGCTCTCCTTC 1

RESULT 241
US-08-535-249-101/c
Sequence 101, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7

FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-101

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCAC 1984
DB 14 GGTATTGATGGCAC 1

RESULT 242
US-08-535-249-103/c
Sequence 103, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-103

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1997 CAGTGGTGATCAGA 2010
Db      14 CAGTGGTGATCAGA 1
|||||

RESULT 243
US-08-535-249-106/c
; Sequence 106, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-106

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2046 AAGACCCCATCT 2059
Db      14 AAGACCCCATCT 2059
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|||||
Db      14 AAGACCCCATCT 1
|||||

RESULT 244
US-08-535-249-122/c
; Sequence 122, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-122

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2278 GGAGTTCAGACACT 2291
Db      14 GGAGTTCAGACACT 1
|||||

RESULT 245
US-08-535-249-136/c
; Sequence 136, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
```

APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS: 137
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-136

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 246
US-09-475-947A-310
Sequence 310, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTS00667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 310
LENGTH: 14
TYPE: DNA
ORGANISM: human
US-09-475-947A-310

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 931 AAAAAAAAAACAAA 944
Db 1 AAAAAAAAAACAAA 14
RESULT 247
US-08-182-968A-299/c
Sequence 299, Application US/08182968A
Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/277
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 299:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-182-968A-299

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCGAGAGGCT 3223
Db 15 TGCCGAGAGGCT 2

RESULT 248
US-08-182-968A-300/c
Sequence 300, Application US/08182968A
Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION

; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-300

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCGAGAGGCT 3223
Db 14 TGCCGAGAGGCT 1

RESULT 249
US-08-292-620A-359/c
; Sequence 359, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwigen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION DATA: including application
; APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-359

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAT 2589
Db 15 AAAAAAAAAAAAT 2

RESULT 250
US-08-292-620A-360/c
; Sequence 360, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwigen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
FILING DATE: December 7, 1992

two

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 360:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-360

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0;

QY 2576 AAAAAAAAAAAT 2589

Db 14 AAAAAAAAAAAT 1

RESULT 251

US-08-292-620A-364/C
Sequence 364, Application US/08292620A
Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

two

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 364:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-364

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0;

QY 2801 TGAIAAAAAAAAAA 2814

Db 15 TGAIAAAAAAAAAA 2

RESULT 252

US-08-292-620A-365/C
Sequence 365, Application US/08292620A
Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

two

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 365;
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-365

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TCAAAAAAAAAA 2814
DB 14 TCAAAAAAAAAA 1

RESULT 253
US-08-774-306A-299/c
Sequence 299, Application US/08774306A
Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
INHIBITING HEPATITIS C
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774.306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 299;
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-299

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223
DB 15 TGCCCAAGGCCT 2

RESULT 254
US-08-774-306A-300/c
Sequence 300, Application US/08774306A
Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
INHIBITING HEPATITIS C
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774.306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 300;
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-300

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223
DB 14 TGCCCAAGGCCT 1

RESULT 255
US-08-886-456-1/c
Sequence 1, Application US/08886456
Patent No. 5959090
GENERAL INFORMATION:
APPLICANT: Guzaev, Andrei
APPLICANT: Azhayev, Alex

APPLICANT: Lomborg, Harri
TITLE OF INVENTION: Chemical Phosphorylation of Oligonucleotides and
FILE OF INVENTION: Reactants Used Therefor
FILE REFERENCE: 05566.0009-00
CURRENT APPLICATION NUMBER: US/08/886,456
CURRENT FILING DATE: 1997-07-01
EARLIER APPLICATION NUMBER: 60/021,099

; EARLIER FILING DATE: 1996-07-02
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Rattus rattus
US-08-886-456-1

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2524 ACGACCATGATGTT 2537
Db 15 ACGACCATGATGTT 2

RESULT 256
US-08-832-021-18/c
; Sequence 18, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-18

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587
Db 14 TTAATAAAAAAAAAA 1

RESULT 257
US-08-832-021-19
; Sequence 19, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-19

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAG 2758
Db 2 TTTTNTTTTAAAG 15

RESULT 258
US-08-832-021-19/c
; Sequence 19, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-19

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587
Db 14 TTAATAAAAAAAAAA 1

RESULT 259
US-08-832-021-20/c
; Sequence 20, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-20

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587

```

; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-24

Query Match          0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
DB 14 TGAATAAAAAAAAAA 1

RESULT 263
US-09-064-156A-299/c
; Sequence 299, Application US/09064156A
; Patent No 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 299:

```

```

; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-21

Query Match          0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
DB 14 TGAATAAAAAAAAAA 1

RESULT 261
US-08-832-021-23/c
; Sequence 23, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-23

Query Match          0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
DB 14 TGAATAAAAAAAAAA 1

RESULT 262
US-08-832-021-24/c
; Sequence 24, Application US/08832021

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-064-156A-299

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCGAGAGGCCT 3223
Db 15 TGCCGAGAGGCCT 2

RESULT 264
US-09-064-156A-300/c
; Sequence 300, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 300:

/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-064-156A-300

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCGAGAGGCCT 3223
Db 14 TGCCGAGAGGCCT 1

RESULT 265
US-09-071-845-359/c
; Sequence 359, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-359

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAT 2589
Db 15 AAAAAAAAAAAT 2

RESULT 266
US-09-071-845-360/c
; Sequence 360, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:

```

; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-360

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAT 2589
Db 14 AAAAAAAAAAAAT 1

RESULT 267
US-09-071-845-364/c
; Sequence 364, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS

```

```

; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 364:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-364

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814
Db 15 TGAIAAAAAAAAAA 2

RESULT 268
US-09-071-845-365/c
; Sequence 365, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

```

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/009,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 365:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-365

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814
Db 14 TGAIAAAAAAAAAA 1

RESULT 269
US-08-242-664-30/c
Sequence 30, Application US/08242664
Patent No. 5571937
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-242-664-30

Query Match 0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1169 TTTTCTTACTTT 1182
Db 15 TTTTCTTACTTT 2

RESULT 270
US-08-484-138-30/c
Sequence 30, Application US/08484138
Patent No. 5652350
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-2/JPW/WJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-138-30

Query Match 0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1169 TTTTCTTACTTT 1182
|||||

```

Db      15 TTTTCTTACTTT 2

RESULT 271
PCT-US95-06379-30/c
; Sequence 30, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-30

Query Match      0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1169 TTTTCTTACTTT 1182
        |||||
Db      15 TTTTCTTACTTT 2

RESULT 272
US-09-300-958A-63/c
; Sequence 63, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85

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```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-63

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2575 TAAAAAAAAAAAAA 2588
        |||||
Db      17 TAAAAAAAAAAAAA 4

RESULT 273
US-09-090-672B-105/c
; Sequence 105, Application US/09090672B
; Patent No. 6828428
; GENERAL INFORMATION:
; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
US-09-090-672B-105

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2575 TAAAAAAAAAAAAA 2588
        |||||
Db      17 TAAAAAAAAAAAAA 4

```

```
RESULT 274
US-09-300-958A-63
; Sequence 63, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-63

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3263 ATTTTTCCTTTTA 3279
Db 1 ATTTTTCCTTTTA 17

RESULT 275
US-08-281-940-54
; Sequence 54, Application US/08281940
; Patent No. 5589330
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: METHOD FOR MULTIPLE ALLELE-SPECIFIC
; TITLE OF INVENTION: DISEASE ANALYSIS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY P.C.
; STREET: 805 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,940
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUDWIG, S. PETER
; REGISTRATION NUMBER: 25351
; REFERENCE/DOCKET NUMBER: 0372/09696
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/527-7700
; TELEFAX: 212/753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
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```
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; IMMEDIATE SOURCE:
; CLONE: 2184GAN
US-08-281-940-54

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
Db 1 GATTGTATATTGTTTC 17

RESULT 276
US-08-758-306-1333
; Sequence 1333, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1333:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-1333

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.4e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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```
QY 3761 ACCTGGGTCCATTCCTC 3777
|||:|||||:|:|
Db 1 ACCUGGCUCCAUGCUC 17

RESULT 277
US-08-710-134-54
; Sequence 54, Application US/08710134
; Patent No. 5834181
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,134
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-8.1
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-8415
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-710-134-54

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
|||:|||||:|:|
Db 1 GATTGTTTTTGTTC 17

RESULT 278
US-08-485-885-54
; Sequence 54, Application US/08485885
; Patent No. 5849483
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
|||:|||||:|:|
Db 1 GATTGTTTTTGTTC 17

RESULT 279
US-08-985-162-647/c
; Sequence 647, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McGswiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,885
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-12.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-485-885-54

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
|||:|||||:|:|
Db 1 GATTGTTTTTGTTC 17

RESULT 279
US-08-985-162-647/c
; Sequence 647, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McGswiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
```



```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 647:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-985-162-647
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3058 GATGGCTTAAGGAGTTT 3074
Db 17 GATGGCTAAAGGAGATT 1

RESULT 280
US-08-998-099-52
; Sequence 52, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-08-998-099-52
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.4e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 903 GAGCCACTCACCTCTC 919
Db 1 GAGCCCCCUCACCCUUUC 17

RESULT 281
US-09-135-020-7
; Sequence 7, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29

;
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-135-020-7
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1344 CAGATCCTGAGCAAGCT 1360
Db 1 CAGATCCTGAGGATGCT 17

RESULT 282
US-09-135-010A-7
; Sequence 7, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/135,010A
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-135-010A-7
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1344 CAGATCCTGAGCAAGCT 1360
Db 1 CAGATCCTGAGGATGCT 17

RESULT 283
US-09-444-871-7
; Sequence 7, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
```

```
/ TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
/ FILE REFERENCE: 2323-131
/ CURRENT APPLICATION NUMBER: US/09/444,871
/ CURRENT FILING DATE: 1999-11-22
/ EARLIER APPLICATION NUMBER: US 09/135,020
/ EARLIER FILING DATE: 1998-08-17
/ EARLIER APPLICATION NUMBER: 08/921,068
/ EARLIER FILING DATE: 1997-08-29
/ EARLIER APPLICATION NUMBER: 08/739,383
/ EARLIER FILING DATE: 1996-10-29
/ EARLIER APPLICATION NUMBER: 60/019,014
/ EARLIER FILING DATE: 1995-12-22
/ EARLIER APPLICATION NUMBER: 60/094,477
/ EARLIER FILING DATE: 1998-07-29
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-444-871-7

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAGCT 1360
Db 1 CAGATCCTGAGGATGCT 17

RESULT 284
US-08-584-040-1690/c
/ Sequence 1690, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 114:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-584-040-1690
```

```
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1690:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-584-040-1690

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4228 AGGTTTTGAACACATT 4244
Db 17 AGGTTTTTAACACATT 1

RESULT 285
US-08-584-040-2186/c
/ Sequence 2186, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2186:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-584-040-2186

Query Match      0.3%; Score 13.8; DB 1; Length 17;
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```
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTGAAAAAAGCA 2816
Db 17 GTCAAAAAAGCA 1

RESULT 286
US-08-584-040-2315
; Sequence 2315, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2315:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2315

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 862 ACTGAACCTCATTCTT 878
Db 1 ACUUAACUCAAUUCUU 17

RESULT 287
US-08-584-040-2544/c
; Sequence 2544, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2544:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2544/c

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2579 AAAAAAATTCGAGA 2595
Db 17 AAAAAAAGTAGAGA 1

RESULT 288
US-08-584-040-2545/c
; Sequence 2545, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2544:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2544
```

```

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2545:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2545

```

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Caps 0;

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QY 2578 AAAAAAAAAAATTGGAG 2594
|||||
DB 17 AAAAAAAAAAAGTAGAG 1

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RESULT 289
US-08-584-040-2546/c
; Sequence 2546, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

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```

; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2546:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2546

```

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Caps 0;

```

```

QY 2577 AAAAAAAAAAATTGGA 2593
|||||
DB 17 AAAAAAAAAAAGTAGA 1

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```

RESULT 290
US-08-584-040-2547/c
; Sequence 2547, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2547:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-2547

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAATTGG 2592
Db 17 AAAAAAAAAAAGTAG 1

RESULT 291
US-08-584-040-2551/c
; Sequence 2551, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2551:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2551

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 GAGAAAAAAACAA 944
Db 17 GAAAAAAACAAAAA 1

RESULT 292
US-08-584-040-2552/c
; Sequence 2552, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2552:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2552

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGAGAAAAAAACAA 943
Db 17 GAAAAAAACAAAAA 1

RESULT 293
US-08-584-040-2556/c
; Sequence 2556, Application US/08584040

```

; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2556:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2556

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```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2798 ATGTGAAAAA 2814
Db 17 ATTTGAAAAA 1

```

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RESULT 294
US-08-584-040-2727
; Sequence 2727, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2727:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2727

```

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 2.4e+02;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3702 TTTTATATCTTC 3718
Db 1 UUUUGUACCAUUC 17

```

```

RESULT 295
US-08-584-040-4005
; Sequence 4005, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible

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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4030 TATGGACTCTTTGCC 4046
    :|||||:|:|
Db 1 UCUGGACUCUCUGCC 17

RESULT 298
US-08-584-040-5563
; Sequence 5563, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5563:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-5563

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 246 TCGAAGCTAGGAGAAGC 262
    :|||||:|:|
Db 1 UGGCAGCUGAAGAAGC 17

RESULT 299
US-08-584-040-5963
; Sequence 5963, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5963:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-5963

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTGGCGTTCA 4051
    ||:|:|:|:|:|
Db 1 ACUCUCUUUCCAUAUCA 17

RESULT 300
US-08-584-040-7626/c
; Sequence 7626, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5963:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-5963

```


NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7626:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-7626

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 GAGCTGCTGAACTGCC 50
|||||
Db 17 GAGCTGCTGACACTGTC 1

RESULT 301
US-08-679-645-878/c
Sequence 878, Application US/08679645
Patent No. 6350934
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 878:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-878

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 931 AAAAAAAAAACCAACT 947
|||||
Db 17 AAAAAAACAACCAAGCT 1

RESULT 302
US-09-597-735-7
Sequence 7, Application US/09597735
Patent No. 6420124
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/597,735
CURRENT FILING DATE: 2000-06-19
EARLIER APPLICATION NUMBER: 09/135,010
EARLIER FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-597-735-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360
|||||
Db 1 CAGATCCTGAGGATGCT 17

RESULT 303
US-09-444-295-7
; Sequence 7, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN mink WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/444,295
; CURRENT FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-295-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360
|||||
Db 1 CAGATCCTGAGGATGCT 17

RESULT 304
US-09-597-732-7
; Sequence 7, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29

; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-732-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360
|||||
Db 1 CAGATCCTGAGGATGCT 17

RESULT 305
US-09-475-947A-118/c
; Sequence 118, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 17
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-118

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 CGAGAGAAAAAACA 943
|||||
Db 17 GAAAAA 1

RESULT 306
US-09-474-432B-757/c
; Sequence 757, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 757
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-757

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCCGAAGG 3220
||| |||||
Db 17 GGCAGATGCCCGAAGG 1

RESULT 307

US-09-371-772B-235/c
; Sequence 235, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-235

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4228 AGGTTTGAAGACATT 4244
||||| |||||
Db 17 AGGTTTGAAGACATT 1

RESULT 308

US-09-371-772B-731/c
; Sequence 731, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-731

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTGAAAAAACA 2816
||| |||||
Db 17 GTCAAAAAACA 1

RESULT 309

US-09-371-772B-860
; Sequence 860, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 860
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-860

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 862 ACTGAACCTCCATTCTT 878
||: |||: |||: |||:
Db 1 ACUAAACUAAUUUCUU 17

RESULT 310

US-09-371-772B-1068/c
; Sequence 1068, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08

```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1068
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1068

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2579 AAAAAAAAAAATTGGAGA 2595
    |||||
Db 17 AAAAAAAAAAAGTAGAGA 1

RESULT 311
US-09-371-772B-1069/c
; Sequence 1069, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1069
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1069

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594
    |||||
Db 17 AAAAAAAAAAAGTAGAG 1

RESULT 312
US-09-371-772B-1070/c
; Sequence 1070, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225

```

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1070
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1070

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAAAAAATTGGA 2593
    |||||
Db 17 AAAAAAAAAAAGTAGA 1

RESULT 313
US-09-371-772B-1071/c
; Sequence 1071, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1071

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAATTGG 2592
    |||||
Db 17 AAAAAAAAAAAGTAG 1

RESULT 314
US-09-371-772B-1075/c
; Sequence 1075, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 1075
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 GAGAAAAAACAATA 944
 |||||
Dd 17 GAAAAAAACAAA 1

RESULT 315

US-09-371-772B-1076/c
; Sequence 1076, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MCSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MBHB00.876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772.25
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 60/005,974
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: Patent in version 3.0

```

; COLIMARS: 100
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA

```

; ORGANISM: Homo sapiens
US-09-371-772B-1076

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels

Qy 927 GGAGAAAAA AAAAACA 943
||| ||||| ||||| |||
Db 17 GGAAAAA AAAAACA 1

RESULT 316

US-09-371-772B-1080/S
; Sequence 1080, Application US/09371772B
; Patent No. 8566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00.876-J (237/198)

```

CURRENT APPLICATION NUMBER: US/09/371,772.28
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 60/005,974
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: Patent in version 3.0

; SEQ ID NO 1080

; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM:
 US-09-371-772B

```
Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2798 ATGTGAAAAAAAAAAAAA 2814
 |||
 Db 17 ATTTGGAATAAAAAAAAAA 1

RESULT 317

US-09-371-772B-1251
; Sequence 1251, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MCSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
;
; FILE REFERENCE: MBHB00_876-J (237/198)
;

```

```

, , CURRENT APPLICATION NUMBER: US/09/371,772EN
, , CURRENT FILING DATE: 1999-08-10
, , PRIOR APPLICATION NUMBER: US 60/005,974
, , PRIOR FILING DATE: 1995-10-26
, , PRIOR APPLICATION NUMBER: US 08/584,040
, , PRIOR FILING DATE: 1996-01-08
, , NUMBER OF SEQ ID NOS: 14225
, , SOFTWARE: PatentIn version 3.0
, , SEQ ID NO 1251

```

```
;
; LENGTH: 17
; TYPE: RNA
; ORGANISM: M
```

US-09-371-772B-1251

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 2.4e+02;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Qy 3702 TTTTATATACTATCTTC 3718
db 1 UUUUGUAUACCAUCUC 17

RESULT 318

```

US-09-371-772B-1772
; Sequence 1772, Application US/09371772B
; Patent No. 656127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```

```

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Res
;
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
;
; FILE REFERENCE: MBHB00, 876-J (237/198)

```

CURRENT APPLICATION NUMBER: US/09/371,772/23
CURRENT FILING DATE: 1999-08-10
PRIORITY APPLICATION NUMBER: US 60/005,974
PRIORITY FILING DATE: 1999-10-26
PRIORITY APPLICATION NUMBER: US 08/584,040
PRIORITY FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1772

; LENGTH: 17

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1772

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GCTCTCTTCGAGTGCA 1827
    | : : | : : | : : | : : | : : |
Db 1 GAUCUCCUCCACGUGA 17

RESULT 319
US-09-371-772B-1781/c
; Sequence 1781, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1781
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1781

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1849 TTCACCACCAAGACAGG 1865
    | : : | : : | : : | : : | : : |
Db 17 TGCACCACCAAGACAGC 1.

RESULT 320
US-09-371-772B-2067
; Sequence 2067, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2067
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
; ORGANISM: Homo sapiens
US-09-371-772B-2067

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.4e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4030 TATGGACTCTCTTGCC 4046
    : : : : | : : | : : | : : | : : |
Db 1 UCUGGACUCUCUCUGCC 17

RESULT 321
US-09-371-772B-2453
; Sequence 2453, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2453
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2453

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 246 TGAAGCTAGGAGAGC 262
    : : | : : | : : | : : | : : |
Db 1 UGGCAGCUAGAGAGC 17

RESULT 322
US-09-371-772B-2800
; Sequence 2800, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2800
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
```

US-09-371-772B-2800

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTTCCGTTCA 4051
||:|::|:|:|:
Db 1 ACUCUCUUUCAUCA 17

RESULT 323

US-09-371-772B-3418/c
; Sequence 3418, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3418
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3418

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAACTGCC 50
|||||||
Db 17 GAGCTGCTGACACTGTC 1

RESULT 324

US-09-371-772B-5235
; Sequence 5235, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5235
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5235

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTTCCGTTCA 4051
||:|::|:|:|:
Db 1 ACUCUCUUUCAUCA 17

RESULT 323

US-09-371-772B-3418/c
; Sequence 3418, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3418
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3418

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAACTGCC 50
|||||||
Db 17 GAGCTGCTGACACTGTC 1

RESULT 324

US-09-371-772B-5235
; Sequence 5235, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5235
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5235

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.4e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 861 CACTGAATCCATTCT 877
||:|::|:|:|:
Db 1 CACUUAACUAAUUCU 17

RESULT 325

US-09-371-772B-5435/c
; Sequence 5435, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5435
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5435

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTGGAGAA 2596
|||||||
Db 17 AAAAAAAGTAGAGAA 1

RESULT 326

US-09-371-772B-5582/c
; Sequence 5582, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5582
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5582

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2750 TTTTAAAGGAAAAA 2766
DB 17 TTATTTTAGGAAAAA 1

RESULT 327
US-09-371-772B-5583/c
; Sequence 5583, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5583
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5583

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2749 TTTTAAAGGAAAAA 2765
DB 17 TTATTTTAGGAAAAA 1

RESULT 328
US-09-371-772B-6814
; Sequence 6814, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6814
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6814

Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTGGC 4045
DB 1 UUCUGACUCUCUGC 17

RESULT 329
US-09-597-731-7
; Sequence 7, Application US/09597731
; Patent No. 6582913
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,731
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-731-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360
DB 1 CAGATCCTGAGCATGCT 17

RESULT 330
US-09-476-387-756/c
; Sequence 756, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29


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; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 756
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-756

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCAGAAG 3220
Db 17 GGCAGATGCCAGAAG 1

RESULT 331
US-09-401-063-647/c
; Sequence 647, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggan, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 647:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-401-063-647

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3058 GATGGCTTAAGGAGTTT 3074
Db 17 GATGGCTTAAGGAGATT 1

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 332
US-09-866-108A-243
; Sequence 243, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-243

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 496 ATCCTCGCGCGCTGTC 512
Db 1 ATCCTCGCGCGCTGTC 17

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 333
US-09-866-108A-1065/c
; Sequence 1065, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
```

```
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 1065
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-1065

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2713 CTACTTCCTTAAGACA 2729
DB 17 CTACGTCCTTAGAGACA 1

RESULT 334
US-09-866-108A-1066/c
/ Sequence 1066, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 1065
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-1065
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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 1066
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-1066

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2712 CCTACTTCCTTAAGAC 2728
DB 17 CCTACGTCCTTAGAGAC 1

RESULT 335
US-09-866-108A-2222
/ Sequence 2222, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 2222
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-2222

Query Match      0.3%; Score 13.8; DB 1; Length 17;
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```
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 675 GTGTGAAGCAGGGCC 691
Db 1 GTGTGATGCACGGTC 17

RESULT 336
US-09-866-108A-8557
; Sequence 8557, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8557
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8557

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1462 CAAGCCGAGGGCAGCC 1478
Db 1 CCAGCCAGAGGGCAGCC 17

RESULT 338
US-09-866-108A-10508/c
; Sequence 10508, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2519 CGATGAGCACCATGATG 2535
Db 1 CGATGAGCACCAGGATG 17

RESULT 337
US-09-866-108A-9226
; Sequence 9226, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
```

/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 10508
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-10508

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2928 CTCCCGCTCCCTTCCTC 2944
DB 17 CTCCCGCTCCCTGGCTC 1

RESULT 339
US-09-866-108A-10509/c
/ Sequence 10509, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aecomica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 10509
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-10509

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2927 CTCCCGCTCCCTTCCT 2943
DB 17 CTCCCGCTCCCTGGCT 1

RESULT 340
US-09-129-603-4/c
/ Sequence 4, Application US/09129603A
/ Patent No. 6790944
/ GENERAL INFORMATION:
/ APPLICANT: Ishiwata, Tetsuyoshi
/ APPLICANT: Sakurada, Mikiko
/ APPLICANT: Nishimura, Ayako
/ APPLICANT: Nakagawa, Satoshi
/ APPLICANT: Kuga, Tetsuro
/ APPLICANT: Nishi, Tatsunari
/ APPLICANT: No. 6790944ura, No. 6790944uo
/ APPLICANT: Sawada, Shigemasa
/ APPLICANT: Nagase, Takahiro
/ APPLICANT: Takei, Masami
/ TITLE OF INVENTION: No. 6790944el Protein
/ FILE REFERENCE: 766.25
/ CURRENT APPLICATION NUMBER: US/09/129,603A
/ CURRENT FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: PCT/JP97/04469
/ EARLIER FILING DATE: 1997-12-05
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: other nucleic acid from homo sapiens, synthesized
/ OTHER INFORMATION: DNA
US-09-129-603-4

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAACAACACC 946
DB 17 GAAAAAACAACACC 1

RESULT 341
US-09-685-664B-235/c
/ Sequence 235, Application US/09685664B
/ Patent No. 6818447
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-K (400/021)
/ CURRENT APPLICATION NUMBER: US/09/685,664B
/ CURRENT FILING DATE: 2000-10-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ PRIOR APPLICATION NUMBER: US 09/371,772
/ PRIOR FILING DATE: 1999-08-10
/ NUMBER OF SEQ ID NOS: 8231
/ SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 235
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-235

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4228 AGCTTTTGAAGACATT 4244
Db 17 AGGTTTITTAACACATT 1

RESULT 342
US-09-685-664B-731/c
; Sequence 731, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-731

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTGAAAAAAGCA 2816
Db 17 GTCAAAAAAGCA 1

RESULT 343
US-09-685-664B-860
; Sequence 860, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
```

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; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 860
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-860

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 862 ACTGAACCTCCATTCTT 878
Db 1 ACUUAACUCAAUUUCUU 17

RESULT 344
US-09-685-664B-1068/c
; Sequence 1068, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1068
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1068

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2579 AAAAAAAATTGAGA 2595
Db 17 AAAAAAAAGTAGAGA 1

RESULT 345
US-09-685-664B-1069/c
; Sequence 1069, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
```

RESULT 347
US-09-685-664B-1071/c
: Sequence 1071, Application US/09685664B
: Patent No. 6818447
: GENERAL INFORMATION:
: APPLICANT: Ribozyme Pharmaceuticals, Inc.
: APPLICANT: Pavco, Pam
: APPLICANT: McSwiggen, Jim
: APPLICANT: Stinchcomb, Dan
: APPLICANT: Stinchcomb, Jaime
: TITLE OF INVENTION: Method and Reagent for
: TITLE OF INVENTION: Levels of Vascular En
: FILE REFERENCE: MBHB00-876-K (400/021)
: CURRENT APPLICATION NUMBER: US/09/685,664B

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Qy      928 GAGAAAAAAGAAAAACAAA 944
      || |||||
Db      17 GAAAAAAGAAAAAAGAAAAA 1
      || |||||

RESULT 349
US-09-685-664B-1076/c
; Sequence 1076, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Payco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent fo

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; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1076

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGNAGAAAAAACA 943
DB 17 GGNAAAAA 1

RESULT 350
US-09-685-664B-1080/c
; Sequence 1080, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1080
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1080

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2798 ATGTGAAAAA 2814
DB 17 ATTTGAAAAA 1

RESULT 351
US-09-685-664B-1251
; Sequence 1251, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1251
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1251

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 2.4e+02;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 3702 TTTTATATCTTC 3718
DB 1 UUUUGUACCAUUC 17

RESULT 352
US-09-685-664B-1772
; Sequence 1772, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1772
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1772

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GCTCTCTTCGACGTGA 1827
DB 1 GAUCCUCCUCCGACGUGA 17

RESULT 353
US-09-685-664B-1781/c
; Sequence 1781, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
```

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1781
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1781

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1849 TTACCCACAAAGACAGG 1865
DB 17 TGCACCACAAAGACAGC 1

RESULT 354
US-09-685-664B-2067
; Sequence 2067, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2067
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-2067

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.4e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4030 TATGGACTCTTTGGC 4046
DB 1 UCUGGACUCUCUCUGCC 17

RESULT 355
US-09-685-664B-2453
```

```
; Sequence 2453, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2453
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2453

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 246 TCGAAGCTAGGAGAGC 262
DB 1 UGGCAGCUAGAGAGC 17

RESULT 356
US-09-685-664B-2800
; Sequence 2800, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2800
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2800

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTTGGCTTCA 4051
DB 1 ACUCUCUUUCCAUA 17
```



```
RESULT 357
US-09-685-664B-3418/c
; Sequence 3418, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHBB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685.664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3418
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3418

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 GAGCTGCTGAACTGCC 50
Db 17 GAGCTGCTGACATGTC 1

RESULT 358
US-09-090-672B-107/c
; Sequence 107, Application US/09090672B
; Patent No. 6828428
; GENERAL INFORMATION:
; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoehi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
US-09-090-672B-107

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAACAACCC 946
Db 17 GAAAAAACAACCC 1

RESULT 359
US-09-750-401-29/c
; Sequence 29, Application US/09750401
; Patent No. 6635422
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 33
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-29

Query Match          0.3%; Score 13.8; DB 1; Length 33;
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2737 AAAACATCTTTTAAAAAGGAAAAAATTA 2769
Db 33 AAGAACCATTACAAATTAAGGAAAAAATA 1

RESULT 360
US-08-882-649A-8/c
; Sequence 8, Application US/08882649A
; Patent No. 6344316
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; APPLICANT: Chee, Mark
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chaoqiang, Lai
; APPLICANT: Wodicka, Lisa
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Lee, Danny
; APPLICANT: Tran, Huu M.
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Joe Liebeschuetz
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,649A
FILING DATE: 25-Jun-1997
CLASSIFICATION: 435-006.000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,471
FILING DATE: 23-JAN-1996
APPLICATION NUMBER: US 60/035,170
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: PCT/US97/01603
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-019410US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
(ix) Features:
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-882-649A-8

Query Match 0.3%; Score 13.6; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAAACC 946
Db 16 AAAAAAAAAAAAAABC 1

RESULT 361
US-09-644-827B-10/C
; Sequence 10, Application US/09644827B
; Patent No. 6762283
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: SCHUCHMANN, Marcus
; APPLICANT: GONCHAROV, Tanya
; TITLE OF INVENTION: Caspase-8 Interacting Proteins
; FILE REFERENCE: WALLACH=26
; CURRENT APPLICATION NUMBER: US/09/644, 827B
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 132105
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 127721
; PRIOR FILING DATE: 1998-12-24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:

OTHER INFORMATION: synthetic
US-09-644-827B-10
Query Match 0.3%; Score 13.6; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 975 CCCCCCAGCCGCCCC 990
Db 16 CCCCCCAGCCGCCCC 1
RESULT 362
US-08-363-240A-33
; Sequence 33, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-33
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 829 TTCAGATCAGCCACT 843
Db 1 UCCAGCAUCCGACCU 15

RESULT 363
US-08-292-620A-356/C

; Sequence 356, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-356

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAAAACTCAAA 2821
Db 15 AAAAAAAAAATCAAA 1

RESULT 364
US-08-292-620A-357/c
; Sequence 357, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 357:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-357

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2806 AAAAAAAAACTCAA 2820
Db 15 AAAAAAAAAATCAA 1

RESULT 365
US-08-292-620A-358/c
; Sequence 358, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-358

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two

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Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2805 AAAAAAAAAACATCA 2819
Db 15 AAAAAAAAAACATCA 1

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RESULT 366
US-08-292-620A-363/c
; Sequence 363, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

```

```

; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 363:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-363

```

```

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 930 GAAAAAAAAACAAA 944
Db 15 GAAAAAAAAACAAA 1

```

```

RESULT 367
US-08-292-620A-366/c
; Sequence 366, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1

```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 366:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-366

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2799 TGTGAAAAA 2813
Db 15 TCTGAAAAA 1

RESULT 368
US-08-585-684B-824/c
; Sequence 824, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 825:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-825

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2510 TAATGACGATGA 2524
Db 15 CAACGATGACGACGA 1
```

```
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 824:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-824

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2516 CAACGATGACGACCA 2530
Db 15 CAACGATGACGACGA 1

RESULT 369
US-08-585-684B-825/c
; Sequence 825, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 825:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-825

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2510 TAATGACGATGA 2524
Db 15 CAACGATGACGACGA 1
```

Best Local Match	Similarity	Local Match	Indels	Gaps
Matches	14: Conservative	0: Mismatches	1: Indels	0: Gaps

```
; APPLICATION NUMBER: US/08/893.204C
; FILING DATE: 7/15/97
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenberg Morton
; REGISTRATION NUMBER: 26,049
; REFERENCE/DOCKET NUMBER: MR2493-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (410) 465-6678
; TELEFAX: (410) 461-3067
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; ORIGINAL SOURCE: synthetic
; PUBLICATION INFORMATION:
; AUTHORS: Katherine Meyer-Siegler
; OTHERS: Perry Hudson
; TITLE: Enhanced Expression of Macrophage Migration
; TITLE: Inhibitory Factor in Prostatic Adenocarcinoma Metastases
; JOURNAL: Urology
; VOLUME: 48
; ISSUE: 3
; PAGES: 448-452
; DATE: 1996
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 15
; US-08-893-204C-2

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 929 AGAAAAAAACAA 943
Db 15 AGAAAAAAACAA 1

RESULT 373
US-08-832-021-25/c
; Sequence 25, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832.021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-25

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAAACAA 2587
Db 15 TTTAAAAAAACAA 1

RESULT 376
US-08-832-021-34/c
; Sequence 34, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
```

```
RESULT 374
US-08-832-021-26/c
; Sequence 26, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832.021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-26

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2800 GTCAAAAAACAA 2814
Db 15 GTCAAAAAACAA 1

RESULT 375
US-08-832-021-29/c
; Sequence 29, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832.021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-29

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAAACAA 2587
Db 15 TTTAAAAAAACAA 1

RESULT 376
US-08-832-021-34/c
; Sequence 34, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
```

```

; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-34

```

```

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      2800 GTGAAAAAATAAAAA 2814
DB      15 GCGAAAAAATAAAAA 1

```

```

RESULT 377
US-08-832-021-36/c
; Sequence 36, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-36

```

```

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      926 AGGAAAAAATAAAAA 940
DB      15 AGGAAAAAATAAAAA 1

```

```

RESULT 378
US-08-832-021-41/c
; Sequence 41, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382

```

```

; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-41

```

```

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2573 TTTAAAAAATAAAAA 2597
DB      15 TCTAAAAAATAAAAA 1

```

```

RESULT 379
US-08-832-021-43
; Sequence 43, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-43

```

```

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2745 TTTTAAAAAAGG 2759
DB      1 TTTTAAAAAAGG 15

```

```

RESULT 380
US-08-832-021-46/c
; Sequence 46, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: DNA

```


; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-46

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814
| ||||| |||||
Db 15 GCGAAAAAAAAAAAAA 1

RESULT 381
US-08-832-021-53/c
; Sequence 53, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-53

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAAAAAAAAA 2587
| ||||| |||||
Db 15 TATAAAAAAAAAAAAA 1

RESULT 382
US-08-832-021-58/c
; Sequence 58, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-58

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 928 GAGAAAAAAAAACA 942
| ||||| |||||
Db 15 GAGAAAAAAAAAAA 1

RESULT 383
US-08-675-119-2
; Sequence 2, Application US/08675119
; Patent No. 6054442
; GENERAL INFORMATION:
; APPLICANT: Chen, Shih-Fong
; APPLICANT: Maine, Ira
; APPLICANT: Kerwin, Sean M.
; APPLICANT: Fletcher, Terace
; APPLICANT: Salazar, Miguel
; APPLICANT: Mamiya, Blain
; APPLICANT: Wajima, Makoto
; APPLICANT: Windle, Bradford E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: MODULATION AND INHIBITION OF HUMAN
; TITLE OF INVENTION: TELOMERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,119
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: CTCR:028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-675-119-2

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1680 CAAAACCCCAAGCC 1694
| ||||| |||||
Db 1 CAAAACCCCAAGCC 15

RESULT 384
US-08-851-843A-43
; Sequence 43, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "RNA"
US-08-851-843A-43

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15

RESULT 385
US-08-851-843A-45
Sequence 45, Application US/08051843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lirngner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "RNA"
US-08-851-843A-45

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15

RESULT 386
US-09-071-845-356/c
Sequence 356, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 356:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-356

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAACATCAAA 2821
Db 15 AAAAAAACATCAAA 1

RESULT 387
US-09-071-845-357/c
Sequence 357, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-357

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2806 AAAAAAACATCAAA 2820
Db 15 AAAAAAACATCAAA 1

RESULT 388
US-09-071-845-358/c
Sequence 358, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:

```
/
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 358:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-071-845-358

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2805 AAAAAAAAAACATCA 2819
Db 15 AAAAAAAAAAAATCA 1

RESULT 389
US-09-071-845-363/C
/ Sequence 363, Application US/09071845
/ Patent No. 6132967
/ GENERAL INFORMATION:
/ APPLICANT: Susan Grimm
/ APPLICANT: Dan T. Stinchcomb
/ APPLICANT: James McSwiggen
/ APPLICANT: Sean Sullivan
/ APPLICANT: Kenneth G. Draper
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF
/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,845
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 358:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-071-845-358
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/
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 363:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-071-845-363

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 930 GAAAAAAAAACAAA 944
Db 15 GAAAAAAAAAAAAA 1

RESULT 390
US-09-071-845-366/C
/ Sequence 366, Application US/09071845
/ Patent No. 6132967
/ GENERAL INFORMATION:
/ APPLICANT: Susan Grimm
/ APPLICANT: Dan T. Stinchcomb
/ APPLICANT: James McSwiggen
/ APPLICANT: Sean Sullivan
/ APPLICANT: Kenneth G. Draper
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF
/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,845
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 363:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-071-845-363
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; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 366:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-366
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2799 TGTGAAAAA 2813
Db 15 TCTGAAAAA 1

RESULT 391
US-08-974-549A-113
; Sequence 113, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 824:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-974-549A-113
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15

RESULT 392
US-09-038-073-824/c
; Sequence 824, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Fast-Seq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 824:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-824
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2516 CAACGATGACGACCA 2530
Db 15 CAACGATGACGACGA 1

RESULT 393
US-09-038-073-825/c
; Sequence 825, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 825:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-825
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2510 TAATGACACGATGA 2524
Db 15 TGATGACACGATGA 1

RESULT 394
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US-09-038-073-1392/c
; Sequence 1392, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1392:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-1392
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1207 CTTTAAAAAACATGC 1221
Db 15 CTTTAAAAACACGC 1

RESULT 395
US-08-854-050-43
; Sequence 43, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
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;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/854,050
;/ FILING DATE: 09-MAY-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/851,843
;/ FILING DATE: 06-MAY-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/846,017
;/ FILING DATE: 25-APR-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/844,419
;/ FILING DATE: 18-APR-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/724,643
;/ FILING DATE: 01-OCT-1996
;/ CLASSIFICATION: 536
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002930US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 43:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: other nucleic acid
;/ DESCRIPTION: /desc = "RNA"
;/ US-08-854-050-43

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred.No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGGCC 1694
|||||
Db 1 CAAACCCCAAGGCC 15

RESULT 396
US-08-854-050-45
;/ Sequence 45, Application US/08854050
;/ Patent No. 6261836
;/ GENERAL INFORMATION:
;/ APPLICANT: Cech, Thomas R.
;/ APPLICANT: Lingner, Joachim
;/ APPLICANT: Nakamura, Toru
;/ APPLICANT: Chapman, Karen B.
;/ APPLICANT: Morin, Gregg B.
;/ APPLICANT: Harley, Calvin
;/ APPLICANT: Andrews, William H.
;/ TITLE OF INVENTION: No. 6261836el Telomerase
;/ NUMBER OF SEQUENCES: 225
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco

;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/854,050
;/ FILING DATE: 09-MAY-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/851,843
;/ FILING DATE: 06-MAY-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/846,017
;/ FILING DATE: 25-APR-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/844,419
;/ FILING DATE: 18-APR-1997
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/724,643
;/ FILING DATE: 01-OCT-1996
;/ CLASSIFICATION: 536
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002930US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 45:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: other nucleic acid
;/ DESCRIPTION: /desc = "RNA"
;/ US-08-854-050-45

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred.No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGGCC 1694
|||||
Db 1 CAAACCCCAAGGCC 15

RESULT 397
US-09-430-323-43
;/ Sequence 43, Application US/09430323
;/ Patent No. 6309867
;/ GENERAL INFORMATION:
;/ APPLICANT: Cech, Thomas R.
;/ APPLICANT: Lingner, Joachim
;/ APPLICANT: Nakamura, Toru
;/ APPLICANT: Chapman, Karen B.
;/ APPLICANT: Morin, Gregg B.
;/ APPLICANT: Harley, Calvin
;/ APPLICANT: Andrews, William H.
;/ TITLE OF INVENTION: No. 6309867el Telomerase
;/ NUMBER OF SEQUENCES: 225
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/ STATE: California

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;
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "RNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-430-323-43
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAAACCCCAAGCC 1694
Db 1 CAAAACCCCAAGCC 15
|||||
RESULT 398
US-09-430-323-45
; Sequence 45, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "RNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-430-323-45
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAAACCCCAAGCC 1694
Db 1 CAAAACCCCAAGCC 15
|||||
RESULT 399
US-09-467-932-2
; Sequence 2, Application US/09467932
; Patent No. 6593306
; GENERAL INFORMATION:
; APPLICANT: Chen, Shih-Fong
; APPLICANT: Maine, Ira
; APPLICANT: Kerwin, Sean M.
; APPLICANT: Fletcher, Terace
; APPLICANT: Salazar, Miguel
; APPLICANT: Mamiya, Makoto
; APPLICANT: Wajima, Bradford E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATION
; TITLE OF INVENTION: AND INHIBITION OF HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/09/467,932
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/879,457
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kitchell, Barbara S.
/ REGISTRATION NUMBER: 33,928
/ REFERENCE/DOCKET NUMBER: CTCR:030
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (713) 789-2679
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-467-932-2

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15

RESULT 400
US-09-402-181B-113
/ Sequence 113, Application US/09402181B
/ Patent No. 6610839
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181B
/ FILING DATE: 29-Sep-1997
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
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/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ausenhus, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015389-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-402-181B-113

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15

RESULT 401
US-09-721-456-113
/ Sequence 113, Application US/09721456
/ Patent No. 6617110
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/721,456
/ FILING DATE: 22-No. 6617110-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-721-456-113

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15
|||||
RESULT 402
US-09-766-253-43
Sequence 43, Application US/09766253
Patent No. 680880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 680880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "RNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-766-253-43

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15
|||||
RESULT 403
US-09-766-253-45
Sequence 45, Application US/09766253
Patent No. 680880
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 680880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "RNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-07-766-253-45
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1680 CAAAACCCCAAGCC 1694
Db 1 CAAAACCCCAAAACC 15

RESULT 404
US-08-087-387-6/c
; Sequence 6, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applic
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/087,387
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-087-387-6
Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAAGT 1

RESULT 405
US-08-455-627-6/c
; Sequence 6, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
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; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-6
Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAAGT 1

RESULT 406
US-08-311-760A-375
; Sequence 375, Application US/08311760A
; Patent No. 5593706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-760A-375

```

Query Match 0.3%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 73.3%; Pred. No. 2.4e+02;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1540 TGCGTCCACCTCC 1554
Db 2 UGCCGUGCACCUC 16

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; RESULT 407
; US-08-311-760A-383
; Sequence 383, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwigen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

```

```

; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 383:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-760A-383

```

Query Match 0.3%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 73.3%; Pred. No. 2.4e+02;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1540 TGCGTCCACCTCC 1554
Db 2 UGCCGUGCACCUC 16

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; RESULT 408
; US-08-461-271-6/c
; Sequence 6, Application US/08461271
; Patent No. 5741643
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,271
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-461-271-6

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Query Match 0.3%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2576 AAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAGT 1

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```

; RESULT 409
; US-08-713-685A-6/c
; Sequence 6, Application US/08713685A

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; Patent No. 5817795
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; APPLICATION NUMBER: US/08/713,685A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-713-685A-6

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAAGT 1

RESULT 410
US-08-689-856-6/c
; Sequence 6, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-689-856-6

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAAGT 1

RESULT 411
US-08-774-310-375
; Sequence 375, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwigen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,310
; FILING DATE: December 23, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,760
; FILING DATE: September 23, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-310-375

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 73.3%; Pred. No. 2.4e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1540 TGCCGTCCACCTCC 1554
:||||:|||||
Db 2 UGCCGUGGCACCUCC 16

RESULT 412
US-08-774-310-383
; Sequence 383, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ranharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,310
; FILING DATE: December 23, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,760
; FILING DATE: September 23, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 383:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-310-383

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 73.3%; Pred. No. 2.4e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1540 TGCCGTCCACCTCC 1554
:||||:|||||
Db 2 UGCCGUGGCACCUCC 16

RESULT 413
US-08-947-317-4
; Sequence 4, Application US/08947317
; Patent No. 5972610
; GENERAL INFORMATION:
; APPLICANT: BUCHARDT, Ole
; APPLICANT: EGHOLM, Michael
; APPLICANT: NIELSEN, Peter Eigil
; APPLICANT: BERG, Rolf H
; APPLICANT: STANLEY, Christopher J
; TITLE OF INVENTION: USE OF NUCLEIC ACID ANALOGUES IN THE INHIBITION OF
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: 1614-7062
; CURRENT APPLICATION NUMBER: US/08/947,317
; CURRENT FILING DATE: 1997-10-08
; EARLIER APPLICATION NUMBER: PCT/EP93/01435
; EARLIER FILING DATE: 1993-06-07
; EARLIER APPLICATION NUMBER: GB/9211979.1
; EARLIER FILING DATE: 1992-06-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer.
US-08-947-317-4

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2741 CATCTTTTTTTTTT 2755
|||||
Db 1 CATCTTTTTTTTTT 15

RESULT 414
US-09-070-477-6/c
; Sequence 6, Application US/09070477
; Patent No. 6048974
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/713,685
; FILING DATE:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:

; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-070-477-6

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAAGT 1

RESULT 415
US-09-411-628-1
; Sequence 1, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Anchored primer
US-09-411-628-1

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTATTTT 2756
Db 2 AGCTTTTATTTT 16

RESULT 416
US-08-535-249-109/c
; Sequence 109, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA: EP 93 107 849.7
; APPLICATION NUMBER:
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-109

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2088 CTGGAGTCACACAG 2102
Db 16 CTTGAGTCACACAG 2

RESULT 417
US-08-535-249-131/c
; Sequence 131, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:

```
;
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-131

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2435 GATTGCAAGTCTTG 2449
Db 16 GATTGTAAGTCTTG 2

RESULT 418
US-09-300-958A-57
; Sequence 57, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; PRIOR FILING DATE: 1999-04-27
; PRIOR FILING DATE: 1998-04-27
; PRIOR FILING DATE: 1998-08-27
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 57
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-300-958A-57

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTCTTTT 2756
Db 2 AGCTTTTCTTTT 16

RESULT 419
US-09-300-958A-57
; Sequence 57, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; PRIOR FILING DATE: 1999-04-27
; PRIOR FILING DATE: 1998-04-27
; PRIOR FILING DATE: 1998-08-27
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 57
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-300-958A-57

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTCTTTT 2756
Db 2 AGCTTTTCTTTT 16

RESULT 420
US-09-527-972-16
; Sequence 16, Application US/09527972
; Patent No. 6642438
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Kellogg, Jill A.
; APPLICANT: Phan, Chau B.
; APPLICANT: Mathews, Helena V.
; APPLICANT: Webb, Nancy M.
; TITLE OF INVENTION: Banana and Melon Promoters for
; FILE REFERENCE: 4257-0019.30
; CURRENT APPLICATION NUMBER: US/09/527,972
; PRIOR FILING DATE: 2000-03-17
; EARLIER APPLICATION NUMBER: US 60/125,310
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-09-527-972-16

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTCTTTT 2756
Db 2 AGCTTTTCTTTT 16
```



```
RESULT 421
US-09-479-005A-395/c
; Sequence 395, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH800-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 395
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-479-005A-395

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1212 AAAAAATGCACTAC 1226
    ||||| |||||
Db 16 AAAAAATGCACTAC 2

RESULT 422
US-10-174-794-1
; Sequence 1, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Anchored primer
US-10-174-794-1

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTITTTT 2756
    ||||| |||||
Db 2 AGCTTTTITTTT 16

RESULT 423
5262177-6
; Patent No. 5262177
; APPLICANT: BROWN, J OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHIU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889/c
; Sequence 60889, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889
```

```
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889/c
; Sequence 60889, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889
```

Query Match 0.3%; Score 13.4; DB 1; Length 25;
 Best Local Similarity 73.9%; Pred. No. 4.8e+02;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3969 AAGAACTCTCAACTCAGAGTCTTA 3991
 Db 25 AAGACTCTGAGTTGAGATTCCTTA 3

RESULT 426
 US-09-300-958A-65/c
 ; Sequence 65, Application US/09300958A
 ; Patent No. 6495319
 ; GENERAL INFORMATION:
 ; APPLICANT: McClelland, Michael
 ; APPLICANT: Welsh, John
 ; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
 ; FILE OF INVENTION: Using Same
 ; FILE REFERENCE: P-PH 3457
 ; CURRENT APPLICATION NUMBER: US/09/300,958A
 ; CURRENT FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/083,331
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/098,070
 ; PRIOR FILING DATE: 1998-08-27
 ; PRIOR APPLICATION NUMBER: 60/118,624
 ; PRIOR FILING DATE: 1999-02-04
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 65
 ; LENGTH: 14
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-09-300-958A-65

Query Match 0.3%; Score 13.2; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.8e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAAA 2588
 Db 14 BAAAAAATAAAAAA 1

RESULT 427
 US-08-832-021-5
 ; Sequence 5, Application US/08832021
 ; Patent No. 6045998
 ; GENERAL INFORMATION:
 ; APPLICANT: Combates, N.
 ; APPLICANT: Pardini, J.
 ; APPLICANT: Parimoo, S.
 ; APPLICANT: Prouty, S.
 ; APPLICANT: Stenn, K.
 ; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
 ; FILE REFERENCE: JBP-382
 ; CURRENT APPLICATION NUMBER: US/08/832,021
 ; CURRENT FILING DATE: 1997-04-02
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 14
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 US-08-832-021-5

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2745 TTTTITTTTTTTTAA 2757
 Db 2 TTTTITTTTTTTTAA 14

RESULT 428
 US-08-724-466B-17
 ; Sequence 17, Application US/08724466B
 ; Patent No. 6063606
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; ZIP: M5L 1A9
 ; COUNTRY: Canada
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,466B
 ; FILING DATE: October 1, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667,546
 ; FILING DATE: June 21, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 50767/00004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-724-466B-17

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTITTTTTTTTAA 2757
 Db 2 TTTTITTTTTTTTAA 14

RESULT 429
 US-08-882-164D-17
 ; Sequence 17, Application US/08882164D
 ; Patent No. 6306624
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5L 1A9

Query Match 0.3%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAA 2757
 Db 2 TTTTNTTTTAA 14

RESULT 433
 US-08-832-021-20
 ; Sequence 20, Application US/08832021
 ; Patent No. 6045998
 ; GENERAL INFORMATION:
 ; APPLICANT: Combates, N.
 ; APPLICANT: Pardinas, J.
 ; APPLICANT: Parimoo, S.
 ; APPLICANT: Prouty, S.
 ; APPLICANT: Stenn, K.
 ; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
 ; FILE REFERENCE: JBP-382
 ; CURRENT APPLICATION NUMBER: US/08/832,021
 ; CURRENT FILING DATE: 1997-04-02
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 15
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 US-08-832-021-20

Query Match 0.3%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAA 2757
 Db 2 TTTTNTTTTAA 14

RESULT 434
 US-08-832-021-43/c
 ; Sequence 43, Application US/08832021
 ; Patent No. 6045998
 ; GENERAL INFORMATION:
 ; APPLICANT: Combates, N.
 ; APPLICANT: Pardinas, J.
 ; APPLICANT: Parimoo, S.
 ; APPLICANT: Prouty, S.
 ; APPLICANT: Stenn, K.
 ; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
 ; FILE REFERENCE: JBP-382
 ; CURRENT APPLICATION NUMBER: US/08/832,021
 ; CURRENT FILING DATE: 1997-04-02
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 43
 ; LENGTH: 15
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 US-08-832-021-43

Query Match 0.3%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAA 2587
 Db 13 TAAAAAATAA 1

RESULT 435
 US-08-087-387-6
 ; Sequence 6, Application US/08087387
 ; Patent No. 5473060
 ; GENERAL INFORMATION:
 ; APPLICANT: Sergei M. Gryaznov
 ; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applica
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
 ; STREET: 465 Lincoln Centre Drive
 ; CITY: Foster City
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch diskette
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: Windows 3.1/DOS 5.0
 ; SOFTWARE: Microsoft Word for Windows, vers. 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/087,387
 ; FILING DATE: 19930702
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stephen C. Macevicz
 ; REGISTRATION NUMBER: 30,285
 ; REFERENCE/DOCKET NUMBER: 104
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 358-7855
 ; TELEFAX: (415) 358-7794
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 nucleotides
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-087-387-6
 Query Match 0.3%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2740 ACAATCTTTTCTTTT 2755
 Db 1 ACTTTTCTTTTCTTTT 16
 RESULT 436
 US-08-455-627-6
 ; Sequence 6, Application US/08455627
 ; Patent No. 5571677
 ; GENERAL INFORMATION:
 ; APPLICANT: Sergei M. Gryaznov
 ; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward LLP
 ; STREET: Five Palo Alto Square, 3000 El Camino Real
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08/455,627
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-455-627-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTT 2755
Db 1 ACTTTTTTTTTTTT 16

RESULT 437
US-08-461-271-6
Sequence 6, Application US/08461271
Patent No. 5741643
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
CITY: Foster City
STATE: California
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
FILING DATE: 2-Jul-93
PRIOR APPLICATION NUMBER: US/08/461,271
CLASSIFICATION: 435
APPLICATION DATA:
FILING DATE: 2-Jul-93
APPLICATION NUMBER: 08/087,387
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevitz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELEPHONE: (415) 358-7855
TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-461-271-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2740 ACATCTTTTTTTTTT 2755
Db 1 ACTTTTTTTTTTTT 16
RESULT 438
US-08-713-685A-6
Sequence 6, Application US/08713685A
Patent No. 5817795
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
CITY: Foster City
STATE: California
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
FILING DATE: 2-Jul-93
PRIOR APPLICATION NUMBER: US/08/713,685A
CLASSIFICATION: 435
APPLICATION DATA:
FILING DATE: 2-Jul-93
APPLICATION NUMBER: 08/087,387
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevitz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELEPHONE: (415) 358-7855
TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-713-685A-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTT 2755
Db 1 ACTTTTTTTTTTTT 16

RESULT 439
US-08-689-856-6
Sequence 6, Application US/08689856
Patent No. 5830658
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward LLP
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,856
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,627
FILING DATE: 31-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-689-856-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTTTT 2755
Db 1 ACTTTTTTTTTTTT 16

RESULT 440
US-09-070-477-6
Sequence 6, Application US/09070477
Patent No. 6048974
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
CITY: Foster City
STATE: California
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/713,685
FILING DATE:
APPLICATION NUMBER: 08/461,271
FILING DATE:

APPLICATION NUMBER: 08/087,387
FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevitz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-7855
TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-070-477-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTTTT 2755
Db 1 ACTTTTTTTTTTTT 16

RESULT 441
US-09-411-628-1/c
Sequence 1, Application US/09411628
Patent No. 6428994
GENERAL INFORMATION:
APPLICANT: University of Southern California
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: US 60/102,906
EARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Anchored primer
US-09-411-628-1

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAAATT 2590
Db 16 TAAAAAATAAAAAAGCTT 1

RESULT 442
US-09-300-958A-57/c
Sequence 57, Application US/09300958A
Patent No. 6495319
GENERAL INFORMATION:
APPLICANT: McClelland, Michael
APPLICANT: Welsh, John
APPLICANT: Trenkle, Thomas
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
TITLE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27

; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 57
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-57

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAATT 2590
|||||
Db 16 TAAAAAATAAAAGCTT 1

RESULT 443
US-09-300-958A-85/c
; Sequence 85, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 85
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-85

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAATT 2590
|||||
Db 16 TAAAAAATAAAAGCTT 1

RESULT 444
US-09-527-972-16/c
; Sequence 16, Application US/09527972
; Patent No. 6642438
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Kellogg, Jill A.
; APPLICANT: Phan, Chau B.
; APPLICANT: Mathews, Helena V.
; APPLICANT: Webb, Nancy M.
; TITLE OF INVENTION: Banana and Melon Promoters for
; TITLE OF INVENTION: Expression of Transgenes in Plants

; FILE REFERENCE: 4257-0019.30
; CURRENT APPLICATION NUMBER: US/09/527,972
; CURRENT FILING DATE: 2000-03-17
; EARLIER APPLICATION NUMBER: US 60/125,310
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-09-527-972-16

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAATT 2590
|||||
Db 16 TAAAAAATAAAAGCTT 1

RESULT 445
US-10-174-794-1/c
; Sequence 1, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Anchored primer
US-10-174-794-1

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAATT 2590
|||||
Db 16 TAAAAAATAAAAGCTT 1

RESULT 446
US-09-090-672B-105
; Sequence 105, Application US/09090672B
; Patent No. 6828428
; GENERAL INFORMATION:
; APPLICANT: Iehiwa, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tateunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York

; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
; US-09-090-672B-105

Query Match 0.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTT 3279
Db 2 TTTTTCCTTTT 17

RESULT 447
US-09-725-265-20
; Sequence 20, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

Query Match 0.3%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2802 GAAAAAAAAAACAT 2817
Db 1 GAAAAAAAAATATAT 16

RESULT 448
US-09-556-127-20
; Sequence 20, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-20

Query Match 0.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2802 GAAAAAAAAAACAT 2817
Db 1 GAAAAAAAAATATAT 16

RESULT 449
US-08-486-057B-6/c
; Sequence 6, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:


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, APPLICATION NUMBER: US 08/486, 0576
, FILING DATE: 07-JUN-1995
, CLASSIFICATION: 514
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/201,703
, FILING DATE: 25-FEB-1994
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/960,309
, FILING DATE: 13-OCT-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/621,502
, FILING DATE: 03-DEC-1990
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: GB 8927546.5
, FILING DATE: 06-DEC-1989
, ATTORNEY/AGENT INFORMATION:
, NAME: No. 5650494ak, Henry P.
, REGISTRATION NUMBER: 33200
, REFERENCE/DOCKET NUMBER: 4-17861/+
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (908) 277-5110
, TELEFAX: (908) 277-4306
, INFORMATION FOR SEQ ID NO: 6:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 39 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
US-08-486-0576-6

```

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Query Match      0.3%; Score 12.8; DB 1; Length 39;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 12; Indels
```

Qy 2131 ATGCTGCCTACTGCTTTTAGAAATGTGCAGGAT 2162
||| ||| ||| ||| ||| ||| ||| |||
Dδ 39 ATCCTGCACATTTCATAAGCAATAGGCCGCAT 8

```

RESULT 450
US-08-789-588-6/c
; Sequence 6, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005

```

```

; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: Patent In Release #1.0, Version #1.30
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/789,588
; ; FILING DATE:
; ; CLASSIFICATION: 530
; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: US 08/486,057
; ; FILING DATE: 07-JUN-1995
; ; APPLICATION NUMBER: US 08/201,703

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1  FILING DATE: 25-FEB-1994
2  PRIOR APPLICATION DATA:
3  APPLICATION NUMBER: US 07/960,309
4  FILING DATE: 13-OCT-1992
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: US 07/621,502
7  FILING DATE: 03-DEC-1990
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: GB 8927546.5
10 FILING DATE: 08-DEC-1989
11 ATTORNEY/AGENT INFORMATION:
12 NAME: NO. 5922846ak, Henry P.
13 REGISTRATION NUMBER: 33200
14 REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont.3
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (908) 277-5110
17 TELEFAX: (908) 277-4306
18 INFORMATION FOR SEQ ID NO: 6:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 39 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: cDNA
25 US-08-789-588-6
26
27 Query Match 0.3%; Score 12.8; D
28 Best Local Similarity 62.5%; Pred. No. 3.7e
29 Matches 20; Conservative 0; Mismatches
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100

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RESULT 451
US-09-725-265-42
; Sequence 42, Application US/09725265

```

/ GENERAL INFORMATION:
/ APPLICANT: KURANE, RYUICHIRO
/ APPLICANT: KANAGAWA, TAKAHIRO
/ APPLICANT: KAWAGATA, YOICHI
/ APPLICANT: YAMADA, KAZUTAKA
/ APPLICANT: YOKOMAKU, TOYOKAZU
/ APPLICANT: KOYAMA, OSAMU
/ APPLICANT: FURUSHO, KENTA
/ TITLE OF INVENTION: METHOD FOR DETERMINING
/ TITLE OF INVENTION: NUCLEIC ACID PROBES
/ TITLE OF INVENTION: THE METHOD
/ FILE REFERENCE: 199953USOXDIV
/ CURRENT APPLICATION NUMBER: US/09/725,265
/ CURRENT FILING DATE: 2000-11-29
/ PRIOR APPLICATION NUMBER: US 09/556,127
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: JP 1999-111601
/ PRIOR FILING DATE: 1999-04-20
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 42
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: ARTIFICIAL SEQUENCE
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-42

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Query Match 0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. NO. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels

Qy 2793 TAATTATGTGAAAAAAA 2811

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Db      2 TATATATATAAAAAAAAA 20

RESULT 452
US-09-823-634A-13/c
; Sequence 13, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      20 TTTTTCACAAATTTT 2

RESULT 453
US-09-823-634A-14/c
; Sequence 14, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      19 TTTTTCACAAATTTT 1

RESULT 454
US-09-823-647B-13/c
; Sequence 13, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
```

```
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      20 TTTTTCACAAATTTT 2

RESULT 455
US-09-823-647B-14/c
; Sequence 14, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      19 TTTTTCACAAATTTT 1

RESULT 456
US-09-556-127-42
; Sequence 42, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
```


GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-789-588-7

Query Match 0.3%; Score 12.6; DB 1; Length 39;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1987 CTACATATGCCAGTGTGATCGAATAACTATAAG 2021
DB 5 CTGCAATTGCAAGACTTTTCAATCATATTAGAAAG 39

RESULT 460
US-08-292-620A-359
Sequence 359, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-359

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 7.1%; Pred. No. 2.8e+02;
Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTITTTTTT 2755
DB 2 AUUUUUUUUUUU 15

RESULT 461
US-08-292-620A-360
Sequence 360, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-360

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 7.1%; Pred. No. 2.8e+02;
Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTCCTTTT 2755
Db 1 AUUUUUUUUUUUUU 14

RESULT 462
US-08-292-620A-365
Sequence 365, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```

```

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 365:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-365

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTTCCTTTTTCCTT 2758
Db 2 UUUUUUUUUUUUCAG 15

RESULT 463
US-08-832-021-23
Sequence 23, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardinas, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-23

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTTCCTTTTTCCTT 2758

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Db 2 TTTTTTTTTTTCAG 15

RESULT 464

US-09-071-845-359

; Sequence 359, Application US/09071845

; Patent No. 6132967

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/071,845

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620

; FILING DATE: August 17, 1994

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 359:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-071-845-359

Query Match 0.3%; Score 12.4; DB 1; Length 15;

Best Local Similarity 7.1%; Pred. NO. 2.8e+02;

Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTCAG 15

Db 2 AAAAAAAAAUUUUU 15

RESULT 465

US-09-071-845-360

; Sequence 360, Application US/09071845

; Patent No. 6132967

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/071,845

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620

; FILING DATE: August 17, 1994

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 360:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-071-845-360

Query Match 0.3%; Score 12.4; DB 1; Length 15;

Best Local Similarity 7.1%; Pred. NO. 2.8e+02;

Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTCAG 15

Db 1 AAAAAAAAAUUUUU 14

RESULT 466

US-09-071-845-365

; Sequence 365, Application US/09071845

; Patent No. 6132967

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,845
/ FILING DATE: December 7, 1992
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 365:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-071-845-365

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTITTTTTTAAG 2758
Db 2 UUUUUUUUUUCAG 15

RESULT 467
US-08-292-620A-366
/ Sequence 366, Application US/08292620A
/ Patent No. 5837542
/ GENERAL INFORMATION:
/ APPLICANT: Susan Grimm
/ APPLICANT: Dan T. Stinchcomb
/ APPLICANT: James McSwiggen
/ APPLICANT: Sean Sullivan
/ APPLICANT: Kenneth G. Draper
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF
/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon

/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620A
/ FILING DATE: August 17, 1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: including application
/ PRIOR APPLICATION DATA: described below:
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 366:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-292-620A-366

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTITTTTTTAAG 2758
Db 1 UUUUUUUUUUCAG 14

RESULT 468
US-08-832-021-41
/ Sequence 41, Application US/08832021
/ Patent No. 6045998
/ GENERAL INFORMATION:
/ APPLICANT: Combates, N.
/ APPLICANT: Pardini, J.
/ APPLICANT: Parimoo, S.
/ APPLICANT: Prouty, S.
/ APPLICANT: Stenn, K.
/ TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
/ FILE REFERENCE: JBP-382
/ CURRENT APPLICATION NUMBER: US/08/832,021
/ CURRENT FILING DATE: 1997-04-02
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 41
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer
/ US-08-832-021-41

Query Match 0.3%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAG 2758
Db 1 TTTTNTTTTAAAG 14

RESULT 469

US-09-071-845-366
; Sequence 366, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 366:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-071-845-366

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAG 2758
Db 1 UUUUUUUUUUCAG 14

RESULT 470

US-08-584-040-2186
; Sequence 2186, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-584-040-2186

Query Match 0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 14.3%; Pred. No. 3.7e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2744 CTTTNTTTTAA 2757

Db 3 CUUUUUUUUUUGA 16

RESULT 471

US-09-371-772B-731
; Sequence 731, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel.


```

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH000,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-731

Query Match          0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 14.3%; Pred. No. 3.7e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2744 CTTTTTTTTTTAA 2757
Db 3 CUUUUUUUUUUGA 16

RESULT 472
US-09-685-664B-731
; Sequence 731, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH000-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-731

Query Match          0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 14.3%; Pred. No. 3.7e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2744 CTTTTTTTTTTAA 2757
Db 3 CUUUUUUUUUUGA 16

RESULT 473
US-08-330-000-1
; Sequence 1, Application US/08330000
; Patent No. 5686242
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; APPLICANT: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5686242ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,000
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 755,485
; FILING DATE: September 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07489
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca Lynne
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1723
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-330-000-1

Query Match          0.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTTTTTT 2755
Db 3 ATGTTTTTTTTTT 16

RESULT 474
US-08-965-908-1
; Sequence 1, Application US/08965908
; Patent No. 6022691
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; APPLICANT: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 6022691ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,908

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;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330,000
; FILING DATE:
; APPLICATION NUMBER: 755,485
; FILING DATE: September 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07489
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca Lynne
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1723
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-965-908-1

Query Match          0.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTTCCTTTT 2755
Db 3 ATGTTTTTTCCTTTT 16

RESULT 475
US-09-725-265-17
; Sequence 17, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953US0XDIV
; CURRENT FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17
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Query Match          0.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2576 AAAAAAAAAAAAAAT 2589
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Db 1 AAAAAAAAAAAATAT 14

RESULT 476
US-09-556-127-17
; Sequence 17, Application US/09556127
; Patent No. 6695661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 0163-0758-0X
; CURRENT FILING DATE: 2002-06-17
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-17
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Query Match          0.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2576 AAAAAAAAAAAAAAT 2589
|||||
Db 1 AAAAAAAAAAAATAT 14
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Search completed: February 25, 2005, 09:40:33
Job time : 20 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 09:52:48 ; Search time 11 Seconds
(without alignments)

3.661 Million cell updates/sec

Title: US-10-633-163-47

Perfect score: 4267

Sequence: 1 gggtactctgctggcagcagg.....tgacggctgattaaaaaaa 4267

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 314 seqs, 4719 residues

Total number of hits satisfying chosen parameters: 628

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 366 summaries

Database : fetchrst47.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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C 2	20.2	0.5	25	1	AI307726
C 3	20.2	0.5	25	1	BZ764590
C 4	19.8	0.5	24	1	CD743368
C 5	19.2	0.4	24	1	AW247159
C 6	19.2	0.4	24	1	AZ458112
C 7	19.2	0.4	24	1	AZ621257
C 8	19.2	0.4	25	1	BZ764590
C 9	18.8	0.4	23	1	CF310247
C 10	18.8	0.4	23	1	CF310247
C 11	18.8	0.4	23	1	CF310999
C 12	18.8	0.4	23	1	CF310999
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C 14	18.8	0.4	23	1	AZ316719
C 15	17	0.4	25	1	AI307726
C 16	16.8	0.4	20	1	AZ835133
C 17	16.8	0.4	20	1	AZ835133
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C 19	16.8	0.4	21	1	AJ661013
C 20	16.8	0.4	21	1	CN763587
C 21	16.8	0.4	21	1	CN763587
C 22	16.8	0.4	21	1	CL693164
C 23	16.8	0.4	21	1	CL693165
C 24	16.8	0.4	21	1	CW020436
C 25	16.6	0.4	24	1	AW247159
C 26	16.6	0.4	24	1	AZ621257
C 27	16.4	0.4	19	1	CF295672
C 28	16.4	0.4	19	1	CF323353
C 29	16.4	0.4	19	1	AZ766990
C 30	16.4	0.4	20	1	AZ468873
C 31	16.4	0.4	20	1	AZ468899
C 32	16.4	0.4	20	1	AZ845320
C 33	16	0.4	16	1	CF312586

ACCESSION:CF298591	1	CF298591	18	0.4	16	C 34
ACCESSION:CF278272	1	CF278272	19	0.4	16	C 35
ACCESSION:AZ458112	24	AZ458112	24	0.4	16	C 36
ACCESSION:CF308042	19	CF308042	19	0.4	15.8	C 37
ACCESSION:AZ654747	1	AZ654747	19	0.4	15.8	C 38
ACCESSION:AZ764511	1	AZ764511	19	0.4	15.8	C 39
ACCESSION:AZ858877	1	AZ858877	40	0.4	15.8	C 40
ACCESSION:AZ858877	1	AZ858877	41	0.4	15.8	C 41
ACCESSION:AZ962226	1	AZ962226	42	0.4	15.8	C 42
ACCESSION:BG673623	1	BG673623	43	0.4	15.4	C 43
ACCESSION:AI471695	1	AI471695	44	0.4	15.4	C 44
ACCESSION:AZ427731	1	AZ427731	45	0.4	15.4	C 45
ACCESSION:AZ650212	1	AZ650212	46	0.4	15.4	C 46
ACCESSION:CD743368	24	CD743368	47	0.4	15.2	C 47
ACCESSION:AW246551	1	AW246551	48	0.4	15	C 48
ACCESSION:CF299675	1	CF299675	49	0.4	15	C 49
ACCESSION:AJ600267	1	AJ600267	50	0.4	15	C 50
ACCESSION:AW248796	1	AW248796	51	0.4	15	C 51
ACCESSION:CF301359	1	CF301359	52	0.3	14.8	C 52
ACCESSION:BM658913	1	BM658913	53	0.3	14.8	C 53
ACCESSION:AI685758	26	AI685758	54	0.3	14.8	C 54
ACCESSION:AW248540	1	AW248540	55	0.3	14.4	C 55
ACCESSION:AW248958	1	AW248958	56	0.3	14.4	C 56
ACCESSION:CF317778	1	CF317778	57	0.3	14.4	C 57
ACCESSION:AW246518	1	AW246518	58	0.3	14.4	C 58
ACCESSION:CF299997	1	CF299997	59	0.3	14.4	C 59
ACCESSION:AW246528	1	AW246528	60	0.3	14.4	C 60
ACCESSION:CF299997	1	CF299997	61	0.3	14.4	C 61
ACCESSION:CF300456	1	CF300456	62	0.3	14.4	C 62
ACCESSION:CF292885	1	CF292885	63	0.3	14.4	C 63
ACCESSION:AW249689	1	AW249689	64	0.3	14	C 64
ACCESSION:CF295100	1	CF295100	65	0.3	14	C 65
ACCESSION:CF301470	1	CF301470	66	0.3	14	C 66
ACCESSION:CR789161	1	CR789161	67	0.3	14	C 67
ACCESSION:BO590507	1	BO590507	68	0.3	14	C 68
ACCESSION:BO593369	1	BO593369	69	0.3	14	C 69
ACCESSION:CF296130	1	CF296130	70	0.3	14	C 70
ACCESSION:CF314013	1	CF314013	71	0.3	14	C 71
ACCESSION:CF29320	1	CF29320	72	0.3	14	C 72
ACCESSION:AW245664	1	AW245664	73	0.3	14	C 73
ACCESSION:BO590128	1	BO590128	74	0.3	14	C 74
ACCESSION:BO591181	1	BO591181	75	0.3	14	C 75
ACCESSION:BO591588	1	BO591588	76	0.3	14	C 76
ACCESSION:CF291802	1	CF291802	77	0.3	14	C 77
ACCESSION:CF294668	1	CF294668	78	0.3	14	C 78
ACCESSION:CF295988	1	CF295988	79	0.3	14	C 79
ACCESSION:CF311499	1	CF311499	80	0.3	14	C 80
ACCESSION:CF319075	1	CF319075	81	0.3	14	C 81
ACCESSION:CF336950	1	CF336950	82	0.3	14	C 82
ACCESSION:AW247976	1	AW247976	83	0.3	13.8	C 83
ACCESSION:CF302447	1	CF302447	84	0.3	13.8	C 84
ACCESSION:CF313013	1	CF313013	85	0.3	13.8	C 85
ACCESSION:CF298591	1	CF298591	86	0.3	13.8	C 86
ACCESSION:CF278272	1	CF278272	87	0.3	13.8	C 87
ACCESSION:AW245585	1	AW245585	88	0.3	13.4	C 88
ACCESSION:AW250976	1	AW250976	89	0.3	13.4	C 89
ACCESSION:BO588758	1	BO588758	90	0.3	13.4	C 90
ACCESSION:CF329379	1	CF329379	91	0.3	13.4	C 91
ACCESSION:CF543203	1	CF543203	92	0.3	13.4	C 92
ACCESSION:CF312586	1	CF312586	93	0.3	13.4	C 93
ACCESSION:CF291803	1	CF291803	94	0.3	13.4	C 94
ACCESSION:CF295672	1	CF295672	95	0.3	13.4	C 95
ACCESSION:AZ766990	1	AZ766990	96	0.3	13.4	C 96
ACCESSION:AZ962226	1	AZ962226	97	0.3	13.4	C 97
ACCESSION:AZ426873	1	AZ426873	98	0.3	13.4	C 98
ACCESSION:AZ654747	1	AZ654747	99	0.3	13.2	C 99
ACCESSION:AA918967	1	AA918967	100	0.3	13	C 100
ACCESSION:BQ583549	1	BQ583549	101	0.3	13	C 101
ACCESSION:BQ589180	1	BQ589180	102	0.3	13	C 102
ACCESSION:BQ590337	1	BQ590337	103	0.3	13	C 103
ACCESSION:CF278426	1	CF278426	104	0.3	13	C 104
ACCESSION:CF280420	1	CF280420	105	0.3	13	C 105
ACCESSION:CF280707	1	CF280707	106	0.3	13	C 106

c 107	13	0.3	13	1	CF280757	ACCESSION:CF280757	c 180	13	0.3	13	1	CF329946	ACCESSION:CF329946
c 108	13	0.3	13	1	CF282369	ACCESSION:CF282369	c 181	13	0.3	13	1	CF329988	ACCESSION:CF329988
c 109	13	0.3	13	1	CF290970	ACCESSION:CF290970	c 182	13	0.3	13	1	CF330023	ACCESSION:CF330023
c 110	13	0.3	13	1	CF290971	ACCESSION:CF290971	c 183	13	0.3	13	1	CF330725	ACCESSION:CF330725
c 111	13	0.3	13	1	CF291011	ACCESSION:CF291011	c 184	13	0.3	13	1	CF331041	ACCESSION:CF331041
c 112	13	0.3	13	1	CF291060	ACCESSION:CF291060	c 185	13	0.3	13	1	CF331266	ACCESSION:CF331266
c 113	13	0.3	13	1	CF291061	ACCESSION:CF291061	c 186	13	0.3	13	1	CF331273	ACCESSION:CF331273
c 114	13	0.3	13	1	CF291167	ACCESSION:CF291167	c 187	13	0.3	13	1	CF331903	ACCESSION:CF331903
c 115	13	0.3	13	1	CF291214	ACCESSION:CF291214	c 188	13	0.3	13	1	CF332079	ACCESSION:CF332079
c 116	13	0.3	13	1	CF291427	ACCESSION:CF291427	c 189	13	0.3	13	1	CF332695	ACCESSION:CF332695
c 117	13	0.3	13	1	CF291469	ACCESSION:CF291469	c 190	13	0.3	13	1	CF332696	ACCESSION:CF332696
c 118	13	0.3	13	1	CF291479	ACCESSION:CF291479	c 191	13	0.3	13	1	CF333486	ACCESSION:CF333486
c 119	13	0.3	13	1	CF291514	ACCESSION:CF291514	c 192	13	0.3	13	1	CF333972	ACCESSION:CF333972
c 120	13	0.3	13	1	CF291515	ACCESSION:CF291515	c 193	13	0.3	13	1	CF333973	ACCESSION:CF333973
c 121	13	0.3	13	1	CF291596	ACCESSION:CF291596	c 194	13	0.3	13	1	CF334347	ACCESSION:CF334347
c 122	13	0.3	13	1	CF291597	ACCESSION:CF291597	c 195	13	0.3	13	1	CF337022	ACCESSION:CF337022
c 123	13	0.3	13	1	CF291726	ACCESSION:CF291726	c 196	13	0.3	13	1	CN546046	ACCESSION:CN546046
c 124	13	0.3	13	1	CF291903	ACCESSION:CF291903	c 197	13	0.3	13	1	CN749468	ACCESSION:CN749468
c 125	13	0.3	13	1	CF298590	ACCESSION:CF298590	c 198	13	0.3	13	1	CN752228	ACCESSION:CN752228
c 126	13	0.3	13	1	CF298592	ACCESSION:CF298592	c 199	13	0.3	13	1	CN752875	ACCESSION:CN752875
c 127	13	0.3	13	1	CF298736	ACCESSION:CF298736	c 200	13	0.3	13	1	CN753196	ACCESSION:CN753196
c 128	13	0.3	13	1	CF298764	ACCESSION:CF298764	c 201	13	0.3	14	1	BQ586422	ACCESSION:BQ586422
c 129	13	0.3	13	1	CF298795	ACCESSION:CF298795	c 202	13	0.3	14	1	BQ587890	ACCESSION:BQ587890
c 130	13	0.3	13	1	CF298908	ACCESSION:CF298908	c 203	13	0.3	14	1	BQ589191	ACCESSION:BQ589191
c 131	13	0.3	13	1	CF299133	ACCESSION:CF299133	c 204	13	0.3	14	1	BQ590242	ACCESSION:BQ590242
c 132	13	0.3	13	1	CF299359	ACCESSION:CF299359	c 205	13	0.3	14	1	BQ590261	ACCESSION:BQ590261
c 133	13	0.3	13	1	CF299937	ACCESSION:CF299937	c 206	13	0.3	14	1	BQ591168	ACCESSION:BQ591168
c 134	13	0.3	13	1	CF300118	ACCESSION:CF300118	c 207	13	0.3	14	1	BQ591176	ACCESSION:BQ591176
c 135	13	0.3	13	1	CF300587	ACCESSION:CF300587	c 208	13	0.3	14	1	BQ591207	ACCESSION:BQ591207
c 136	13	0.3	13	1	CF300658	ACCESSION:CF300658	c 209	13	0.3	14	1	BQ591380	ACCESSION:BQ591380
c 137	13	0.3	13	1	CF300929	ACCESSION:CF300929	c 210	13	0.3	14	1	BQ591482	ACCESSION:BQ591482
c 138	13	0.3	13	1	CF301247	ACCESSION:CF301247	c 211	13	0.3	14	1	BQ591949	ACCESSION:BQ591949
c 139	13	0.3	13	1	CF301286	ACCESSION:CF301286	c 212	13	0.3	14	1	BQ593052	ACCESSION:BQ593052
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c 141	13	0.3	13	1	CF302830	ACCESSION:CF302830	c 214	13	0.3	14	1	CF278001	ACCESSION:CF278001
c 142	13	0.3	13	1	CF302898	ACCESSION:CF302898	c 215	13	0.3	14	1	CF278452	ACCESSION:CF278452
c 143	13	0.3	13	1	CF310516	ACCESSION:CF310516	c 216	13	0.3	14	1	CF279473	ACCESSION:CF279473
c 144	13	0.3	13	1	CF310517	ACCESSION:CF310517	c 217	13	0.3	14	1	CF279992	ACCESSION:CF279992
c 145	13	0.3	13	1	CF312721	ACCESSION:CF312721	c 218	13	0.3	14	1	CF281958	ACCESSION:CF281958
c 146	13	0.3	13	1	CF313171	ACCESSION:CF313171	c 219	13	0.3	14	1	CF282350	ACCESSION:CF282350
c 147	13	0.3	13	1	CF314239	ACCESSION:CF314239	c 220	13	0.3	14	1	CF294449	ACCESSION:CF294449
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c 149	13	0.3	13	1	CF315395	ACCESSION:CF315395	c 222	13	0.3	14	1	CF296120	ACCESSION:CF296120
c 150	13	0.3	13	1	CF316439	ACCESSION:CF316439	c 223	13	0.3	14	1	CF297969	ACCESSION:CF297969
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c 153	13	0.3	13	1	CF318290	ACCESSION:CF318290	c 226	13	0.3	14	1	CF300542	ACCESSION:CF300542
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c 157	13	0.3	13	1	CF319919	ACCESSION:CF319919	c 230	13	0.3	14	1	CF302675	ACCESSION:CF302675
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c 159	13	0.3	13	1	CF320018	ACCESSION:CF320018	c 232	13	0.3	14	1	CF308006	ACCESSION:CF308006
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c 164	13	0.3	13	1	CF327339	ACCESSION:CF327339	c 237	13	0.3	14	1	CF311201	ACCESSION:CF311201
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c 178	13	0.3	13	1	CF329801	ACCESSION:CF329801	c 251	13	0.3	14	1	CF329217	ACCESSION:CF329217
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C 257	13	0.3	14	1	CF33214	ACCESSION:CF33214	C 330	13	0.3	16	1	CF328223	ACCESSION:CF328223
C 258	13	0.3	14	1	CF333215	ACCESSION:CF333215	C 331	13	0.3	16	1	CF333386	ACCESSION:CF333386
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C 260	13	0.3	14	1	CF334202	ACCESSION:CF334202	C 333	13	0.3	16	1	CR786853	ACCESSION:CR786853
C 261	13	0.3	14	1	CF334281	ACCESSION:CF334281	C 334	13	0.3	17	1	BG673623	ACCESSION:BG673623
C 262	13	0.3	14	1	CF334290	ACCESSION:CF334290	C 335	13	0.3	17	1	CF299675	ACCESSION:CF299675
C 263	13	0.3	14	1	CF335781	ACCESSION:CF335781	C 336	13	0.3	21	1	CL693164	ACCESSION:CL693164
C 264	13	0.3	14	1	CF336094	ACCESSION:CF336094	C 337	13	0.3	21	1	CL693165	ACCESSION:CL693165
C 265	13	0.3	14	1	CF336106	ACCESSION:CF336106	C 338	13	0.3	21	1	CW020436	ACCESSION:CW020436
C 266	13	0.3	14	1	CF336287	ACCESSION:CF336287	C 339	12.8	0.3	16	1	BQ590507	ACCESSION:BQ590507
C 267	13	0.3	14	1	CF336906	ACCESSION:CF336906	C 340	12.8	0.3	16	1	BQ595369	ACCESSION:BQ595369
C 268	13	0.3	15	1	AJ690565	ACCESSION:AJ690565	C 341	12.8	0.3	16	1	CF296130	ACCESSION:CF296130
C 269	13	0.3	15	1	BE230585	ACCESSION:BE230585	C 342	12.8	0.3	16	1	CF314013	ACCESSION:CF314013
C 270	13	0.3	15	1	BQ582543	ACCESSION:BQ582543	C 343	12.8	0.3	16	1	CF329320	ACCESSION:CF329320
C 271	13	0.3	15	1	BQ585820	ACCESSION:BQ585820	C 344	12.8	0.3	16	1	AW246487	ACCESSION:AW246487
C 272	13	0.3	15	1	BQ590410	ACCESSION:BQ590410	C 345	12.8	0.3	16	1	AW246487	ACCESSION:AW246487
C 273	13	0.3	15	1	BQ590656	ACCESSION:BQ590656	C 346	12.8	0.3	16	1	AW246490	ACCESSION:AW246490
C 274	13	0.3	15	1	BQ591170	ACCESSION:BQ591170	C 347	12.8	0.3	16	1	AW251049	ACCESSION:AW251049
C 275	13	0.3	15	1	BQ591178	ACCESSION:BQ591178	C 348	12.8	0.3	16	1	BQ590688	ACCESSION:BQ590688
C 276	13	0.3	15	1	BQ591223	ACCESSION:BQ591223	C 349	12.8	0.3	17	1	BQ590128	ACCESSION:BQ590128
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C 281	13	0.3	15	1	CF291029	ACCESSION:CF291029	C 354	12.8	0.3	17	1	CF319075	ACCESSION:CF319075
C 282	13	0.3	15	1	CF291103	ACCESSION:CF291103	C 355	12.8	0.3	17	1	CF336950	ACCESSION:CF336950
C 283	13	0.3	15	1	CF291717	ACCESSION:CF291717	C 356	12.8	0.3	17	1	AW247976	ACCESSION:AW247976
C 284	13	0.3	15	1	CF291798	ACCESSION:CF291798	C 357	12.8	0.3	19	1	CF308042	ACCESSION:CF308042
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C 286	13	0.3	15	1	CF292461	ACCESSION:CF292461	C 359	12.4	0.3	17	1	BQ591588	ACCESSION:BQ591588
C 287	13	0.3	15	1	CF296652	ACCESSION:CF296652	C 360	12.2	0.3	17	1	AW246528	ACCESSION:AW246528
C 288	13	0.3	15	1	CF298148	ACCESSION:CF298148	C 361	12	0.3	15	1	AW246551	ACCESSION:AW246551
C 289	13	0.3	15	1	CF298630	ACCESSION:CF298630	C 362	12	0.3	15	1	AW245585	ACCESSION:AW245585
C 290	13	0.3	15	1	CF298733	ACCESSION:CF298733	C 363	12	0.3	16	1	AW248540	ACCESSION:AW248540
C 291	13	0.3	15	1	CF298805	ACCESSION:CF298805	C 364	12	0.3	16	1	CF319827	ACCESSION:CF319827
C 292	13	0.3	15	1	CF298889	ACCESSION:CF298889	C 365	12	0.3	16	1	AW251049	ACCESSION:AW251049
C 293	13	0.3	15	1	CF299602	ACCESSION:CF299602	C 366	12	0.3	18	1	CF301359	ACCESSION:CF301359
C 294	13	0.3	15	1	CF299608	ACCESSION:CF299608							
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C 296	13	0.3	15	1	CF300361	ACCESSION:CF300361							
C 297	13	0.3	15	1	CF300992	ACCESSION:CF300992							
C 298	13	0.3	15	1	CF302034	ACCESSION:CF302034							
C 299	13	0.3	15	1	CF302124	ACCESSION:CF302124							
C 300	13	0.3	15	1	CF302182	ACCESSION:CF302182							
C 301	13	0.3	15	1	CF307923	ACCESSION:CF307923							
C 302	13	0.3	15	1	CF311159	ACCESSION:CF311159							
C 303	13	0.3	15	1	CF311907	ACCESSION:CF311907							
C 304	13	0.3	15	1	CF313319	ACCESSION:CF313319							
C 305	13	0.3	15	1	CF313320	ACCESSION:CF313320							
C 306	13	0.3	15	1	CF316251	ACCESSION:CF316251							
C 307	13	0.3	15	1	CF318035	ACCESSION:CF318035							
C 308	13	0.3	15	1	CF327434	ACCESSION:CF327434							
C 309	13	0.3	15	1	CF330195	ACCESSION:CF330195							
C 310	13	0.3	15	1	CF330668	ACCESSION:CF330668							
C 311	13	0.3	15	1	CF332178	ACCESSION:CF332178							
C 312	13	0.3	15	1	CF336202	ACCESSION:CF336202							
C 313	13	0.3	15	1	CR547282	ACCESSION:CR547282							
C 314	13	0.3	16	1	BQ590166	ACCESSION:BQ590166							
C 315	13	0.3	16	1	BQ590207	ACCESSION:BQ590207							
C 316	13	0.3	16	1	BQ592600	ACCESSION:BQ592600							
C 317	13	0.3	16	1	BQ592965	ACCESSION:BQ592965							
C 318	13	0.3	16	1	BQ595717	ACCESSION:BQ595717							
C 319	13	0.3	16	1	CF279325	ACCESSION:CF279325							
C 320	13	0.3	16	1	CF311057	ACCESSION:CF311057							
C 321	13	0.3	16	1	CF314377	ACCESSION:CF314377							
C 322	13	0.3	16	1	CF315789	ACCESSION:CF315789							
C 323	13	0.3	16	1	CF316056	ACCESSION:CF316056							
C 324	13	0.3	16	1	CF317718	ACCESSION:CF317718							
C 325	13	0.3	16	1	CF318894	ACCESSION:CF318894							

ALIGNMENTS

RESULT 1

BM658913/c

LOCUS

BM658913

DEFINITION

LQ602768282.R1 CSEQFXL36 fetal brain Sus scrofa cdNA, mRNA

ACCESSION

BM658913

VERSION

BM658913.1

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

REFERENCE

1 (bases 1 to 26)

AUTHORS

Adelson,D.L. and Gill,C.A.

TITLE

Porcine ESTs

JOURNAL

Unpublished (2002)

COMMENT

Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
1..26
/organism="Sus scrofa"

```

/mol_type="mRNA"
/db_xref="taxon:9823"
/dev stage="fetal"
/clone_lib="CSEOPXL36 fetal brain"
/note="Organ: brain; Vector: pBluescript SK+; Site_1:
NotI; Site_2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNInsert)
GCCAATTGGAGCTCCACCGCGGTGGCGCGCGCTCGAG. Sequence 3' of
the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."

Query Match      0.5%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.7;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAATTCGAGAAAAAAA 2601
Db 26 AAAAAAAAAAAGAGAAAAAAA 1

RESULT 2
AI307726/c
LOCUS      25 bp      mRNA      linear      EST 08-APR-1999
DEFINITION tb36d11.x1 NCI CGAP HSC2 Homo sapiens cDNA clone IMAGE:2056437 3'
            similar to TR:020155 O20155 ORF41C. ;, mRNA sequence.
ACCESSION  AI307726
VERSION     AI307726
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 25)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapsb-r@mail.nih.gov
          Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
          M.D., Ph.D.
          cDNA Library Preparation: David B. Krizman, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Insert Length: 494 Std Error: 0.00
          Seq primer: -40UP from Gibco
          High quality sequence stop: 1.
          Location/Qualifiers
            1..25
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:2056437"
              /tissue type="stem cell 34+/38+"
              /dev stage="adult"
              /lab_host="DH10B"
              /clone_lib="NCI CGAP HSC2"
              /note="Organ: bone marrow; Vector: pMP1; mRNA made from
              bone marrow, stem cells 34+/38+, cDNA made by oligo-dT
              priming. Directionally cloned. Size-selected on agarose
              gel, average insert size 400 bp. Primary library,
              non-amplified."
          Query Match      0.5%; Score 20.2; DB 1; Length 25;
          Best Local Similarity 88.0%; Pred. No. 3.7;
          Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2745 TTTTITTTTTTAAGGAAAAAATAA 2769
Db 25 TTTTITTTTTTTTGAAAAAATAA 1

```

```

RESULT 3
BZ764590
LOCUS      25 bp      DNA      linear      GSS 13-MAR-2003
DEFINITION SALK_125759.44.00.x Arabidopsis thaliana TDNA insertion lines
          Arabidopsis thaliana genomic clone SALK_125759.44.00.x, genomic
          survey sequence.
ACCESSION  BZ764590
VERSION     BZ764590.1 GI:28937143
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE  1 (bases 1 to 25)
AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
          Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
          Shinn,P., Zimmerman,J. and Ecker,J.R.
          A Sequence-Indexed Library of Insertion Mutations in the
          Arabidopsis Genome
          Unpublished (2001)
          Contact: Joseph R. Ecker
          Salk Institute Genomic Analysis Laboratory (SIGnAL)
          The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Fax: 858 558 6379
          Email: ecker@salk.edu
          This is single pass sequence recovered from the left border of
          TDNA. This sequence lies within 300 bases of the 5' end of
          At1951830.
          Class: TDNA tagged.
          Location/Qualifiers
            1..25
              /organism="Arabidopsis thaliana"
              /mol_type="genomic DNA"
              /ecotype="Col-0"
              /db_xref="taxon:3702"
              /clone="SALK_125759.44.00.x"
              /clone_lib="Arabidopsis thaliana TDNA insertion lines"
              /note="PCR was performed on Arabidopsis thaliana lines
              each of which contains one or more TDNA insertion
              elements. The resultant fragment for each line was
              directly sequenced to determine the genomic sequence at
              the site of insertion. Details of the protocols used can
              be found at http://signal.salk.edu/tdna_protocols.html"
          Query Match      0.5%; Score 20.2; DB 1; Length 25;
          Best Local Similarity 88.0%; Pred. No. 3.7;
          Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAAAGAAACATCTTTTTTTTTT 2755
Db 1 AAAAAAAAAAATTTTTTTTTT 25

RESULT 4
CD743368/c
LOCUS      24 bp      mRNA      linear      EST 25-JUN-2004
DEFINITION CD743368 IRB8_072 Infected Rat Blood-fed (IRB) An.gam. 30 hr
          Abdomen Library Anopheles gambiae cDNA 5', mRNA sequence.
ACCESSION  CD743368
VERSION     CD743368.1 GI:49247179
KEYWORDS   EST.
SOURCE     Anopheles gambiae (African malaria mosquito)
ORGANISM   Anopheles gambiae
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
          Anopheles.
          Reference 1 (bases 1 to 24)
          Authors Dana,A.N., Lobo,N.F., Hillenmeyer,M.E. and Collins,F.H.

```

TITLE Hematophagy-associated gene expression patterns in adult female
JOURNAL Anopheles gambiae mosquitoes
COMMENT Unpublished (2003)
 Contact: Dana A.N.
 Frank H. Collins Laboratory
 University of Notre Dame
 Center for Tropical Disease Research and Training, Dept. of Biol.
 Sci., Notre Dame, IN 46556, USA
 Tel: 574 - 631 - 3241
 Fax: 574 - 631 - 3996
 Email: adana@nd.edu

PCR Primers
FORWARD: ctcggaagcgccattgtgttg
BACKWARD: atacgactacataggcgcaattggc
Seq primer: ctcggaagcgccattgtgttg.

FEATURES

source

1..24
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="4Arr"
 /db_xref="taxon:7165"
 /sex="female"
 /tissue_type="Abdomens"
 /dev_stage="Female adult 5-7 days post eclosion"
 /lab_host="E. coli XL1-Blue"
 /clone_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr
 Abdomen library"
 /notes="Vector: lambdaTriplex2 (Clontech); Site 1: Sfi IA;
 Site 2: Sfi IB; Plasmidium berghei-infected rat blood-fed
 adult female An. gambiae mosquitoes were flash frozen
 after a 30 hour incubation of adult mosquitoes at 19
 degrees Celsius. Total RNA extracted from abdomens
 separated from remaining carcass. CDNA inserts >500 bp
 cloned directionally into lTriplex2; Sfi IA site is 5'.
 Non-normalized and Non-amplified phagemid library. Single
 pass sequencing reactions from 5' end."

Query Match 0.5%; Score 19.8; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATCAAAACAAA 2826
 |||||
Db 24 AAAAAAAAAAAATAAAAAAAAAA 1

RESULT 5
AW247159/c
LOCUS 2819627.3prxime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819627 3',
DEFINITION mRNA sequence.
ACCESSION AW247159.1 GI:6590152
VERSION EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS NIH-MGC http://img.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2819627.5prine
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross_match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 24
 contiguous PHRED high quality bases following vector sequence. Very
 Low Quality Sequence: Trace file contained 24 contiguous distinct
 peaks following vector sequence. Polyadenylation: Based upon the
 presence of a XhoI site followed by a run of 14 or more T residues
 at the beginning of the sequence, this cDNA insert was
 polyadenylated.
 Plate: LCM2 row: B column: 12
 High quality sequence stop: 24.

FEATURES

source

1..24
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2819627"
 /tissue_type="small cell carcinoma"
 /cell_line="MGCC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5',
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2804 AAAAAAAAAAACATCAAAACAAA 2827
 |||||
Db 24 AAAAAAAAAAAATAAAAAAAAAA 1

RESULT 6
AZ458112/c
LOCUS 1M0261E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0261E24 R, genomic survey sequence.

ACCESSION AZ458112
VERSION AZ458112.1 GI:10616237
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0261 row: E column: 24
 Seq primer: CACACAGGAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

```

source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M045E23"
/lab host="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAACATCAAAACAAA 2826
|||||
Db 24 AAAAAAAAAATAAAAAAAAAA 1

RESULT 7
AZ621257/c      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS
DEFINITION
IM0454E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454E23 F, genomic survey sequence.
ACCESSION
AZ621257
VERSION
AZ621257.1 GI:11743447
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: E column: 23
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
source
1. .24
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M045E23"
/lab host="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2804 AAAAAAAAAACATCAAAACAAA 2827
|||||
Db 24 AAAAAAAAAATAAAAAAAAAA 1

RESULT 8
BZ764590/c      25 bp      DNA      linear      GSS 13-MAR-2003
LOCUS
DEFINITION
SALK 125759.44.00 x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_125759.44.00.x, genomic survey sequence.
ACCESSION
BZ764590
VERSION
BZ764590.1 GI:28937143
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
REFERENCE
1 (bases 1 to 25)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At1G51830.
Class: TDNA tagged.
FEATURES
source
1. .25
Location/Qualifiers

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

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/ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_125759.44.00.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 0.4%; Score 19.2; DB 1; Length 25;
 Best Local Similarity 87.5%; Pred. No. 10;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2731 AAAAAGAAACATCTTTTTTTTT 2754

Db 24 AAAAAAAAAATTTTTTTTTT 1

RESULT 9
 CF310247
 LOCUS
 DEFINITION
 ABF--04-M19_g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--04-M19, mRNA sequence.
 CF310247
 CF310247.1 GI:33682008

EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 23)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--04-M19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."
 Location/Qualifiers

Query Match 0.4%; Score 18.8; DB 1; Length 23;
 Best Local Similarity 90.9%; Pred. No. 8.7;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTNTTTTAAAGAAAAA 2766
 Db 2 TTTTNTTTTAAAGAAAAA 23

Query Match 0.4%; Score 18.8; DB 1; Length 23;
 Best Local Similarity 90.9%; Pred. No. 8.7;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTNTTTTAAAGAAAAA 2766

Db 2 TTTTNTTTTAAAGAAAAA 23

RESULT 10
 CF310247/c
 LOCUS
 DEFINITION

ABF--04-M19_g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--04-M19, mRNA sequence.
 CF310247
 CF310247.1 GI:33682008

EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 23)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--04-M19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."
 Location/Qualifiers

Query Match 0.4%; Score 18.8; DB 1; Length 23;
 Best Local Similarity 90.9%; Pred. No. 8.7;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTNTTTTAAAGAAAAA 2766
 Db 23 TTTTNTTTTAAAGAAAAA 2

RESULT 11
 CF310999
 LOCUS
 DEFINITION

ABF--05-P22_g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--05-P22, mRNA sequence.
 CF310999
 CF310999.1 GI:33682760

EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 23)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--04-M19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."
 Location/Qualifiers

Query Match 0.4%; Score 18.8; DB 1; Length 23;
 Best Local Similarity 90.9%; Pred. No. 8.7;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTNTTTTAAAGAAAAA 2766
 Db 23 TTTTNTTTTAAAGAAAAA 2

RESULT 11
 CF310999
 LOCUS
 DEFINITION

ABF--05-P22_g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--05-P22, mRNA sequence.
 CF310999
 CF310999.1 GI:33682760

EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 23)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Query Match 0.4%; Score 18.8; DB 1; Length 23;
 Best Local Similarity 90.9%; Pred. No. 8.7;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTNTTTTAAAGAAAAA 2766
 Db 2 TTTTNTTTTAAAGAAAAA 23

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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source
  1. .23
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--05-P22"
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    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

Query Match      0.4%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTTCATTTTAAAGGAAAAA 2766
Db 1 TTTTTCATTTTAAAGGAAAAA 22

RESULT 12
CF310999/c
LOCUS
DEFINITION
  CF310999 23 bp mRNA linear EST 15-AUG-2003
  ABF--05-P22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
  library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
  ABF--05-P22, mRNA sequence.
CF310999
ACCESSION
  CF310999.1 GI:33682760
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 23)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
  source
    1. .23
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="ABF--05-P22"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="ABF3-overexpressing transgenic rice plasmid
      cDNA library (ABF)"
      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
      for 2hrs. Oligo-capped mRNA was reverse transcribed and

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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.4%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTTCATTTTAAAGGAAAAA 2766
Db 22 TTTTTCATTTTAAAGGAAAAA 1

RESULT 13
AZ316719
LOCUS
DEFINITION
  AZ316719 23 bp DNA linear GSS 29-SEP-2000
  1M0035A01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0035A01 F, genomic survey sequence.
AZ316719
ACCESSION
  AZ316719 GI:10364814
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 23)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah
    University of Utah
    Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0035 row: A column: 01
    Seq primer: CGTTGTAACACGACGCCAGT
    Class: plasmid ends
    High quality sequence stop: 23.
    Location/Qualifiers
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        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0035A01"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adapted DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (GI4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adapted vector DNA, and transformed into

```

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 615 GCGCGCGGCACGACGCGCGC 636
|||||
Db 2 GCGCGCGCGCGCGCGCGC 23

RESULT 14
AZ316719/c
LOCUS
DEFINITION
1M0035A01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0035A01 F, genomic survey sequence.

ACCESSION
AZ316719
VERSION
AZ316719.1 GI:10364814
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Iglam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: A column: 01

Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES
source

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035A01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 615 GCGCGCGGCACGACGCGCGC 636
|||||
Db 23 GCGCGCGCGCGCGCGCGC 2

RESULT 15
AI307726

LOCUS
DEFINITION
AI307726 25 bp mRNA linear EST 08-APR-1999
td36d11.x1 NCI CGAP HSC2 Homo sapiens cDNA clone IMAGE:2056437 3'
similar to TR:020155 O20155 ORF41C. i, mRNA sequence.

ACCESSION
AI307726
VERSION
AI307726.1 GI:4001931

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 25)

AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,

M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 494 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2056437"
/tissue_type="stem cell 34+/38+"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP HSC2"
/note="Organ: bone marrow; Vector: pAMPl; mRNA made from
bone marrow, stem cells 34+/38+, cDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 400 bp. Primary library,
non-amplified."

Query Match 0.4%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2745 TTTTTCCTTAAAGGAAAAATAA 2769
|||||
Db 1 TTTTTCCTTTCCTTAAAAAATAA 25

RESULT 16
AZ835133

LOCUS
DEFINITION
AZ835133 20 bp DNA linear GSS 20-FEB-2001
2M0129008F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0129008 F, genomic survey sequence.

ACCESSION
AZ835133

VERSION
AZ835133.1 GI:13005041

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Roste,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weises,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

AUTHORS
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLcU, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduwn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0129 row: 0 column: 08
Seq primer: CGTTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

TITLE

JOURNAL

COMMENT

FEATURES
source
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0129O08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /Clone_lib="Mouse 10kb plasmid UUC1M library"
 /note=Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptoered DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptoered mouse DNA was annealed to
adaptoered vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTTTTTTTTAAGCAAAAAA 2765
||||||| ||||| ||||| |||||
Db 1 TTTTTTTTTTTAAAAAAA 20

RESULT 17
AZ8351133/c
LOCUS AZ8351133
DEFINITION ZMW129O08F Mouse 10kb plasmid UUC1M library Mus musculus genomic
Clone UUGC2M0129O08 F, genomic survey sequence.
ACCESSION AZ8351133
VERSION AZ8351133.1
KEYWORDS GI:13005041
GSS.

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ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE     1 (bases 1 to 21)
AUTHORS       Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE         Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL       Unpublished (2004)
COMMENT       Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES     source
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             /clone_lib="CSEQRAN09"
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             constructed from pooled tissue from day 30 placentas."
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2745 TTTTCTTTTAAAGGAAAAA 2764
Db      2 TTTTCTTTTAAAGGAAAAA 21

RESULT 19
AJ661013/c      21 bp mRNA linear EST 28-JUN-2004
LOCUS           AJ661013 CSEQRAN09 Sus scrofa cDNA clone C0000935_H04, mRNA
DEFINITION      sequence.
ACCESSION       AJ661013
VERSION         AJ661013.1 GI:49345046
KEYWORDS        EST.
SOURCE          Sus scrofa (pig)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE       1 (bases 1 to 21)
AUTHORS         Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE           Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL         Unpublished (2004)
COMMENT         Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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               /mol_type="mRNA"
               /db_xref="taxon:9823"
               /db_xref="taxon:9823"

ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE     1 (bases 1 to 21)
AUTHORS       Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE         Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL       Unpublished (2004)
COMMENT       Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES     source
             1..21
             /organism="Sus scrofa"
             /mol_type="mRNA"
             /db_xref="taxon:9823"
             /db_xref="taxon:9823"
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/clone="C0000935_H04"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/notes="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2747 TTTTCTTTTAAAGGAAAAA 2766
Db      21 TTTTCTTTTAAAGGAAAAA 2

RESULT 20
CN763587
LOCUS           CN763587 21 bp mRNA linear EST 20-MAY-2004
DEFINITION      ID0AAA7BH12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA7BH12 5',
mRNA sequence.
ACCESSION       CN763587
VERSION         CN763587.1 GI:47537510
KEYWORDS        EST.
SOURCE          Acyrthosiphon pisum (pea aphid)
ORGANISM        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE       1 (bases 1 to 21)
AUTHORS         Hunter,W., Martinez-Torres,D., Rabbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
TITLE           An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
JOURNAL         Unpublished (2004)
COMMENT         Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Plate: 7 row: H column: 12.
FEATURES       source
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               /clone="ID0AAA7BH12"
               /tissue_type="whole insect"
               /dev_stage="nymphs and adults (parthenogenetic females)"
               /lab_host="XLI-Blue"
               /clone_lib="ApMS"
               /note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
               Sample name: ID0AAA ; Plant growth place: Department of
               Ecology & Evolutionary Biology, Princeton University ;
               Soil conditions: Soil ; Sowing date: 01/06/1999 ;
               Harvesting date: 01/06/1999 ; Stress date: no stress ;
               Description: Aphids inoculated on one-week old Vicia faba
               under non-sterile conditions. All parthenogenetic stages
               and both winged and wingless adults were collected for
               library construction. ; experimental condition: long
               photoperiod (16-hr light/8-hr dark at 18 c)"
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy	2747	TTTTTTTTTAAAGGAAAAA	2766
Db	1		20
RESULT 21			
CN763587/c			
LOCUS			
DEFINITION	CN763587	21 bp mRNA linear	EST 20-MAY-2004
	ID0AAA7BH12RM1	ApMs Acyrthosiphon pisum cDNA clone	ID0AAA7BH12 5',
	mRNA sequence.		
ACCESSION	CN763587		
VERSION	CN763587.1	GI:47537510	
KEYWORDS	EST.		
SOURCE	Acyrthosiphon pisum (pea aphid)		
ORGANISM	Acyrthosiphon pisum		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;		
	Aphidoidea; Aphididae; Macrocephali; Acyrthosiphon.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,		
	Stern, D., Tagu, D. and Wincker, P.		
TITLE	An expressed sequence tags database for the pea aphid Acyrthosiphon		
	pisum		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: D. Tagu		
	INRA Rennes		
	UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France		
	Tel: +33.2.23.48.51.65		
	Fax: +33.2.23.48.51.50		
	Risk of contamination by bacterial sequences from obligatory		
	(Buchner) or facultative endosymbionts. These sequences were		
	obtained in the frame of the International Consortium of Aphid		
	Genomics in collaboration with Genoscope		
	PCR Primers		
	FORWARD: CAGGAACACGTATGACC		
	Plate: 7	row: H	column: 12.
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="Acyrthosiphon pisum"		
	/mol_type="mRNA"		
	/cultivar="developmentstage"		
	/db_xref="taxon:7029"		
	/clone="ID0AAA7BH12"		
	/tissue_type="whole insect"		
	/dev_stage="nymphs and adults (parthenogenetic females)"		
	/lab_host="X11-Blue"		
	/clone_lib="ApMs"		
	/note=vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;		
	Sample name: ID0AAA ; Plant growth place: Department of		
	Ecology & Evolutionary Biology, Princeton University ;		
	Soil conditions: Soil ; Sowing date: 01/06/1999 ;		
	Harvesting date: 01/06/1999 ; Stress date: no stress ;		
	Description: Aphids inoculated on one-week old Vicia faba		
	under non-sterile conditions. All parthenogenetic stages		
	and both winged and wingless adults were collected for		
	library construction. ; experimental condition: long		
	photoperiod (16-hr light/8-hr dark at 18 C)"		
Query Match	0.4%	Score 16.8;	DB 1; Length 21;
Best Local Similarity	90.0%	Pred. No. 36;	
Matches	18;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
Qy	2745	TTTTTTTTTAAAGGAAAAA	2764
Db	20		1
RESULT 22			
CL693164			
LOCUS			
DEFINITION	CL693164	21 bp DNA linear	GSS 10-JUL-2004
	PRIO160a_G09_2 - PRIO160a.BR (21) Mixed stage foamid library of P.		
	pacificus var. California Pristionchus pacificus genomic, genomic		
	survey sequence.		

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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="vector: pEpifos-5 Fosmid vector"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACHTCAAAA 2822
Db 2 AAAAAAAAAAACHTCAAAAA 21

RESULT 24
LOCUS
DEFINITION
GC0698 TIGEM gene trap library Mus musculus cDNA clone A012.A8,
mRNA sequence.
ACCESSION
VERSION
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Cobellis,G., Nicolaus,G., Marra,E., Barbarisi,M., Sardiello,M., Di
Giorgio,F.P., Iovino,N., Zollo,M., Ballabio,A. and Cortese,R.
Tagging genes with cassette-exchange sites
Unpublished (2004)
Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="A012.A8"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="vector: pFLIP1"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2747 TTTTAAAAAGGAAAAA 2766
Db 1 TTTTAAAAAGGAAAAA 20

RESULT 25
LOCUS
DEFINITION
AW247159 24 bp mRNA linear EST 07-JAN-2000
2819627.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819627 3',
mRNA sequence.

```

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 24)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819627.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 24
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM2 row: B column: 12
High quality sequence stop: 24.
FEATURES
source
Location/Qualifiers
1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819627"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Query Match      0.4%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1152 TTTCTTTTATATATATTTT 1174
Db 1 TTTTATATATATATATTTT 23

RESULT 26
LOCUS
DEFINITION
AZ621257 24 bp DNA linear GSS 13-DEC-2000
1M0454E23F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0454E23 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS   1 (bases 1 to 24)
           Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
           Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
           Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
           Niederhausen,A. and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
           University of Utah Genome Center
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: E column: 23
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES   Location/Qualifiers
           1..24
           /organism="Mus musculus"
           /mol_type="genomic DNA"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="UTGCM0454E23"
           /sex="Male"
           /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
           /clone_lib="Mouse 10kb plasmid UGCM library"
           /notes="Vector: PWD42nv; Purified genomic DNA from M.
           musculus C57BL/6J (male) was obtained from the Jackson
           Laboratory Mouse DNA Resource
           (http://www.jax.org/resources/documents/dnares/). The DNA
           was hydrodynamically sheared by repeated passage through a
           0.005 inch orifice at constant velocity. The sheared DNA
           was blunt end-repaired with T4 DNA polymerase and T4
           polynucleotide kinase. Adaptor oligonucleotides were
           ligated to the blunt ends in high molar excess. The
           adaptor DNA was purified and size-selected for a 9.5 to
           10.5 kb range using preparative agarose gel
           electrophoresis. Vector DNA was prepared from a derivative
           of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
           inducible derivative of plasmid R1. The vector was ligated
           with adaptors complementary to the insert adaptors and
           purified. The sheared, adaptor mouse DNA was annealed to
           adaptor vector DNA, and transformed into
           chemically-competent E. coli XL10-Gold (Stratagene) cells
           and selected for ampicillin resistance."
Query Match      0.4%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATATATATTTT 1174
      ||| ||||| ||||| |||||
Db 1 TTTTATTTTATTTTATTTT 23

RESULT 27
CF295672/c
LOCUS      CF295672
DEFINITION 30DGS--05-L12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
           sativa (japonica cultivar-group) cDNA clone 30DGS--05-L12, mRNA
           sequence.
ACCESSION  CF295672
VERSION     CF295672.1 GI:33664705
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS   19 bp mRNA linear EST 14-AUG-2003
           Song,S.I., Jun,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
           1..19
           /organism="Oryza sativa (japonica cultivar-group)"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:39947"
           /clone="30DGS--05-L12"
           /tissue_type="leaf"
           /dev_stage="30 days after germination"
           /lab_host="E.coli DH10B"
           /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
           /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."
Query Match      0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2797 TATGTGAAAAA 2814
      ||||| ||||| |||||
Db 19 TATGTTAAAAA 2

RESULT 28
CF323353/c
LOCUS      CF323353
DEFINITION HDN--03-K01.g1 OshDAC1-overexpressing transgenic rice lambda phage
           cDNA library II (HDN) Oryza sativa (japonica cultivar-group) CDNA
           clone HDN--03-K01, mRNA sequence.
ACCESSION  CF323353
VERSION     CF323353.1 GI:33794946
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS   1 (bases 1 to 19)
           Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
           1..19
           /organism="Oryza sativa (japonica cultivar-group)"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:39947"
           /clone="HDN--03-K01"
           /tissue_type="callus"
           /dev_stage="proliferated callus on 2N6 media for 2 weeks"
           /lab_host="E.coli SOLR"

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Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
           1..19
           /organism="Oryza sativa (japonica cultivar-group)"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:39947"
           /clone="30DGS--05-L12"
           /tissue_type="leaf"
           /dev_stage="30 days after germination"
           /lab_host="E.coli DH10B"
           /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
           /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."
Query Match      0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2797 TATGTGAAAAA 2814
      ||||| ||||| |||||
Db 19 TATGTTAAAAA 2

RESULT 28
CF323353/c
LOCUS      CF323353
DEFINITION HDN--03-K01.g1 OshDAC1-overexpressing transgenic rice lambda phage
           cDNA library II (HDN) Oryza sativa (japonica cultivar-group) CDNA
           clone HDN--03-K01, mRNA sequence.
ACCESSION  CF323353
VERSION     CF323353.1 GI:33794946
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS   1 (bases 1 to 19)
           Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
           1..19
           /organism="Oryza sativa (japonica cultivar-group)"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:39947"
           /clone="HDN--03-K01"
           /tissue_type="callus"
           /dev_stage="proliferated callus on 2N6 media for 2 weeks"
           /lab_host="E.coli SOLR"

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/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCGCGCCCC 990
|||||
Db 18 CCCCCCCCCCGCGCCCC 1

RESULT 29
AZ766990
LOCUS
DEFINITION
A2766990 19 bp DNA linear GSS 16-FEB-2001
clone UUGC1M0564H19 R, genomic survey sequence.
ACCESSION
A2766990
VERSION
A2766990.1 GI:12884624
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: H column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564H19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAATTGGA 2593
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Db 1 AAAAAAAAAAATTGGA 18

RESULT 30
AZ426873/C
LOCUS
DEFINITION
AZ426873 20 bp DNA linear GSS 03-OCT-2000
clone UUGC1M0208L05 R, genomic survey sequence.
ACCESSION
AZ426873
VERSION
AZ426873.1 GI:10550886
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0208 row: L column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0208L05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* Xli10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCGCCC 990
      |||||
Db 1 CCCCCCCCCCGCGCCC 18

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RESULT 32	20 bp	DNA	linear	GSS 20-FEB-2001
AZ845320/c				
LOCUS	AZ845320	20kb plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	2M0145W02F	Mouse	clone UUGC2M0145W02 F,	genomic survey sequence.

ACCESSION NUMBER	VERSION NUMBER	SOURCE	ORGANISM	REFERENCE
AZ845320		GSS.	Mus musculus (house mouse)	
AZ845320.1	GI:13015228			
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus. (bases to 20)				

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE	Mouse whole genome scaffolding with paired end reads from 10kbp Plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112-9011 Tel: 801-585 5606

Email: dunn@genetics.utah.edu
 Fax: 801 595 7177
 Insert Length: 10000 Std Error: 0.00
 Plate: 0145 row: M column: 02
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

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FEATURES
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    1..20
    Location/Qualifiers
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0145M02"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/42nvrec1). The DNA

```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|9B|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and the sheared, adaptor mouse DNA was annealed to the purified, adaptor DNA.

adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 974 CCCCCCACCAGCCGCCCA 991
|||||
Db 20 CCCCCCACCAGCCGCCCA 3

RESULT 33
CF312586/c
LOCUS
DEFINITION ABP--08-G13-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-G13, mRNA sequence.

ACCESSION CF312586
VERSION CF312586.1 GI:33684347
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 16)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="ABP--08-G13"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_hosts="E.coli DH10B"
/clone_libs="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588
|||||
Db 16 TTTAAAAA 1

RESULT 34
CF298591/c
LOCUS
DEFINITION 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA sequence.
ACCESSION CF298591

VERSION CF298591.1 GI:33670352
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 18)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="7LEAF--02-A20"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_hosts="E.coli DH10B"
/clone_libs="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588
|||||
Db 18 TTTAAAAA 3

RESULT 35
CF278272/c
LOCUS
DEFINITION 14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-C01, mRNA sequence.

ACCESSION CF278272
VERSION CF278272.1 GI:33655658
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"
 /db_xref="taxon:39947"
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 16; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTTAAAAA 2588
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 Db 18 TTTTAAAAA 3

RESULT 36
 AZ458112 24 bp DNA linear GSS 04-OCT-2000
 LOCUS
 DEFINITION IM0261E24R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0261E24 R, genomic survey sequence.

ACCESSION AZ458112
 VERSION A2458112.1 GI:10616237
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0261 row: E column: 24
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGCLM0261E24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nb; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16; DB 1; Length 24;
 Best Local Similarity 79.2%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1153 TTCTTTTATATATATTTTCT 1176
 |||||
 Db 1 TTTTITTTATTTTITTTT 24

RESULT 37
 CF308042/c 19 bp mRNA linear EST 15-AUG-2003
 LOCUS
 DEFINITION ABF--01-L07 b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-L07, mRNA sequence.

ACCESSION CF308042
 VERSION CF308042.1 GI:33679803
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers
 1..19
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--01-L07"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

source

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 50;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2798 ATGTGAAAAA 2816
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 Db 19 ATGTGAAAAA 1

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RESULT 38
AZ654747/c
LOCUS
DEFINITION
  AZ654747
  1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0529F08 F, genomic survey sequence.
ACCESSION
  AZ654747
VERSION
  AZ654747.1 GI:11791893
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
REFERENCE
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0529 row: F column: 08
    Seq primer: CGTGTAAACGACGGCCAGT
    Class: plasmid ends
    High quality sequence stop: 19.
FEATURES
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    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clones="UUGC1M0529F08"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptored DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptored mouse DNA was annealed to
    adaptored vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
    Query Match 0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 50;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2804 AAAAAAAAAAACATCAAAA 2822
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Db 19 AAAAAAAAAAATATAAAA 1

RESULT 39

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AZ764511/c
LOCUS
DEFINITION
  AZ764511
  1M0560B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0560B08 R, genomic survey sequence.
ACCESSION
  AZ764511
VERSION
  AZ764511.1 GI:12879549
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
REFERENCE
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0560 row: B column: 08
    Seq primer: CACACAGGAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 19.
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    /organism="Mus musculus"
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    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clones="UUGC1M0560B08"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptored DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptored mouse DNA was annealed to
    adaptored vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
    Query Match 0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 50;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2737 AAAACATCTTTT TTTT 2755
    |||||
Db 19 AAAAAATTTT TTTT 1

RESULT 40
AZ856877

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LOCUS
 DEFINITION 2M0164D14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0164D14 F, genomic survey sequence.
 ACCESSION AZ858877
 VERSION AZ858877
 KEYWORDS AZ858877.1 GI:13052498
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Stokes,R., Tingley,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0164 row: D column: 14
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0164D14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 50;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 615 GCGGCGCGCGCACGCGCG 633
 Db 1 GCGGCGCGCGCGCGCGCG 19

RESULT 41
 AZ858877/c
 LOCUS AZ858877 19 bp DNA linear GSS 21-FEB-2001

DEFINITION 2M0164D14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0164D14 F, genomic survey sequence.
 ACCESSION AZ858877
 VERSION AZ858877
 KEYWORDS AZ858877.1 GI:13052498
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Stokes,R., Tingley,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0164 row: D column: 14
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0164D14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 50;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 616 GCGGCGCGCGCACGCGCG 634
 Db 19 GCGGCGCGCGCGCGCGCG 1

RESULT 42
 AZ962226
 LOCUS AZ962226 19 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUC2M0231A02 F, genomic survey sequence.
ACCESSION A2962226
VERSION A2962226.1 GI:13833453
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedernauser,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0231 row: A column: 02
Seq primer: CGTTGTAACAGCAGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0231A02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2584 AAAAAATCGACAAAAAAA 2602
|||||
Db 1 AAAAAATCGAAAAAAA 19
RESULT 43
BG673623 17 bp mRNA linear EST 30-APR-2001
LOCUS DRNAQC09 Rat DRG Library Rattus norvegicus cDNA clone DRNAQC09 5', mRNA sequence.
DEFINITION

ACCESSION BG673623
VERSION BG673623.1 GI:13895722
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 17)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C., Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D., Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE 22056133
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguag (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.
FEATURES
source
1..17
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNAQC09"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2571 TGTTTAAAAAAA 2587
|||||
Db 1 TTTTAAAAAAA 17
RESULT 44
AI471695 19 bp mRNA linear EST 09-MAR-1999
LOCUS t199f04.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2155231 3' similar to SW:LA17 YEAST Q12446 PROLINE-RICH PROTEIN LAS17.
DEFINITION ;contains element MSRI repetitive element ;, mRNA sequence.
ACCESSION AI471695
VERSION AI471695.1 GI:4333785
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1. .19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:215231"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col4"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; Salt: Site 2: NoI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 974 CCCCCCACCACCCGCCCC 990
||||| |||||||
Db 1 CCCCCCACCACCCGCCCC 17

RESULT 45

AZ427731

LOCUS

DEFINITION 19 bp DNA linear GSS 03-OCT-2000
clone UUGC1M0209G19 R, genomic survey sequence.

ACCESSION AZ427731

VERSION AZ427731.1 GI:10551744

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0209 row: G column: 19

Seq primer: CACACGAAACACCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0209G19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 74;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 974 CCCCCCACCACCCGCCCC 990

||||| |||||||

Db 1 CCCCCCACCACCCGCCCC 17

RESULT 46

AZ650212

LOCUS

DEFINITION 19 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0520G13 F, genomic survey sequence.

ACCESSION AZ650212

VERSION AZ650212.1 GI:11784470

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0520 row: G column: 13

Seq primer: CCTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"


```

/db_xref="taxon:10090"
/clones="UUGC1M0520G13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1|] a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCCCCCCC 989
Db 3 CCCCCCCCCCCCCCCC 19

RESULT 47
LOCUS CD743368 24 bp mRNA linear EST 25-JUN-2004
DEFINITION IRB8_E10_IRB8_072 Infected Rat Blood-fed (IRB) An.gam. 30 hr Abdomen Library Anopheles gambiae cDNA 5', mRNA sequence.
ACCESSION CD743368
VERSION CD743368.1 GI:49247179
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
1 (bases 1 to 24)
Dana, A.N., Lobo, N.F., Hillenmeyer, M.E. and Collins, F.H. Hematophagy-associated gene expression patterns in adult female Anopheles gambiae mosquitoes
Unpublished (2003)
Contact: Dana A.N.
Frank H. Collins Laboratory
University of Notre Dame
Center for Tropical Disease Research and Training, Dept. of Biol. Sci., Notre Dame, IN 46556, USA
Tel.: 574 - 631 - 3241
Fax: 574 - 631 - 3996
Email: adana@nd.edu
PCR Primers
FORWARD: ctccgggaagcgcgcattgtgtgg
BACKWARD: ataccatcactataggcgaaattggc
Seq primer: ctccgggaagcgcgcattgtgtgg.
Location/Qualifiers
1. .24
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4Atr"
/db_xref="taxon:7165"
/sex="female"
/tissue_type="Abdomens"
/dev_stage="Female adult 5-7 days post eclosion"

```

```

/lab_host="E. coli XL1-Blue"
/clone_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr Abdomen Library"
/notes="Vector: lamdaTriplex2 (Clontech); Site 1: Sfi IA; Site 2: Sfi IB; Plasmodium berghei-infected rat blood-fed adult female An. gambiae mosquitoes were flash frozen after a 30 hour incubation of adult mosquitoes at 19 degrees Celsius. Total RNA extracted from abdomens separated from remaining carcasses. CDNA inserts >500 bp cloned directionally into lTriplex2; Sfi IA site is 5'. Non-normalized and Non-amplified phagemid library. Single pass sequencing reactions from 5' end."

Query Match      0.4%; Score 15.2; DB 1; Length 24;
Best Local Similarity 81.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4079 TTTTCTTTTAATGTTTTTTT 4099
Db 1 TTTTCTTTTAATGTTTTTTT 21

RESULT 48
LOCUS AW246551/c 15 bp mRNA linear EST 07-JAN-2000
DEFINITION 2822090.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822090 3', mRNA sequence.
ACCESSION AW246551
VERSION AW246551.1 GI:6589544
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822090.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-x@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubium Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu/Low Quality Sequence: 14 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LICM8 row: I column: 3
High quality sequence stop: 14.
Location/Qualifiers
1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822090"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5'

```

FEATURES
source

adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2571 TGTTTAAAAA 2585
Db 15 TGTTTAAAAA 1

RESULT 49
LOCUS CF299675 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-M14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA sequence.

ACCESSION CF299675
VERSION CF299675.1 GI:33671436

KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-M14"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2587
Db 3 TTTAAAAA 17

RESULT 50
LOCUS AJ600267 18 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 503E07, genomic survey sequence.

ACCESSION AJ600267
VERSION AJ600267.1 GI:37949895

KEYWORDS GSS; right border; T-DNA flanking sequence.

SOURCE ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosoids; euroside II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

MEDLINE 22363535

PUBMED 12446565

REFERENCE 2 (bases 1 to 18)

AUTHORS Balzergue, S.

TITLE Direct Submission

JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobioigen.fr>).

FEATURES

source

1. .18
Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Massillewskija"

/db_xref="taxon:3702"

/clone="503E07"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature 1. .18

/note="T-DNA flanking sequence"

right border"

Query Match 0.4%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1160 TTATATATATTTT 1174

Db 3 TTATATATATTTT 17

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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: B column: 08

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0560B08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 15; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAATT 2590

|||||

Db 1 AAAAAAAAAAAAAATT 15

RESULT 52

AW248796

LOCUS

DEFINITION AW248796 18 bp mRNA linear EST 07-JAN-2000

mRNA sequence.

ACCESSION AW248796

VERSION AW248796.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2820768.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/FTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 12
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 18 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.

Plate: LHCMS row: B column: 1

High quality sequence stop: 12.

FEATURES

source

1..18

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGS:2820768"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 93;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2746 TTTTITTTTAAAGGAAAA 2763

|||||

Db 1 TTTTITTTTGGGAAAA 18

RESULT 53

CF301359/c

LOCUS

DEFINITION CF301359 18 bp mRNA linear EST 15-AUG-2003

7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa (japonica cultivar-group) cDNA clone 7LEAF-06-D05, mRNA

sequence.

ACCESSION CF301359

VERSION CF301359.1

KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Yeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

```

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-D05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 93;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 926 AGGAGAGAAAAAACAACAA 943
    |||||
Db 18 AGGAAAAA

RESULT 54
BM658913
LOCUS      26 bp      mRNA      linear      EST 27-FEB-2002
DEFINITION LQ6602768282.R1 CSEQFXL36 fetal brain Sus scrofa cDNA, mRNA
sequence.
ACCESSION  BM658913
VERSION    BM658913.1 GI:18959184
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 26)
AUTHORS   Adelson,D.L. and Gill,C.A.
TITLE     Porcine ESTs
JOURNAL   Unpublished (2002)
COMMENT   Contact: David L. Adelson
          Animal Breeding and Genetics
          Texas A&M University
          Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
          USA
          Tel: 9798452616
          Fax: 9798456970
          Email: david.adelson@tamu.edu.
FEATURES             source
     source
     1..26
     /organism="Sus scrofa"
     /mol_type="mRNA"
     /db_xref="taxon:9823"
     /dev_stage="fetal"
     /clone_lib="CSEQFXL36 fetal brain"
     /note="Organ: brain; Vector: pBluescript SK+; Site_1:
     NotI; Site 2: EcoRI; sequence 5' of the insert
     (5'-NNN_NNNinsert)
     GCGAATGGAGCTCCACCGCGGTGGCGCGCGCTCGAG. Sequence 3' of
     the inserts (AAGAAATCGATACAGCTATCATCGATACCGTCGACCTCGAG.
     non-normalized library, sequenced 3' with M13R primer."

Query Match      0.3%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1152 TTTCTTTTATATATTTTCTT 1177
    |||||
Db 1 TTTTCTTCTCTTTTCTTTTCTT 26

RESULT 55
A1685758
LOCUS      16 bp      mRNA      linear      EST 27-MAY-1999
DEFINITION tu37909.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:253280 3',
similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL
SEQUENCE MOTIF PROTEIN 1 ; contains element LTR4 repetitive element

```

```

; mRNA sequence.
ACCESSION  A1685758
VERSION    A1685758.1 GI:4897052
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: csapbs-x@mail.nih.gov
          Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          cDNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES             source
     source
     1..16
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="IMAGE:2253280"
     /sex="male"
     /dev_stage="adult"
     /lab_host="DH10B"
     /clone_lib="NCI CGAP Pr28"
     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
     with a modified polylinker; Plasmid DNA from the
     normalized library NCI CGAP_Pr22 was prepared, and ss
     circles were made in vitro. Following RAP purification,
     this DNA was used as tracer in a subtractive hybridization
     reaction. The driver was PCR-amplified cDNAs from a pool
     of 5,000 clones made from the same library (clonesIDs
     985608-986759, 1101192-1101959, and 1217928-1220615).
     Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match      0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 644 CACACATCCACAGCA 659
    |||||
Db 1 CACACATACACAGCA 16

RESULT 56
AW248540/c
LOCUS      16 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION 2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
mRNA sequence.
ACCESSION  AW248540
VERSION    AW248540.1 GI:6591533
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NIH-MGC http://mgc.ncbi.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT   Other_ESTs: 2820844.5prime

```

Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://www-bio.llnl.gov/bbrp/image.html> Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCMS5 row: E column: 5
High quality sequence stop: 15.
Location/Qualifiers

FEATURES

source

```
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820844"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"

```

/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2570 GTGTTTAAAAA 2585

Db 16 GTTTTAAAAA 1

RESULT 57
LOCUS AW248958 16 bp mRNA linear EST 07-JAN-2000
DEFINITION AW248958.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819454 3', mRNA sequence.

ACCESSION AW248958

VERSION AW248958.1 GI:6591951

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2819454.5prime

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM1 row: K column: 7
High quality sequence stop: 15.
Location/Qualifiers

FEATURES

source

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1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819454"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"

```

/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2746 TTTTATTTTAAAGGAA 2761

Db 1 TTTTATTTTAAAGGAA 16

RESULT 58

CF317778/c

LOCUS

DEFINITION

HD--07-J13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--07-J13, mRNA sequence.

ACCESSION CF317778

VERSION CF317778.1 GI:33689539

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

source

1. .16

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

Best Local Similarity 93.8%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2570 GTGTTTAAAAA 2585
Db 16 GTTTTAAAAA 1

RESULT 61
LOCUS CF299997/c
DEFINITION 7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-D19, mRNA sequence.
ACCESSION CF299997
VERSION CF299997.1 GI:33671758
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-D19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 62
LOCUS CF300456/c
DEFINITION 7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA sequence.
ACCESSION CF300456
VERSION CF300456.1 GI:33672217
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 929 AGAAAAAACA 944
Db 18 AGAAAAAACA 3

RESULT 63
LOCUS CF329285/c
DEFINITION NACL--04-122.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-122, mRNA sequence.
ACCESSION CF329285
VERSION CF329285.1 GI:33806806
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-122"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  929 AGAAAAAAACAAAA 944
Db  17 AGAAAAAAACAAAAA 2

RESULT 64
AW249689/c
LOCUS
DEFINITION      15 bp mRNA linear EST 07-JAN-2000
                  2819706.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819706 3',
                  mRNA sequence.
ACCESSION      AW249689
VERSION        AW249689.1 GI:6592682
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT      Other ESTs: 2819706.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nhl.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 13
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 15 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LICM2 row: E column: 19
High quality sequence stop: 13.
Location/Qualifiers
1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819706"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_hosts="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  2799 TGTCAAAAAA 2812
Db  14 TGTCAAAAAA 1

RESULT 65
CF295100/c
LOCUS
DEFINITION      15 bp mRNA linear EST 14-AUG-2003
                  30DGS--04-002.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
                  sativa (japonica cultivar-group) cDNA clone 30DGS--04-002, mRNA
                  sequence.
ACCESSION      CF295100
VERSION        CF295100.1 GI:33664133
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
                  Oryza sativa (japonica cultivar-group)
                  Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
                  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                  of Bioscience and Bioinformatics, Myongji University
                  Yongin, Kyeonggi, Korea
                  Tel: 82 31 330 6193
                  Fax: 82 31 321 6355
                  Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--04-002"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_hosts="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  2575 TAAAAA 2588
Db  15 TAAAAA 2

RESULT 66
CF301470/c
LOCUS
DEFINITION      15 bp mRNA linear EST 15-AUG-2003
                  7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                  sativa (japonica cultivar-group) cDNA clone 7LEAF--06-F15, mRNA
                  sequence.
ACCESSION      CF301470
VERSION        CF301470.1 GI:33673231
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
                  Oryza sativa (japonica cultivar-group)
                  Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs

```


JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 1. .15
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF-06-F15"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2803 AAAAAAAAAAACA 2816
 Db 14 AAAAAAAAAAACA 1

RESULT 67
 CR789161
 LOCUS CR789161 15 bp mRNA linear EST 01-OCT-2004
 DEFINITION DKFZp468J1632_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
 CR789161
 VERSION DKFZp468J1632 5', mRNA sequence.
 KEYWORDS CR789161.1 GI:53708043
 EST.

SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Ansoerge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
 Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and
 Wiemann, S.
 TITLE Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 JOURNAL Unpublished (2004)
 COMMENT Contact: MIPS

MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468J1632
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES
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 Location/Qualifiers
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp468J1632"
 /tissue_type="heart"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="468 (synonym: phrt1)"
 /notes="vector: pSPori_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 0.3%; Score 14; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 61;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2803 AAAAAAAAAAACA 2816
 Db 2 AAAAAAAAAAACA 15

RESULT 68
 BQ590507/c
 LOCUS BQ590507 16 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
 ACCESSION BQ590507
 VERSION BQ590507.1 GI:26120090
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Anaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert length: 16 Std Error: 0.00
 Plate: 19 row: M column: 04
 Seq primer: T7; GTAATACGACTCTACTATAGGCG.

FEATURES
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 1. .16
 Location/Qualifiers
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:189608"
 /db_xref="taxon:161934"
 /clone="024-019-M04"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinvanleberer Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2575 TAAAAAAAAAAAAA 2588
 Db 16 TAAAAAAAAAAAAA 3

RESULT 69
 BQ595369/c

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LOCUS      BQ595369                16 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION S01317-024-022-P02-T7 MPZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION  BQ595369
VERSION    BQ595369.1      GI:26124952
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
JOURNAL   fingerprinting allows access to 25 000 potential sugar beet genes
MEDLINE   Plant J. 32 (5), 845-857 (2002)
PUBMED    22362189
COMMENT   Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 16 Std Error: 0.00
            Plate: 22 row: P column: 02
            Seq primer: T7; GTAATACGACTCATTATAGGC.
            Location/Qualifiers
FEATURES   source
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                /mol_type="mRNA"
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                /db_xref="taxon:161934"
                /clone="024-022-P02"
                /tissue_type="developing root"
                /lab_host="EMDH10B"
                /clone_lib="MPZ-ADIS-024-developing root"
                /note="Vector: PCWVSPT6; Site 1: Sali; Site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPP/GABI-Primary database: http://gabi.rzpd.de"
Query Match      0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2575 TAAAAAATAAAAA 2588
Db      16 TAAAAAATAAAAA 3
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RESULT 70
LOCUS    CF296130/c                16 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION CF296130-06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Orzya
            sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA
            sequence.
ACCESSION  CF296130
VERSION    CF296130.1      GI:33665163
KEYWORDS   EST.
SOURCE     Orzya sativa (japonica cultivar-group)
ORGANISM   Orzya sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

LOCUS    CF296130/c                16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION CF296130-02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Orzya sativa (japonica cultivar-group) cDNA clone
            HD--02-G01, mRNA sequence.
ACCESSION  CF296130
VERSION    CF296130.1      GI:33685774
KEYWORDS   EST.
SOURCE     Orzya sativa (japonica cultivar-group)
ORGANISM   Orzya sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6193
            Fax: 82 31 321 6355
            Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.
            Location/Qualifiers
FEATURES   source
            1..16
                /organism="Orzya sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="30DGS--06-F22"
                /tissue_type="leaf"
                /dev_stage="30 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
Query Match      0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2575 TAAAAAATAAAAA 2588
Db      16 TAAAAAATAAAAA 3
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RESULT 71
LOCUS    CF314013/c                16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION CF314013-02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Orzya sativa (japonica cultivar-group) cDNA clone
            HD--02-G01, mRNA sequence.
ACCESSION  CF314013
VERSION    CF314013.1      GI:33685774
KEYWORDS   EST.
SOURCE     Orzya sativa (japonica cultivar-group)
ORGANISM   Orzya sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6193
            Fax: 82 31 321 6355
            Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.
            Location/Qualifiers
FEATURES   source
            1..16
                /organism="Orzya sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD--02-G01"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6193
            Fax: 82 31 321 6355
            Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.
            Location/Qualifiers
FEATURES   source
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                /organism="Orzya sativa (japonica cultivar-group)"
                /mol_type="mRNA"
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                /db_xref="taxon:39947"
                /clone="30DGS--06-F22"
                /tissue_type="leaf"
                /dev_stage="30 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
Query Match      0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2575 TAAAAAATAAAAA 2588
Db      16 TAAAAAATAAAAA 3
|||||

RESULT 71
LOCUS    CF314013/c                16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION CF314013-02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Orzya sativa (japonica cultivar-group) cDNA clone
            HD--02-G01, mRNA sequence.
ACCESSION  CF314013
VERSION    CF314013.1      GI:33685774
KEYWORDS   EST.
SOURCE     Orzya sativa (japonica cultivar-group)
ORGANISM   Orzya sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6193
            Fax: 82 31 321 6355
            Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.
            Location/Qualifiers
FEATURES   source
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                /organism="Orzya sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD--02-G01"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"

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/lab_host="E.coli DH10B"
/clone_lib="OeHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 0.3%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAATAAAAAA 2588
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 Db 16 TAAAAAATAAAAAA 3

RESULT 72
 CF329320/c
 LOCUS
 DEFINITION NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA sequence.

ACCESSION
 VERSION CF329320.1 GI:33806877
 KEYWORDS EST.

SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.

REFERENCE
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..16
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clones="NACL--04-J17"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAATAAAAAA 2588
 |||||
 Db 16 TAAAAAATAAAAAA 3

RESULT 73
 AW245664/c
 LOCUS
 DEFINITION 2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3', mRNA sequence.

ACCESSION
 VERSION AW245664.1 GI:6588657
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 17)

REFERENCE
 1 (bases 1 to 17)
 NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2822994.5prime

Contact: Robert Strausberg, ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
 project
 Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
 PHRED high quality bases following vector sequence. Very Low
 Quality Sequence: Trace file contained 17 contiguous distinct peaks
 following vector sequence.

Plate: L1CM10 row: N column: 19.

FEATURES
 source
 1..17
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2822994"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACA 2816
 |||||
 Db 17 AAAAAAAAAAACA 4

RESULT 74
 BQ590128/c

LOCUS
 DEFINITION E012843-024-019-E19-T7 MP12-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-E19 3-PRIME, mRNA sequence.

ACCESSION
 VERSION BQ590128.1 GI:26119711

KEYWORDS EST.
 SOURCE Beta vulgaris

ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE
 1 (bases 1 to 17)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 19 row: E column: 19
Seq primer: T7: GTAATACGACTCACTATAGGCG.

FEATURES

source

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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189986"
/db_xref="taxon:161934"
/clone="024-019-E19"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAAAAAAAAA 2588

Db 17 TAAAAAAAAAAAAA 4

RESULT 75
BQ591181/c
LOCUS
DEFINITION
E012715-024-017-H16-T7 MPZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-H16 3-PRIME, mRNA sequence.

ACCESSION
BQ591181
VERSION
BQ591181.1 GI:26120764
KEYWORDS
EST.
SOURCE
Beta vulgaris

ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL
MEDLINE
PUBMED
COMMENT

22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: H column: 16
Seq primer: T7: GTAATACGACTCACTATAGGCG.

FEATURES

source

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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189932"
/db_xref="taxon:161934"
/clone="024-017-H16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAAAAAAAAA 2588

Db 16 TAAAAAAAAAAAAA 3

RESULT 76

BQ591588/c

LOCUS

DEFINITION
E012616-024-017-C15-SP6 MPZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-C15 5-PRIME, mRNA sequence.

ACCESSION
BQ591588
VERSION
BQ591588.1 GI:26121171
KEYWORDS
EST.
SOURCE
Beta vulgaris

ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: C column: 15

Seq primer: SP6: CATACGATTAGTGACACTATAG.
Location/Qualifiers
1. .17

FEATURES

source

```
1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
```


COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS-06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAAAAAA 2588

Db 17 TAAAAAAAAAAAAA 4

RESULT 80
CF311499/c
LOCUS
DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.

ACCESSION CF311499.1 GI:33683260
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-06-L20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression

line."

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAAAAAA 2588

Db 16 TAAAAAAAAAAAAA 3

RESULT 81
CF319075/c
LOCUS
DEFINITION CF319075 17 bp mRNA linear EST 15-AUG-2003
HD--09-H06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.

ACCESSION CF319075
VERSION CF319075.1 GI:33690836
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAAAAAA 2588

Db 16 TAAAAAAAAAAAAA 3

RESULT 82
CF336950/c
LOCUS
DEFINITION CF336950 17 bp mRNA linear EST 18-AUG-2003
JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-D04, mRNA sequence.

ACCESSION CF336950
VERSION CF336950.1 GI:33822280
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--07-D04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ATJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAATAAAAAA 2588
 |||||
Db 17 TAAAAAATAAAAAA 4

RESULT 83
AW247976/c
LOCUS 2820717.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820717 3',
DEFINITION mRNA sequence.
ACCESSION AW247976
VERSION AW247976.1 GI:6591064
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2820717.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
 Project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 0 contiguous

PHRED high quality bases following vector sequence. Very Low
 Quality Sequence: Trace file contained 17 contiguous distinct peaks
 following vector sequence. Polyadenylation: Based upon the presence
 of a XhoI site followed by a run of 14 or more T residues at the
 beginning of the sequence, this cDNA insert was polyadenylated.
 Plate: L1CMA row: 0 column: 22.

FEATURES
 Location/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2820717"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2568 CAGTGTTTAAAAA 2584
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Db 17 CATTGTTTAAAAA 1

RESULT 84
CF302447/c
LOCUS 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA
 sequence.
ACCESSION CF302447
VERSION CF302447.1 GI:33674208
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..17
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /clone="7LEAF--07-P11"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for

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RT-PCR..
Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 928 GAGAAAAAAACAAA 944
Db 17 GAAAAAAACAAA 1

RESULT 85
CF313013/c
LOCUS
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-P19, mRNA sequence.
ACCESSION
CF313013
VERSION
CF313013.1 GI:33684774
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 928 GAGAAAAAAACAAA 944
Db 17 GAAAAAAACAAA 1

RESULT 86
CF298591
LOCUS
DEFINITION
7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA
sequence.
ACCESSION
CF298591
VERSION
CF298591.1 GI:33670352
KEYWORDS
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--02-A20"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTTAA 3280
Db 1 TTTTTCCTTTTAA 17

RESULT 87
CF278272
LOCUS
DEFINITION
14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-C01,
mRNA sequence.
ACCESSION
CF278272
VERSION
CF278272.1 GI:33655658
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-C01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```



```

/clone="14ETL--04-C01"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

Query Match      0.3%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.28; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 3264 TTTTTCCTCTTTAA 3280
      |||||
Db 1 TTTTTCCTCTTTAA 17

```

```

RESULT 88
AW245585
LOCUS
DEFINITION
2822740.3prime NIH_MGC_7 15 bp mRNA linear EST 07-JAN-2000
mRNA sequence.
ACCESSION
AW245585
VERSION
AW245585.1 GI:6588578
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822740.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project

```

```

Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
http://www.genome.washington.edu Low Quality Sequence: 6 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 15 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM10 row: D column: 5
High quality sequence stop: 6.
Location/Qualifiers
1..15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822740"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

```

FEATURES
source

```

```

(Stratagene) and Superscript II RT (Life Technologies)."
Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 3598 TTTTTCCTCTTTAA 3612
      |||||
Db 1 TTTTTCCTCTTTAA 15

```

```

RESULT 89
AW250976/c
LOCUS
DEFINITION
2822229.3prime NIH_MGC_7 15 bp mRNA linear EST 07-JAN-2000
mRNA sequence.
ACCESSION
AW250976
VERSION
AW250976.1 GI:6594065
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822229.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project

```

```

Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
http://www.genome.washington.edu Low Quality Sequence: 11
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 15 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM8 row: N column: 22
High quality sequence stop: 11.
Location/Qualifiers
1..15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822229"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

```

FEATURES
source

```

```

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2798 ATGTGAAAAA 2812

```

```

Db      15 ATCTGAAAAAAAAA 1
|| ||||| ||||| |||||
|| ||||| ||||| |||||

RESULT 90
BQ588758/c
LOCUS      15 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION E012534-024-014-P24-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-014-P24 5-PRIME, mRNA sequence.

ACCESSION BQ588758
VERSION   BQ588758
KEYWORDS  EST.
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 15)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radelof,U.

TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaa@mpiz-koeln.mpg.de
          Insert Length: 15 Std Error: 0.00
          Plate: 14 row: P column: 24
          Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
source
location/Qualifiers
1..15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:187217"
/db_xref="taxon:161934"
/clone="024-014-P24"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPOR16; Site1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPP/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 975 CCCCCCCCCCGCCC 989
|| ||||| ||||| |||||
|| ||||| ||||| |||||

Db      15 CCCCCCCCCCGCCC 1

RESULT 91
CF329379/c
LOCUS      15 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-K23, mRNA
sequence.

```

```

ACCESSION CF329379
VERSION   CF329379.1
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 15)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 321 6193
          Fax: 82 31 321 6355
          Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
location/Qualifiers
1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-K23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAAAC 945
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|| ||||| ||||| |||||

Db      15 AAAAAAAAAACAAAC 1

RESULT 92
CF543203
LOCUS      15 bp      mRNA      linear      EST 22-SEP-2003
DEFINITION S014679-024-030-D05-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-030-D05 5-PRIME, mRNA sequence.

ACCESSION CF543203
VERSION   CF543203.1
KEYWORDS  EST.
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Caryophyllales; Amaranthaceae; Beta.
          1 (bases 1 to 15)
          Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radelof,U.

TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaa@mpiz-koeln.mpg.de
          Insert Length: 15 Std Error: 0.00

```


SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS 1 (bases 1 to 19)
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
 1..19
 /location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="30DGS-05-L12"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2743 TCTTTTTCCTTTTAA 2757
 |||||
Db 1 TTTTTCCTTTTAA 15

RESULT 96
AZ962226/c
LOCUS 19 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0564H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564H19 R, genomic survey sequence.
ACCESSION AZ962226
VERSION AZ962226.1 GI:12884624
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0564 row: H column: 19
 Seq primer: CACACGGAACAGCTATGACC
 Class: plasmid ends

FEATURES
source
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0564H19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2741 CATCTTTTTCCTTTT 2755
 |||||
Db 16 CATTTTTCCTTTT 2

RESULT 97
AZ962226/c
LOCUS 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0231A02 F, genomic survey sequence.
ACCESSION AZ962226
VERSION AZ962226.1 GI:13833453
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0231 row: A column: 02
 Seq primer: CGTTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC2M0231A02"
/sex="female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3278
|||||||
Db 18 TTTTTCCTTTT 4

RESULT 98

AZ426873 20 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION IM0208L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0208L05 R, genomic survey sequence.

AZ426873

VERSION AZ426873.1 GI:10550886

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,R., Stokes,R., Tinge,A., von
Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0208 row: L column: 05

Seq primer: CACACGAAACACCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0208L05"
/sex="male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACAT 2817

|||||||
Db 2 AAAAAAAAAAACAT 16

RESULT 99

AZ654747

LOCUS

DEFINITION IM0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529F08 F, genomic survey sequence.

AZ654747

VERSION AZ654747.1 GI:11791893

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Rilly,M., Rose,R., Stokes,R., Tinge,A., von

Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0529 row: F column: 08

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. .19

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529F08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI-. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1157 TTTTATATATATATATTTT 1174
    ||||| | | |||||
Db 1 TTTTATATATATATATTTT 18

RESULT 100
LOCUS      AA918967/c
DEFINITION o182905.g1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1536152 3'
            similar to TR:Q69566 Q69566 ;contains element PTR7 repetitive
            element ;, mRNA sequence.
ACCESSION  AA918967
VERSION     AA918967.1 GI:3058857
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
            Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
            and Radelof, U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
JOURNAL     22362189
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 13 Std Error: 0.00
            Plate: 5 row: C column: 14
            Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES             source
     1..13
     /organism="Homo sapiens"
     /mol_type="genomic DNA"
     /cultivar="KWS2320 (double haploid, monogerm breeding line)"
     /db_xref="GABI:183152"
     /db_xref="taxon:161934"
     /clone="024-005-C14"
     /tissue_type="inflorescence"
     /lab_host="EMDH108"
     /clone_lib="MPIZ-ADIS-024-inflorescence"
     /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1536152"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kids"
/notes="Organ: kidney; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGATTCCGGCGCGCAATATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 ACACGGCCACACA 649
    ||||| | | |||||
Db 13 ACACGGCCACACA 1

RESULT 101
LOCUS      BQ583549
DEFINITION BQ583549 13 bp mRNA linear EST 06-DEC-2002
            cDNA clone 024-005-C14 5-PRIME, mRNA sequence.
ACCESSION  BQ583549
VERSION     BQ583549.1 GI:26113126
KEYWORDS   EST.
SOURCE      Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
            Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
            and Radelof, U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
JOURNAL     22362189
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 13 Std Error: 0.00
            Plate: 5 row: C column: 14
            Seq primer: SP6; CATACGATTAGTGACACTATAG.

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     /db_xref="GABI:183152"
     /db_xref="taxon:161934"
     /clone="024-005-C14"
     /tissue_type="inflorescence"
     /lab_host="EMDH108"
     /clone_lib="MPIZ-ADIS-024-inflorescence"
     /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

```

SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 102

BQ589180/c

LOCUS

DEFINITION S014009-024-015-122-T7 MP1Z-ADIS-024-storage root Beta vulgaris EST 06-DEC-2002

VERSION BQ589180

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00

Plate: 15 row: I column: 22

Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

1..13

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:18786"

/db_xref="taxon:161934"

/clone="024-015-122"

/tissue_type="storage root"

/lab_host="EMDH108"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: PCWSP0RT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation;

SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 103

BQ590337

LOCUS

DEFINITION E012840-024-019-G12-SP6 MP1Z-ADIS-024-storage root Beta vulgaris

VERSION BQ590337

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00

Plate: 19 row: G column: 12

Seq primer: SP6; CATACGATTAGTGACACTATAG.

Location/Qualifiers

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/cultivar="KWS2320 (double haploid, monogerm breeding line)"

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/clone="024-019-G12"

/tissue_type="storage root"

/lab_host="EMDH108"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: PCWSP0RT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation;

SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 104

CF278426/c

LOCUS

DEFINITION 14ETL--04-F09.bl Rice etiolated leaf plasmid cDNA library (14ETL)

Oriza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F09,

13 bp mRNA linear EST 14-AUG-2003

14ETL--04-F09.bl Rice etiolated leaf plasmid cDNA library (14ETL)

Oriza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F09,

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mRNA sequence.
CF278426
VERSION CF278426.1 GI:33655812
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL-04-F09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
RESULT 105
CF280420/c
LOCUS CF280420.1 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-B11,
mRNA sequence.
ACCESSION CF280420
VERSION CF280420.1 GI:33657806
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL-07-B11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
RESULT 106
CF280707/c
LOCUS CF280707.1 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H19,
mRNA sequence.
ACCESSION CF280707
VERSION CF280707.1 GI:33658093
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
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/clone="14ETL-07-B11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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```

RESULT 107
CF280757/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-I21,
mRNA sequence.
CF280757
CF280757.1 GI:33658143
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/clone="14ETL--07-I21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
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Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 108
CF282369/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--01-D13, mRNA
sequence.
CF282369
CF282369.1 GI:33660003
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--01-D13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
            source
Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 109
CF290970/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
sequence.
CF290970
CF290970.1 GI:33660003
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-D13"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
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Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 109
CF290970/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
sequence.
CF290970
CF290970.1 GI:33660003
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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RT-PCR."

FEATURES
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Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 108
CF282369/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N16,
mRNA sequence.
CF282369
CF282369.1 GI:33659756
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-N16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
            source
Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 108
CF282369/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N16,
mRNA sequence.
CF282369
CF282369.1 GI:33659756
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-N16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
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Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 108
CF282369/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N16,
mRNA sequence.
CF282369
CF282369.1 GI:33659756
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 110
CF290971 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
sequence.
ACCESSION CF290971
VERSION CF290971.1 GI:33660004
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. 13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-E10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 111
CF291011 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E10, mRNA
sequence.
ACCESSION CF291011
VERSION CF291011.1 GI:33660044
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. 13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-D13"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 111
CF291011/c 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E10, mRNA
sequence.
ACCESSION CF291011
VERSION CF291011.1 GI:33660044
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. 13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-E10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 112
CF291060/c 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F11, mRNA
sequence.
ACCESSION CF291060
VERSION CF291060.1 GI:33660093
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1. 13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
| | | | | | | | | | | | | | | | | |
Db 13 AAAAAAAAAAAAAA 1

RESULT 113
CF291061 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F11, mRNA
sequence.

ACCESSION CF291061 GI:33660094
VERSION CF291061
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="root"
/dev_stage="14 days after germination"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 1 AAAAAAAAAAAAAA 13

RESULT 114
CF291167/c 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-H20, mRNA
sequence.

ACCESSION CF291167 GI:33660200
VERSION CF291167
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 13 AAAAAAAAAAAAAA 1

RESULT 115
CF291214/c 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-122.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-122, mRNA
sequence.

ACCESSION CF291214 GI:33660247
VERSION CF291214
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/clone="14ROOT--01-122"
/tissue_type="root"

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/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
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Db 13 AAAAAAAAAAAAAA 1

RESULT 116
CF291427/c
LOCUS      13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
          sativa (japonica cultivar-group) cDNA clone 14ROOT--01-N14, mRNA
          sequence.
ACCESSION  CF291427
VERSION     CF291427.1 GI:33660460
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 13)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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        /dev_stage="14 days after germination"
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Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
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Db 13 AAAAAAAAAAAAAA 1

RESULT 117
CF291469/c
LOCUS      13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-012.b1 Rice root plasmid cDNA library (14ROOT) Oryza
          sativa (japonica cultivar-group) cDNA clone 14ROOT--01-012, mRNA
          sequence.
ACCESSION  CF291469
VERSION     CF291469.1 GI:33660512
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
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          Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 13)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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        /dev_stage="14 days after germination"
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 119
CF291514/c
LOCUS
DEFINITION 14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
          sativa (japonica cultivar-group) cDNA clone 14ROOT--01-P13, mRNA
          sequence.
ACCESSION  CF291514
VERSION     CF291514.1 GI:33660547
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
           1 (bases 1 to 13)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 121
CF291596/c
LOCUS
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          sequence.
ACCESSION  CF291596
VERSION     CF291596.1 GI:33660629
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
           1 (bases 1 to 13)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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     /tissue_type="root"
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     /lab_host="E.coli DH10B"
     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
     /notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 120
CF291515
LOCUS
DEFINITION 14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
          sativa (japonica cultivar-group) cDNA clone 14ROOT--01-P13, mRNA
          sequence.
ACCESSION  CF291515
VERSION     CF291515.1 GI:33660548
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
           1 (bases 1 to 13)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 122
LOCUS CF291597
DEFINITION 14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
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          sequence.
ACCESSION CF291597
VERSION 1.13
KEYWORDS /organism="Oryza sativa (japonica cultivar-group)"
SOURCE Oryza sativa (japonica cultivar-group)
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          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 13)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Gyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
          Location/Qualifiers
            1. .13
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            /tissue_type="root"
            /dev_stage="14 days after germination"
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            /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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            with oligoribonucleotides and then used as templates for
            RT-PCR."

  Query Match
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    /lab_host="E.coli DH10B"
    /clone_lib="Rice root plasmid cDNA library (14ROOT)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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    RT-PCR."

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  Db 13 AAAAAAAAAAAAAA 13

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RESULT 123
LOCUS CF291726/c
DEFINITION 14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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          sequence.
ACCESSION CF291726
VERSION 1.13
KEYWORDS /organism="Oryza sativa (japonica cultivar-group)"
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
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          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 13)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Gyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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  Qy 2576 AAAAAAAAAAAAAA 2588
  Db 13 AAAAAAAAAAAAAA 1

RESULT 124
LOCUS CF291903
DEFINITION 14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
          sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I10, mRNA
          sequence.
ACCESSION CF291903
VERSION 1.13
KEYWORDS /organism="Oryza sativa (japonica cultivar-group)"
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
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          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 13)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

1. 13
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 125
CF298590/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A19, mRNA sequence.
CF298590.1 GI:33670351
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

1. 13
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/tissue_type="leaf"
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Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 126

CF298592/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A21, mRNA sequence.
CF298592.1 GI:33670353
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 127

CF298736/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-E22, mRNA sequence.
CF298736.1 GI:33670497
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

1. 13
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/db_xref="taxon:39947"
/clone="7LEAF--02-E22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 Db 13 AAAAAAAAAAAAAA 1

RESULT 128
 CF298764/c
 LOCUS
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 7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-F20, mRNA
 sequence.

ACCESSION CF298764.1 GI:33670525
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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 /tissue_type="leaf"
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 /lab_host="E.coli DH10B"
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

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 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 Db 13 AAAAAAAAAAAAAA 1

RESULT 129

CF298795/c
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 7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-G14, mRNA
 sequence.

ACCESSION CF298795
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 Db 13 AAAAAAAAAAAAAA 1

RESULT 130

CF298908/c
 LOCUS
 DEFINITION CF298908 13 bp mRNA linear EST 15-AUG-2003
 7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-K03, mRNA
 sequence.

ACCESSION CF298908
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.


```

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 63;
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Qy 2576 AAAAAAAAAAAAAA 2588
      |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 131
CF299133/c
LOCUS
DEFINITION      Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-A06, mRNA
sequence.
ACCESSION      CF299133
VERSION        CF299133.1 GI:33670894
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
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              Fax: 82 31 321 6355
              Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.

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/clone="7LEAF--03-A06"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
      |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 131
CF299133/c
LOCUS
DEFINITION      Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-A06, mRNA
sequence.
ACCESSION      CF299133
VERSION        CF299133.1 GI:33670894
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
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              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.

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/mol_type="mRNA"
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 133
CF299937/c
LOCUS
DEFINITION      Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C12, mRNA
sequence.
ACCESSION      CF299937
VERSION        CF299937.1 GI:33671698
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
      |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 132
CF299359/c
LOCUS
DEFINITION      Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F15, mRNA
sequence.
ACCESSION      CF299359
VERSION        CF299359.1 GI:33671120
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
      |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 133
CF299937/c
LOCUS
DEFINITION      Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C12, mRNA
sequence.
ACCESSION      CF299937
VERSION        CF299937.1 GI:33671698
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)

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LOCUS               CF301286               13 bp   mRNA   linear   EST 15-AUG-2003
DEFINITION          7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                     sativa (japonica cultivar-group) cDNA clone 7LEAF--06-B15, mRNA
                     sequence.
ACCESSION            CF301286
VERSION              CF301286.1   GI:33673047
KEYWORDS
SOURCE
ORGANISM             Oryza sativa (japonica cultivar-group)
                     Oryza sativa (japonica cultivar-group)
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

RESULT 140
CF302158/c
LOCUS               CF302158               13 bp   mRNA   linear   EST 15-AUG-2003
DEFINITION          7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                     sativa (japonica cultivar-group) cDNA clone 7LEAF--07-G20, mRNA
                     sequence.
ACCESSION            CF302158
VERSION              CF302158.1   GI:33673919
KEYWORDS
SOURCE
ORGANISM             Oryza sativa (japonica cultivar-group)
                     Oryza sativa (japonica cultivar-group)
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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LOCUS               CF302158               13 bp   mRNA   linear   EST 15-AUG-2003
DEFINITION          7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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                     sequence.
ACCESSION            CF302158
VERSION              CF302158.1   GI:33673919
KEYWORDS
SOURCE
ORGANISM             Oryza sativa (japonica cultivar-group)
                     Oryza sativa (japonica cultivar-group)
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355

```

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

RESULT 141
CF302830/c
LOCUS               CF302830               13 bp   mRNA   linear   EST 15-AUG-2003
DEFINITION          7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                     sativa (japonica cultivar-group) cDNA clone 7LEAF--08-L16, mRNA
                     sequence.
ACCESSION            CF302830
VERSION              CF302830.1   GI:33674591
KEYWORDS
SOURCE
ORGANISM             Oryza sativa (japonica cultivar-group)
                     Oryza sativa (japonica cultivar-group)
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     RT-PCR."

Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

RESULT 140
CF302158/c
LOCUS               CF302158               13 bp   mRNA   linear   EST 15-AUG-2003
DEFINITION          7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION            CF302158
VERSION              CF302158.1   GI:33673919
KEYWORDS
SOURCE
ORGANISM             Oryza sativa (japonica cultivar-group)
                     Oryza sativa (japonica cultivar-group)
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
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                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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                     /lab_host="E.coli DH10B"
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                     RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
      |||||
Db   13 AAAAAAAAAAAAAA 1

RESULT 140
CF302158/c
LOCUS               CF302158               13 bp   mRNA   linear   EST 15-AUG-2003
DEFINITION          7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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                     sequence.
ACCESSION            CF302158
VERSION              CF302158.1   GI:33673919
KEYWORDS
SOURCE
ORGANISM             Oryza sativa (japonica cultivar-group)
                     Oryza sativa (japonica cultivar-group)
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355

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element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAA 13

RESULT 145
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LOCUS
DEFINITION ABP--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABP--08-J13, mRNA sequence.
ACCESSION CF312721.1 GI:33684482
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE
JOURNAL
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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cDNA library (ABF)"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
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Db 13 AAAAAAAAAAAAAA 13

RESULT 146
CF313171/c
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library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-D10, mRNA sequence.
ACCESSION CF313171.1 GI:33684932
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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line."

Query Match      0.3%; Score 13; DB 1; Length 13;
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Db 13 AAAAAAAAAAAAAA 13

RESULT 147
CF314239/c
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DEFINITION HD--02-L01.b1 OeHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-L01, mRNA sequence.
ACCESSION CF314239.1 GI:33686000
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 13;
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1 | | | | | | | | | |
Db 13 AAAAAAAAAAAAAA 13

RESULT 147
CF314239/c
LOCUS
DEFINITION HD--02-L01.b1 OeHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-L01, mRNA sequence.
ACCESSION CF314239.1 GI:33686000
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
1 | | | | | | | | | |
Db 13 AAAAAAAAAAAAAA 13
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EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
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RESULT 147
CF314239/c
LOCUS
DEFINITION HD--02-L01.b1 OeHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-L01, mRNA sequence.
ACCESSION CF314239.1 GI:33686000
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE
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COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
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derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 13;
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 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 Db 13 AAAAAAAAAAAAAA 1

RESULT 148
 CF314874/c

LOCUS
 DEFINITION HD-03-J07.g1 OshDA1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD-03-J07, mRNA sequence.

ACCESSION CF314874
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

TITLE
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

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 line."

Query Match 0.3%; Score 13; DB 1; Length 13;
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 Db 13 AAAAAAAAAAAAAA 1

RESULT 149
 CF315395/c

LOCUS
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 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD-04-E20, mRNA sequence.

ACCESSION CF315395
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

TITLE
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University

Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES
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 line."

Query Match 0.3%; Score 13; DB 1; Length 13;
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 Db 13 AAAAAAAAAAAAAA 1

RESULT 150
 CF316439/c

LOCUS
 DEFINITION HD-05-L17.b1 OshDA1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD-05-L17, mRNA sequence.

ACCESSION CF316439
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 13 AAAAAAAAAAAAAA 1

RESULT 151
CF316440
LOCUS CF316440 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-L17.gi OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-L17, mRNA sequence.
ACCESSION CF316440
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 152
CF316637/c
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library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-A04, mRNA sequence.
ACCESSION CF316637
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
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line."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 153
CF318290/c

LOCUS CF318290 13 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--08-F19, mRNA sequence.
 ACCESSION CF318290
 VERSION CF318290.1 GI:33690051
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
 FEATURES
 source Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clones="HD--08-F19"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 13 AAAAAAAAAAAAAA 1
 RESULT 154
 LOCUS CF319066/c 13 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--09-H02.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--09-H02, mRNA sequence.
 ACCESSION CF319066
 VERSION CF319066.1 GI:33690827
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 13 AAAAAAAAAAAAAA 1

RESULT 154
 LOCUS CF319066/c 13 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--09-H02.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--09-H02, mRNA sequence.
 ACCESSION CF319066
 VERSION CF319066.1 GI:33690827
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
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 /clones="HD--09-H02"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
 Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 13 AAAAAAAAAAAAAA 1
 RESULT 155
 LOCUS CF319531/c 13 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--10-B03.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-B03, mRNA sequence.
 ACCESSION CF319531
 VERSION CF319531.1 GI:33691292
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
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 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line"

line."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 13 AAAAAAAAAAAAAA 1

RESULT 156
 CF319532
 LOCUS HD--10-B03.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-B03, mRNA sequence.

ACCESSION CF319532
 VERSION CF319532.1 GI:33691293
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--10-B03"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 1 AAAAAAAAAAAAAA 13

RESULT 157
 CF319919
 LOCUS HD--10-J17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-J17, mRNA sequence.

ACCESSION CF319919
 VERSION CF319919.1 GI:33691680
 KEYWORDS EST.

SOURCE

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS 1 (bases 1 to 13)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
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 /clone="HD--10-J17"
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 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 1 AAAAAAAAAAAAAA 13

RESULT 158
 CF320017/c
 LOCUS HD--10-L20.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-L20, mRNA sequence.

ACCESSION CF320017
 VERSION CF320017.1 GI:33691778
 KEYWORDS EST.

SOURCE

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS 1 (bases 1 to 13)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
 1..13
 /organism="Oryza sativa (japonica cultivar-group)"

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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-10-L20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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RESULT 159
CF320018      13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HD--10-L20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-L20, mRNA sequence.

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ACCESSION
CF320018      1 GI:33691779
VERSION
CF320018
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)

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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)

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REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhna@mgbio.com, bhna@mgbio.myongji.ac.kr.

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FEATURES
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/clone="HD-10-L20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2576 AAAAAAAAAAAAAA 2588

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Db 1 AAAAAAAAAAAAAA 13

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RESULT 160
CF320143/c
LOCUS
DEFINITION

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HD--10-O13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-O13, mRNA sequence.

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ACCESSION
CF320143      1 GI:33691904
VERSION
CF320143
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)

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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)

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REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhna@mgbio.com, bhna@mgbio.myongji.ac.kr.

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FEATURES
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derived from rice Histone Deacetylase overexpression
line."

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Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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RESULT 161
CF320938/c
LOCUS
DEFINITION

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HD--12-A06.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--12-A06, mRNA sequence.

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ACCESSION
CF320938      1 GI:33692699
VERSION
CF320938
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)

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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)

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REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 13 AAAAAAAAAAAAAA 1

RESULT 162
 CF326844/C
 LOCUS
 DEFINITION
 NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--01-B12, mRNA
 sequence.
 CF326844.1 GI:33801943
 CF326844
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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 /mol_type="mRNA"
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 /clone="NACL--01-B12"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 13 AAAAAAAAAAAAAA 1

RESULT 163
 CF327070/C
 LOCUS
 DEFINITION
 NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--01-G09, mRNA
 sequence.
 CF327070.1 GI:33802396
 CF327070
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Qy 2576 AAAAAAAAAAAAAA 2588
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 Db 13 AAAAAAAAAAAAAA 1

RESULT 164
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 DEFINITION
 NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA
 sequence.

CF327339.1 GI:33802936
 CF327339
 EST.

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SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 13 AAAAAAAAAAAAAA 1

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CF327340
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DEFINITION Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 13 AAAAAAAAAAAAAA 1

RESULT 165
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DEFINITION Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 166
CF327576/c
LOCUS      CF327576/c
DEFINITION Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 167
CF327888/c
LOCUS      CF327888/c
DEFINITION Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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DEFINITION   NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza
             sativa (japonica cultivar-group) cDNA clone NACL--03-A13, mRNA
             sequence.
ACCESSION   CF328228
VERSION     CF328228.1   GI:33804702
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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REFERENCE   1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

RESULT 171
CF328807/c
LOCUS       CF328807               13 bp   mRNA       linear       EST 18-AUG-2003
DEFINITION   NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
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             sequence.
ACCESSION   CF328807
VERSION     CF328807.1   GI:33806393
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

RESULT 171
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LOCUS       CF328807               13 bp   mRNA       linear       EST 18-AUG-2003
DEFINITION   NACL--03-O07.b1 Rice callus plasmid cDNA library (NACL) Oryza
             sativa (japonica cultivar-group) cDNA clone NACL--03-O07, mRNA
             sequence.
ACCESSION   CF328807
VERSION     CF328807.1   GI:33805856
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

RESULT 172
CF329075/c
LOCUS       CF329075               13 bp   mRNA       linear       EST 18-AUG-2003
DEFINITION   NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
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             sequence.
ACCESSION   CF329075
VERSION     CF329075.1   GI:33806393
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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Db   13 AAAAAAAAAAAAAA 1

RESULT 172
CF329075/c
LOCUS       CF329075               13 bp   mRNA       linear       EST 18-AUG-2003
DEFINITION   NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF329075
VERSION     CF329075.1   GI:33806393
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

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Query Match	0.3%;	Score 13;	DB 1;	Length 13;
Best Local Similarity	100.0%;	Pred. No. 63;		

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Query Match 0.3%; Score 13; DB 1; Length 13;
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QY 2576 AAAAAAAAAAAAAA 2588
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Db 1 AAAAAAAAAAAAAA 13

RESULT 179

CF329869/c 13 bp mRNA linear EST 18-AUG-2003

LOCUS NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-F18, mRNA
 sequence.

ACCESSION CF329869
 VERSION CF329869.1 GI:33807959

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Best Local Similarity 100.0%; Pred. No. 63;
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QY 2576 AAAAAAAAAAAAAA 2588
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Db 13 AAAAAAAAAAAAAA 1

RESULT 180

CF329946/c 13 bp mRNA linear EST 18-AUG-2003

LOCUS NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-H12, mRNA
 sequence.

ACCESSION CF329946
 VERSION CF329946.1 GI:33808114

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
 |||

Db 13 AAAAAAAAAAAAAA 1

RESULT 181

CF329988/c

LOCUS NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-I10, mRNA

sequence.

ACCESSION CF329988.1 GI:33808198

VERSION CF329988

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

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 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..13
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
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 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 182
CF330023/c
LOCUS
DEFINITION
13 bp mRNA linear EST 18-AUG-2003
NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-J05, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

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/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 183
CF330725
LOCUS
DEFINITION
13 bp mRNA linear EST 18-AUG-2003
NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-J01, mRNA
sequence.

ACCESSION
VERSION

CF330725.1 GI:33809672

KEYWORDS

SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

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/db_xref="taxon:39947"
/clone="NACL--06-J01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 184

CF331041/c

LOCUS

DEFINITION

13 bp mRNA linear EST 18-AUG-2003

NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone NACL--07-A04, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
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FEATURES
source

1..13
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/mol_type="mRNA"
/cultivar="Nackdong"

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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 185
CF331266/c 13 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--07-F06, mRNA
sequence.
CF331266.1 GI:33810744
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 187
CF331903/c 13 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--08-D07, mRNA
sequence.
CF331903.1 GI:33812027
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 186
CF331273/q 13 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--07-F09.q1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
sequence.
CF331273.1 GI:33810757
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

```


of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .13
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
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cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 191

CF333486/c

LOCUS

DEFINITION JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-G11, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

JOURNAL

COMMENT

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .13
Location/Qualifiers
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/mol_type="mRNA"
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/clone="JMT--02-G11"
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cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355

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FEATURES

Location/Qualifiers

1..13

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="JMT--03-B12"

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/lab_host="E.coli DH10B"

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cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2576 AAAAAAAAAAAAAA 2588

|||||

Db 1 AAAAAAAAAAAAAA 13

RESULT 194

CF334347/c

LOCUS

DEFINITION

CF334347.1 GI:33817022

EST.

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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of Bioscience and Bioinformatics, Myongji University

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..13

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2576 AAAAAAAAAAAAAA 2588

|||||

Db 1 AAAAAAAAAAAAAA 13

RESULT 196

CF337022/c

LOCUS

DEFINITION

CF337022.1 GI:33822426

EST.

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

/clone="JMT--03-J19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2576 AAAAAAAAAAAAAA 2588

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 195

CF337022/c

LOCUS

DEFINITION

CF337022.1 GI:33822426

EST.

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..13

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--07-E22"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2576 AAAAAAAAAAAAAA 2588

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 196

CF337022/c

LOCUS

DEFINITION

CF337022.1 GI:33822426

EST.

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..13

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

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CN546046/c
LOCUS      CN546046                13 bp    mRNA    linear    EST 30-APR-2004
DEFINITION clone B3CS00RL007H03 3', mRNA sequence.
ACCESSION  CN546046
VERSION    CN546046.1  GI:46910671
SOURCE     EST.
ORGANISM   Vitis vinifera
            Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Ronieu,C. and Terrier,N.
TITLE     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL   Unpublished (2002)
COMMENT   Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: 17.

FEATURES             source
     1..13
     Location/Qualifiers
         1..13
         /organism="Vitis vinifera"
         /mol_type="mRNA"
         /cultivar="Cabernet Sauvignon"
         /db_xref="taxon:29760"
         /clone="B3CS00RL007H03"
         /dev_stage="ripening stage"
         /clone_lib="Ripe Grape Skin Triplex2 Library"
         /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
            SfiI; Site_2: SfiI; Oriented library"

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
Db   13 AAAAAAAAAAAAAA 1

RESULT 197
LOCUS      CN749468                13 bp    mRNA    linear    EST 19-MAY-2004
DEFINITION ApAL3SD-XII-B12 ApAL3SD Acyrthosiphon pisum cDNA clone
            ApAL3SDXIIIB12 5', mRNA sequence.
ACCESSION  CN749468
VERSION    CN749468.1  GI:47514465
KEYWORDS   EST.
SOURCE     Acyrthosiphon pisum (pea aphid)
            Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
            An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
TITLE     Unpublished (2004)
JOURNAL   Contact: D. Tagu
COMMENT   INRA Rennes
            UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65

CN749468
LOCUS      CN749468                13 bp    mRNA    linear    EST 19-MAY-2004
DEFINITION ApAL3SD-XII-B12 ApAL3SD Acyrthosiphon pisum cDNA clone
            ApAL3SDXIIIB12 5', mRNA sequence.
ACCESSION  CN749468
VERSION    CN749468.1  GI:47514465
KEYWORDS   EST.
SOURCE     Acyrthosiphon pisum (pea aphid)
            Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
            An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
TITLE     Unpublished (2004)
JOURNAL   Contact: D. Tagu
COMMENT   INRA Rennes
            UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65

```

```

Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.
PCR Primers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: XII row: B column: 12.

FEATURES             source
     1..13
     Location/Qualifiers
         1..13
         /organism="Acyrthosiphon pisum"
         /mol_type="mRNA"
         /cultivar="yr2"
         /db_xref="taxon:7029"
         /clone="ApAL3SDXIIIB12"
         /tissue_type="antennae"
         /dev_stage="third instar nymph (L3)"
         /lab_host="TOP10"
         /clone_lib="ApAL3SD"
         /note="vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI;
            Sample name: ApAL3SD ; Plant growth place: INRA-Rennes,
            UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
            conditions: peat ; Sowing date: 25/03/2003 ; Harvesting
            date: 10/04/2003 ; Stress date: no stress ; Description:
            aphids inoculated on one-week old Vicia faba germinations
            under non sterile conditions. ; experimental condition:
            short photoperiod (12-hr light/12-hr dark at 18 c)"

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2802 GAAAAAAAAAAAAA 2814
Db   1 GAAAAAAAAAAAAA 13

RESULT 198
LOCUS      CN752228                13 bp    mRNA    linear    EST 19-MAY-2004
DEFINITION ApHL3SD-XXVIII-A5 ApHL3SD Acyrthosiphon pisum cDNA clone
            ApHL3SDXXVIIIAS 5', mRNA sequence.
ACCESSION  CN752228
VERSION    CN752228.1  GI:47517225
KEYWORDS   EST.
SOURCE     Acyrthosiphon pisum (pea aphid)
            Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
            An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
TITLE     Unpublished (2004)
JOURNAL   Contact: D. Tagu
COMMENT   INRA Rennes
            UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR Primers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: XXVIII row: A column: 5.

FEATURES             source
     1..13
     Location/Qualifiers
         1..13
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         /mol_type="mRNA"
         /cultivar="yr2"
         /db_xref="taxon:7029"
         /clone="ApHL3SDXXVIIIAS"
         /tissue_type="head"
         /dev_stage="third instar nymph (L3)"

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/lab_host="TOP10"
/clone_lib="AphL3SD"
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;
Sample name: AphL3SD ; Plant growth place: INRA-Rennes,
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 20/03/2003 ; Harvesting
date: 10/04/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
short photoperiod (12-hr light/12-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 199
CN752875 13 bp mRNA linear EST 19-MAY-2004
LOCUS AphL3LD-VII-H10 AphL3LD Acyrthosiphon pisum cDNA clone
DEFINITION AphL3LDVIIH10 5', mRNA sequence.

ACCESSION CN752875
VERSION CN752875.1 GI:47517872
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 13)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum

JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes

UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.

PCR Primers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: VII row: H column: 10.

FEATURES
source
1..13
Location/Qualifiers
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="AphL3LDVIIH10"
/tissue_type="head"
/dev_stages="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="AphL3LD"
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;
Sample name: AphL3LD ; Plant growth place: INRA-Rennes,
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 18/01/2003 ; Harvesting
date: 03/02/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 200
CN753196

LOCUS 13 bp mRNA linear EST 19-MAY-2004
DEFINITION AphL3LD-XVI-A12 AphL3LD Acyrthosiphon pisum cDNA clone
AphL3LDXVIA12 5', mRNA sequence.

ACCESSION CN753196
VERSION CN753196.1 GI:47518193
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 13)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum

JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes

UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.

PCR Primers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: XVI row: A column: 12.

FEATURES
source
1..13
Location/Qualifiers

/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="AphL3LDXVIA12"
/tissue_type="head"
/dev_stages="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="AphL3LD"
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;
Sample name: AphL3LD ; Plant growth place: INRA-Rennes,
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 18/01/2003 ; Harvesting
date: 03/02/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 201
BQ586422/c

LOCUS 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S013307-024-013-002-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-013-002 3-PRIME, mRNA sequence.

ACCESSION BQ586422
VERSION BQ586422.1 GI:26116004
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
22362189
12472698

COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 13 row: O column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
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1. .14
Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:186441"
/db_xref="taxon:161934"
/clone="024-013-002"
/tissue_type="leaf"
/lab_host="EMDH108"
/clone_lib="MPiZ-ADIS-024-leaf"
/note="Vector: PCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and orientation:
SP6-Sall-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
|||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 202
BQ587890/c
LOCUS
DEFINITION
S013302-024-009-B02-T7 MPiZ-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-B02 3-PRIME, mRNA sequence.

ACCESSION
BQ587890
VERSION
BQ587890.1
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
22362189
12472698

COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 13 row: O column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.

22362189
12472698
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 9 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
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1. .14
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
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/db_xref="taxon:161934"
/clone="024-009-B02"
/tissue_type="leaf"
/lab_host="EMDH108"
/clone_lib="MPiZ-ADIS-024-leaf"
/note="Vector: PCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and orientation:
SP6-Sall-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
|||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 203
BQ589191/c
LOCUS
DEFINITION
S014009-024-015-I20-T7 MPiZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-015-I20 3-PRIME, mRNA sequence.

ACCESSION
BQ589191
VERSION
BQ589191.1
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
22362189
12472698

COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 15 row: I column: 20

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FEATURES
  source
Seq primer: T7; GTAATACGACTCACTATAGGC.
  Location/Qualifiers
    1..14
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      /mol_type="mRNA"
      /cultivar="KWS2320 (double haploid, monogerm breeding line)"
      /db_xref="GABI:187878"
      /db_xref="taxon:161934"
      /clone="024-015-120"
      /tissue_type="storage root"
      /lab_host="EMDH108"
      /clone_lib="MP1Z-ADIS-024-storage root"
      /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
      |||||
Db   14 AAAAAAAAAAAAAA 2

RESULT 205
BQ590261/c
LOCUS      BQ590261
DEFINITION E012844-024-019-E16-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ590261
VERSION   BQ590261.1 GI:26119825
KEYWORDS  EST.
SOURCE    Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
  1 (bases 1 to 14)
  Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
  22362189
  12472698
  Contact: Weisshaar B
  ADIS DNA core facility at MPIZ
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
  Insert Length: 14 Std Error: 0.00
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      /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   14 AAAAAAAAAAAAAA 2

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ACCESSION BQ590242
VERSION   BQ590242.1 GI:26119825
KEYWORDS  EST.
SOURCE    Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
  1 (bases 1 to 14)
  Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
  22362189
  12472698
  Contact: Weisshaar B
  ADIS DNA core facility at MPIZ
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
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project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 206
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ACCESSION
BQ591168
VERSION
BQ591168.1 GI:26120751
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM

REFERENCE
AUTHORS
BQ591168 14 bp mRNA linear EST 06-DEC-2002
E012715-024-017-H18-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-H18 3-PRIME, mRNA sequence.
BQ591168
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
22362189
12472698

COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

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Seq primer: T7: GTAATACGACTCACTATAGGCG.

FEATURES

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/db_xref="taxon:161934"

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/note="Vector: PCVSPORT6; site 1: SalI; Site 2: NotI;

CDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match

Best Local Similarity 100.0%; Pred. No. 1e+02; Length 14;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

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Db 14 AAAAAAAAAAAAAA 2

RESULT 207

BQ591176/c

LOCUS

DEFINITION

E012715-024-017-N20-T7 MP1Z-ADIS-024-storage root Beta vulgaris

CDNA clone 024-017-N20 3-PRIME, mRNA sequence.

ACCESSION

BQ591176

VERSION

BQ591176.1 GI:26120759

KEYWORDS

EST.

SOURCE

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

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Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 17 row: N column: 20

Seq primer: T7: GTAATACGACTCACTATAGGCG.

Location/Qualifiers

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line)"

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/note="Vector: PCVSPORT6; Site 1: SalI; Site 2: NotI;

CDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match

Best Local Similarity 100.0%; Pred. No. 1e+02; Length 14;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||

Db 14 AAAAAAAAAAAAAA 2

KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE Plant J. 32 (5), 845-857 (2002)
PUBMED 22362189
COMMENT 12472698

Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
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/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
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/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
Best Local Similarity 100.0%; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 14 AAAAAAAAAAAAAA 2

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BQ591380/c
LOCUS BQ591380
DEFINITION E012714-024-017-B15-T7 MPiZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION BQ591380
VERSION BQ591380.1 GI:26120963
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE Plant J. 32 (5), 845-857 (2002)
PUBMED 22362189
COMMENT 12472698

Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
Best Local Similarity 100.0%; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 14 AAAAAAAAAAAAAA 2

RESULT 210
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LOCUS BQ591482
DEFINITION E012713-024-017-M04-T7 MPiZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-M04 3-PRIME, mRNA sequence.
ACCESSION BQ591482
VERSION BQ591482.1 GI:26121065
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE Plant J. 32 (5), 845-857 (2002)
PUBMED 22362189
COMMENT 12472698

Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

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Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: M column: 04
Seq primer: T7; GTATACCACTACTATAGGCG.

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            /clone="024-016-C15"
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            Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 211
BQ591949/c
LOCUS
DEFINITION E012580-024-016-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
ACCESSION BQ591949
VERSION BQ591949.1 GI:26121532
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
    1 (bases 1 to 14)
    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
    Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
    and Radelof,U.
REFERENCE
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
    Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED 22362189
COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MPIZ
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weishaa@mpiz-koeln.mpg.de
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    Seq primer: SP6; CATACGATTAGTGACACTATAG.
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            /mol_type="mRNA"
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            line)"

Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: M column: 04
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FEATURES
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            Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAAAAA 2589
Db 13 AAAAAAAAAAAAAA 1

RESULT 212
BQ593052/c
LOCUS
DEFINITION E012375-024-028-C03-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
ACCESSION BQ593052
VERSION BQ593052.1 GI:26122635
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
    1 (bases 1 to 14)
    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
    Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
    and Radelof,U.
REFERENCE
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
    Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED 22362189
COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MPIZ
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weishaa@mpiz-koeln.mpg.de
    Insert Length: 14 Std Error: 0.00
    Plate: 28 row: C column: 03
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            /tissue_type="developing root"
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            Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

```

```

orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 213
CF277935/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-K11,
mRNA sequence.

ACCESSION
CF277935
VERSION
CF277935.1 GI:33655321
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 215
CF278452/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F22,
mRNA sequence.

ACCESSION
CF278452
VERSION
CF278452.1 GI:33655838
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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FEATURES
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 214
CF278001/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-L21,
mRNA sequence.

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ACCESSION
CF278001
VERSION
CF278001.1 GI:33655387
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 215
CF278452/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F22,
mRNA sequence.

ACCESSION
CF278452
VERSION
CF278452.1 GI:33655838
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

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CF278001/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-L21,
mRNA sequence.

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 216
CF279473/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-M14,
mRNA sequence.
ACCESSION
CF279473.1 GI:33656859
VERSION
CF279473.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 216
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-M14,
mRNA sequence.
ACCESSION
CF279473.1 GI:33656859
VERSION
CF279473.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
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Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 218
CF281958/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-D24,
mRNA sequence.
ACCESSION
CF281958.1 GI:33659345
VERSION
CF281958.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

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RESULT 217
CF279992/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--06-I01,
mRNA sequence.
ACCESSION
CF279992.1 GI:33657378
VERSION
CF279992.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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CONTACT: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 218
CF281958/c
LOCUS
DEFINITION
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mRNA sequence.
ACCESSION
CF281958.1 GI:33659345
VERSION
CF281958.1
KEYWORDS
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ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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CONTACT: Nahm B.H.
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Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 219

CF282350/c
LOCUS
DEFINITION
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Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N05,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
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Contact: Nahm B.H.

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FEATURES

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QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 220

CF294449/c
LOCUS
DEFINITION
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sativa (japonica cultivar-group) cDNA clone 30DGS--03-P15, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Contact: Nahm B.H.

TITLE
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COMMENT
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

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Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 221

CF295570/c
LOCUS
DEFINITION
30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--05-J06, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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 Db 14 AAAAAAAAAAAAAA 2

RESULT 222
 CF296120/c
 LOCUS
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ACCESSION CF296120
 VERSION CF296120.1 GI:33665153
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 ORGANISM Oryza sativa (japonica cultivar-group)
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 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES

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 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 Db 14 AAAAAAAAAAAAAA 2

RESULT 223

CF297969/c
 LOCUS
 DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-C16, mRNA
 sequence.

ACCESSION CF297969
 VERSION CF297969.1 GI:33669730
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES

source
 1. 14
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /db_xref="taxon:39947"
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 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 Qy 2576 AAAAAAAAAAAAAA 2588
 Db 14 AAAAAAAAAAAAAA 2

RESULT 224

CF298109/c
 LOCUS
 DEFINITION 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-F19, mRNA
 sequence.

ACCESSION CF298109
 VERSION CF298109.1 GI:33669870
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel.: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. 14

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-F19"

/tissue_type="leaf"

/dev_stage="7 days after germination"

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 0.3%; Score 13; DB 1; Length 14;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 225

CF299368/c

LOCUS

DEFINITION 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F21, mRNA sequence.

ACCESSION CF299368

VERSION CF299368.1 GI:33671129

KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel.: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. 14

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 226

CF300542/c

LOCUS

DEFINITION 7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-B01, mRNA sequence.

ACCESSION CF300542

VERSION CF300542.1 GI:33672303

KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. 14

/organism="Oryza sativa (japonica cultivar-group)"

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 227

CF301020/c

LOCUS

DEFINITION 7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-L10, mRNA sequence.

ACCESSION CF301020

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CF301020.1 GI:33672781
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 229
CF301380/c
LOCUS
DEFINITION
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sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
ACCESSION
CF301380
VERSION
CF301380.1 GI:33673141
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 228
CF301083/c
LOCUS
DEFINITION
7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M19, mRNA
sequence.
ACCESSION
CF301083
VERSION
CF301083.1 GI:33672844
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
ACCESSION
CF302675
VERSION
CF302675.1 GI:33673141
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .14
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
ACCESSION
CF302675
VERSION
CF302675.1 GI:33673141
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
ACCESSION
CF302675
VERSION
CF302675.1 GI:33673141
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
CONTACT: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
ACCESSION
CF302675
VERSION
CF302675.1 GI:33673141
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sper
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DEFINITION 7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-G18, mRNA sequence.
 ACCESSION CF302675
 VERSION CF302675.1 GI:33674436
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
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 Db 14 AAAAAAAAAAAAAA 2

RESULT 231
 CF302846/c
 LOCUS 14 bp mRNA linear EST 15-AUG-2003
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 ACCESSION CF302846
 VERSION CF302846.1 GI:33674607
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 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

Location/Qualifiers
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 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--08-M05"
 /tissue_type="leaf"
 /dev_stages="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
 |||||||||
 Db 14 AAAAAAAAAAAAAA 2

RESULT 232
 CF308006/c
 LOCUS 14 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-K10, mRNA sequence.
 ACCESSION CF308006
 VERSION CF308006.1 GI:33679767
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

Location/Qualifiers
 1..14
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--01-K10"
 /tissue_type="leaf"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588


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/clone.lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 236
CF310714/c
LOCUS
DEFINITION ABF--05-111.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-111, mRNA sequence.
ACCESSION CF310714
VERSION CF310714.1 GI:33682475
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-111"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 237
CF311201/c
LOCUS
DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-D22, mRNA sequence.
ACCESSION CF311813
VERSION CF311813.1 GI:33683574
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

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DEFINITION ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-F09, mRNA sequence.
ACCESSION CF311201
VERSION CF311201.1 GI:33682962
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-F09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 238
CF311813/c
LOCUS
DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-D22, mRNA sequence.
ACCESSION CF311813
VERSION CF311813.1 GI:33683574
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea

```

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES

1. 14
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF-07-D22"
 /tissue_type="leaf"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 14 AAAAAAAAAAAAAA 2

RESULT 239

CF318323/c
 LOCUS
 DEFINITION HD--08-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--08-G13, mRNA sequence.

ACCESSION

VERSION CF318323.1 GI:33690084
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

1. 14
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD-08-G13"
 /tissue_type="callus"
 /dev_stages="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 14 AAAAAAAAAAAAAA 2

RESULT 240

CF318450/c
 LOCUS
 DEFINITION HD--08-J08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--08-J08, mRNA sequence.

ACCESSION

VERSION CF318450

KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

1. 14
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD-08-J08"
 /tissue_type="callus"
 /dev_stages="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
 |||||
 Db 14 AAAAAAAAAAAAAA 2

RESULT 241

CF319826/c
 LOCUS
 DEFINITION HD--10-H16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-H16, mRNA sequence.

ACCESSION

VERSION CF319826

KEYWORDS EST.

SOURCE

Oryza sativa (japonica cultivar-group)


```

ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 14)
              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE         Contact: Nahm B.H.
JOURNAL       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT       of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
              source
                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD-10-G24"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli DH10B"
                /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."
              Query Match      0.3%; Score 13; DB 1; Length 14;
              Best Local Similarity 100.0%; Pred. No. 1e+02;
              Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

RESULT 242
CF321246/C
LOCUS
DEFINITION   HD--12-G24.g1 OshDAC1-overexpressing transgenic rice plasmid
              library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
              HD--12-G24, mRNA sequence.
ACCESSION   CF321246
VERSION     CF321246.1 GI:33693007
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
              source
                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD-10-H16"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli DH10B"
                /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."
              Query Match      0.3%; Score 13; DB 1; Length 14;
              Best Local Similarity 100.0%; Pred. No. 1e+02;
              Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

RESULT 242
CF321246/C
LOCUS
DEFINITION   HD--12-G24.g1 OshDAC1-overexpressing transgenic rice plasmid
              library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
              HD--12-G24, mRNA sequence.
ACCESSION   CF321246
VERSION     CF321246.1 GI:33693007
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
              source
                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD-10-H01"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-12-G24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

RESULT 243
CF327097/C
LOCUS
DEFINITION   NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza
              sativa (japonica cultivar-group) cDNA clone NACL--01-H01, mRNA
              sequence.
ACCESSION   CF327097
VERSION     CF327097.1 GI:33802449
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
              source
                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="NACL--01-H01"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

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Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

RESULT 243
CF327097/C
LOCUS
DEFINITION   NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza
              sativa (japonica cultivar-group) cDNA clone NACL--01-H01, mRNA
              sequence.
ACCESSION   CF327097
VERSION     CF327097.1 GI:33802449
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
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                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="NACL--01-H01"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

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RESULT 244
CF327119/c
LOCUS      14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-H14, mRNA
            sequence.
ACCESSION  CF327119.1      GI:33802493
VERSION     CF327119.1
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
            1..14
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
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            /clone="NACL--01-H14"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            RT-PCR.
            Qy 2576 AAAAAAAAAAAAAA 2588
            Db 14 AAAAAAAAAAAAAA 2

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 245
CF327203/c
LOCUS      14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-J16, mRNA
            sequence.
ACCESSION  CF327203.1      GI:33802665
VERSION     CF327203.1
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL--01-H14"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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            RT-PCR."
            RT-PCR.
            Qy 2576 AAAAAAAAAAAAAA 2588
            Db 14 AAAAAAAAAAAAAA 2

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 246
CF327445/c
LOCUS      14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-O24, mRNA
            sequence.
ACCESSION  CF327445.1      GI:33803149
VERSION     CF327445.1
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL--01-O24"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            RT-PCR.
            Qy 2576 AAAAAAAAAAAAAA 2588
            Db 13 AAAAAAAAAAAAAA 1

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
            1..14
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
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            /db_xref="taxon:39947"
            /clone="NACL--01-J16"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            RT-PCR.
            Qy 2576 AAAAAAAAAAAAAA 2588
            Db 13 AAAAAAAAAAAAAA 1

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 246
CF327445/c
LOCUS      14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-O24, mRNA
            sequence.
ACCESSION  CF327445.1      GI:33803149
VERSION     CF327445.1
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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            /clone="NACL--01-O24"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            RT-PCR.
            Qy 2576 AAAAAAAAAAAAAA 2588
            Db 13 AAAAAAAAAAAAAA 1

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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Db      14 AAAAAAAAAAAAAA 2
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RESULT 247
CF328490/c
LOCUS   14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
          sativa (japonica cultivar-group) cDNA clone NACL--03-G21, mRNA
          sequence.
ACCESSION CF328490.1 GI:33805226
VERSION   CF328490
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
CONTACT:  Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. 14
/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
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          location
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Qy      2576 AAAAAAAAAAAAAA 2588
          |||||||
Db      14 AAAAAAAAAAAAAA 2

RESULT 249
CF328669/c
LOCUS   14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
          sativa (japonica cultivar-group) cDNA clone NACL--03-K23, mRNA
          sequence.
ACCESSION CF328669.1 GI:33805587
VERSION   CF328669
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
CONTACT:  Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. 14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-G21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
          |||||||
Db      14 AAAAAAAAAAAAAA 2

RESULT 248
CF328540/c
LOCUS   14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
          sativa (japonica cultivar-group) cDNA clone NACL--03-H24, mRNA
          sequence.
ACCESSION CF328540.1 GI:33805324
VERSION   CF328540
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
CONTACT:  Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. 14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
          |||||||
Db      14 AAAAAAAAAAAAAA 2

RESULT 248
CF328540/c
LOCUS   14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
          sativa (japonica cultivar-group) cDNA clone NACL--03-H24, mRNA
          sequence.
ACCESSION CF328540.1 GI:33805324
VERSION   CF328540
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
CONTACT:  Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. 14
/organism="Oryza sativa (japonica cultivar-group)"
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/clone="NACL--03-K23"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 250
CF328994/c
LOCUS
DEFINITION
NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-C11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

TITLE
JOURNAL
COMMENT

FEATURES
source
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 252
CF329990
LOCUS
DEFINITION
NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-I11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-I11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

TITLE
JOURNAL
COMMENT

FEATURES
source
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 251
CF329217/c
LOCUS
DEFINITION
NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-H10, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 14)

```

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AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-H10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

TITLE
JOURNAL
COMMENT

FEATURES
source
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 252
CF329990
LOCUS
DEFINITION
NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-I11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/clone="NACL--05-I11"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

TITLE
JOURNAL
COMMENT

FEATURES
source
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 251
CF329217/c
LOCUS
DEFINITION
NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-H10, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 14)

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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 253
CF330198/c
LOCUS
DEFINITION NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-N04, mRNA sequence.

ACCESSION CF330198
VERSION CF330198.1 GI:33808624
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .14
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Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2803 AAAAAAAAAAAC 2815
|||||
Db 14 AAAAAAAAAAAC 2

RESULT 254
CF330784/c
LOCUS
DEFINITION NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-K10, mRNA sequence.

ACCESSION CF330784
VERSION CF330784.1 GI:33809790
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1. .14

/organism="Oryza sativa (japonica cultivar-group)"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 255
CF331272/c
LOCUS
DEFINITION NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA sequence.

ACCESSION CF331272
VERSION CF331272.1 GI:33810755
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL Unpublished (2003)
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Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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 Db 14 AAAAAAAAAAAAAA 2

RESULT 256

CF331861/c

LOCUS

DEFINITION NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-C10, mRNA sequence.

ACCESSION

CF331861

VERSION

CF331861.1 GI:33811945

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 14

/organism="Oryza sativa (japonica cultivar-group)"

/mol type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="NACL--08-C10"

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/lab host="E.coli DH10B"

/clone lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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 Db 14 AAAAAAAAAAAAAA 2

RESULT 257

CF333214/c

LOCUS

DEFINITION JMT--02-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-A10, mRNA sequence.

ACCESSION

CF333214

VERSION

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 14

/organism="Oryza sativa (japonica cultivar-group)"

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/db_xref="taxon:39947"

/clone="JMT--02-A10"

/tissue type="leaf"

/dev stage="14 days after germination"

/lab host="E.coli DH10B"

/clone lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

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Db 14 AAAAAAAAAAAAAA 2

RESULT 258

CF333215

LOCUS

DEFINITION

JMT--02-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-A10, mRNA sequence.

ACCESSION

CF333215

VERSION

CF333215.1 GI:33814709

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 14

Unpublished (2003)
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 2

RESULT 262
CF334290/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa (japonica cultivar-group)"
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cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 262
CF334290/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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was reverse transcribed and then used for PCR. mRNA was
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methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 262
CF334290/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/organism="Oryza sativa (japonica cultivar-group)"
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cDNA library (JMT)"
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was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 14 AAAAAAAAAAAAAA 2

RESULT 262
CF334290/c
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DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/clone="JMT--03-111"
/tissue_type="leaf"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 262
CF334290/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa (japonica cultivar-group)"
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/clone="JMT--03-111"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 262
CF334290/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--03-111"
/tissue_type="leaf"
/dev_stage="14 days after germination


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KEYWORDS
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaah@gbio.com, bhnaah@bio.myongji.ac.kr.

FEATURES             source
                    1..14
                        /organism="Oryza sativa (japonica cultivar-group)"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:39947"
                        /clone="JMT--06-A10"
                        /tissue_type="leaf"
                        /dev_stage="14 days after germination"
                        /lab_host="E.coli DH10B"
                        /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                        cDNA library (JMT)"
                        /notes="vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                        was reverse transcribed and then used for PCR. mRNA was
                        prepared from Arabidopsis Jasmonate Carboxyl
                        methyltransferase overexpression line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
Db   14 AAAAAAAAAAAAAA 2

RESULT 265
CF336106/c
LOCUS      CF336106
DEFINITION JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-A17, mRNA sequence.
ACCESSION  CF336106
VERSION     CF336106.1 GI:33820590
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaah@gbio.com, bhnaah@bio.myongji.ac.kr.

FEATURES             source
                    1..14
                        /organism="Oryza sativa (japonica cultivar-group)"

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RESULT 267
CF336906/c
LOCUS
DEFINITION
    CF336906
    14 bp mRNA linear EST 18-AUG-2003
    JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
    library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
    JMT--07-C05, mRNA sequence.
ACCESSION
    CF336906
VERSION
    CF336906.1 GI:33822182
KEYWORDS
    EST.
SOURCE
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 14)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
    source
    1..14
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="JMT--07-C05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="AtJMT-overexpressing transgenic rice plasmid
    cDNA library (JMT)"
    /note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
    was reverse transcribed and then used for PCR. mRNA was
    prepared from Arabidopsis Jasmonate Carboxyl
    methyltransferase overexpression line."
    Query Match 0.3%; Score 13; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 268
AJ690565/c
LOCUS
DEFINITION
    AJ690565 KN261 Bos taurus cDNA clone KN261-054_B13, mRNA sequence.
ACCESSION
    AJ690565
VERSION
    AJ690565.1 GI:49423173
KEYWORDS
    EST.
SOURCE
    Bos taurus (cow)
    Bos taurus
    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
    Bovinae; Bos.
REFERENCE
    1 (bases 1 to 15)
    Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
    Development of cDNA and EST resources for studying reproduction and
    embryo development in pigs and cattle
    Unpublished (2004)
    Contact: Anderson SI
    Genomics and Bioinformatics

Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI
R. Site2: SmaI 3' Seq Primer M13f Normalised library constructed
from bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
    source
    1..15
    /organism="Bos taurus"
    /mol_type="mRNA"
    /db_xref="taxon:9913"
    /clone="KN261-054_B13"
    /tissue_type="ovary"
    /clone_lib="KN261"
    /note="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2:
    SmaI; Single pass sequencing. Normalised library
    constructed from bovine ovary."
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    Best Local Similarity 100.0%; Pred. No. 1.6e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 269
BE230585
LOCUS
DEFINITION
    BE230585
    15 bp mRNA linear EST 07-JUL-2000
    99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
    (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION
    BE230585
VERSION
    BE230585.1 GI:8956782
KEYWORDS
    EST.
SOURCE
    Oryza sativa (indica cultivar-group)
    Oryza sativa (indica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 15)
    Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
    Nahm,B.H.
    Large-scale Sequencing Analysis of ESTs from Rice Seedling
    Unpublished (1999)
    Contact: Eun M.Y.
    Department of Cytogenetics
    National Inst. of Agri. Sci. and Tech, RDA
    Suwon, Kyunggido, Korea
    Tel: 82 331 290 0301
    Fax: 82 331 290 0307
    Email: myeun@sun20.asti.re.kr.
FEATURES
    source
    1..15
    /organism="Oryza sativa (indica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Milyang 23"
    /db_xref="taxon:39946"
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    /dev_stage="5 days after pollination"
    /lab_host="E. coli SOLR"
    /clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; Directional cDNA library inserted into lambda ZAPII
    vector at 5' end with EcoRI and 3' end with Xho I site"
    Query Match 0.3%; Score 13; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 1.6e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 270
BQ582543/c
LOCUS
DEFINITION S013300-024-007-B02-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris
ACCESSION BQ582543 15 bp mRNA linear EST 06-DEC-2002
VERSION S013300-024-007-B02 3-PRIME, mRNA sequence.
KEYWORDS Beta vulgaris
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS 1 (bases 1 to 15)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 7 row: B column: 02
Seq primer: T7; GTATACGACTCATTATAGGC.
Location/Qualifiers
1. .15
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184162"
/db_xref="taxon:161934"
/clone="024-007-B02"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 271
BQ585820/c
LOCUS
DEFINITION E012533-024-014-H17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION BQ585820 15 bp mRNA linear EST 06-DEC-2002
VERSION E012533-024-014-H17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
KEYWORDS Beta vulgaris
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS 1 (bases 1 to 15)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: T7; GTATACGACTCATTATAGGC.
Location/Qualifiers
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line)"
/db_xref="GABI:184162"
/db_xref="taxon:161934"
/clone="024-007-B02"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION BQ585820
VERSION BQ585820.1 GI:26115402
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS 1 (bases 1 to 15)
Herwig, R., Schulz, B., Weissshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 14 row: H column: 17
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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line)"
/db_xref="GABI:187164"
/db_xref="taxon:161934"
/clone="024-014-H17"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 272
BQ590410/c
LOCUS
DEFINITION E012844-024-019-M08-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION BQ590410
VERSION BQ590410.1 GI:26119993
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS 1 (bases 1 to 15)
Herwig, R., Schulz, B., Weissshaar, B., Hennig, S., Steinfath, M.,

```

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MPiZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissaha@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

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Seq primer: T7; GTAATACGACTCCTACTATAGGC.

FEATURES
source

1. .15
Location/Qualifiers

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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189710"
/db_xref="taxon:161934"
/clone="024-019-M08"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||
Db 15 AAAAAAAAAAAAAA 3

RESULT 273
BQ590656/c

LOCUS

DEFINITION BQ590656 15 bp mRNA linear EST 06-DEC-2002
CNA clone 024-018-L13-SP6 MPiZ-ADIS-024-storage root Beta vulgaris

cDNA clone 024-018-L13 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 15)

REFERENCE
AUTHORS Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MPiZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissaha@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 18 row: L column: 13

Seq primer: SP6; CATACGATTAGTCACACTATAG.

FEATURES
source

1. .15
Location/Qualifiers

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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189464"
/db_xref="taxon:161934"
/clone="024-018-L13"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||
Db 15 AAAAAAAAAAAAAA 3

RESULT 274

BQ591170/c

LOCUS

DEFINITION BQ591170 15 bp mRNA linear EST 06-DEC-2002
E012715-024-017-N18-T7 MPiZ-ADIS-024-storage root Beta vulgaris

cDNA clone 024-017-N18 3-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 15)

REFERENCE

AUTHORS

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MPiZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissaha@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

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Seq primer: T7; GTAATACGACTCCTACTATAGGC.

FEATURES

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Location/Qualifiers

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 Db 15 AAAAAAAAAAAAAA 3

RESULT 277
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LOCUS
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ACCESSION
 VERSION BQ594689

KEYWORDS
 SOURCE EST.

ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 15)
 AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Leirach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weishaar B
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 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weissnaempiz-koeln.mpg.de
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 Seq primer: T7; GTAATAGCACTCACTATAGGCG.

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 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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RESULT 278
 CF277319/c

LOCUS
 DEFINITION 14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION
 VERSION CF277319

KEYWORDS
 SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 15)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

LOCUS
 DEFINITION 14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION
 VERSION CF277319

KEYWORDS
 SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 15)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

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 Db 15 AAAAAAAAAAAAAA 3

RESULT 279
 CF281923/c

LOCUS
 DEFINITION 14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION
 VERSION CF281923

KEYWORDS
 SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 15)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
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QY 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 280
CF290920/c
LOCUS
DEFINITION
14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-C09, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 281
CF291029/c
LOCUS
DEFINITION

15 bp mRNA linear EST 14-AUG-2003
14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E19, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF291029.1 GI:33660062

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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Db 15 AAAAAAAAAAAAAA 3

RESULT 282
CF291103/c
LOCUS
DEFINITION

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14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G10, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF291103.1 GI:33660136

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAAAAAAAAAA 3

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sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E04, mRNA
sequence.
ACCESSION
CF291717.1 GI:33660750
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAAAAAAAAAA 3

RESULT 285
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LOCUS
DEFINITION
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sativa (japonica cultivar-group) cDNA clone 30DGS--01-E17, mRNA
sequence.
ACCESSION
CF292458.1 GI:33661491
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 15)
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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAAAAAAAAAA 3

RESULT 286
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LOCUS
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sativa (japonica cultivar-group) cDNA clone 30DGS--01-E19, mRNA
sequence.
VERSION CF292461.1 GI:33661494
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAAAAAAAAAA 3

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sativa (japonica cultivar-group) cDNA clone 30DGS--01-E19, mRNA
sequence.
VERSION CF292461.1 GI:33661494
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SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 15 AAAAAAAAAAAAAA 3

RESULT 287
CF296652/c
LOCUS
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sativa (japonica cultivar-group) cDNA clone 30DGS--07-C02, mRNA
sequence.
VERSION CF296652.1 GI:33665685
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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Query Match 0.3%; Score 13; DB 1; Length 15;
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RESULT 288
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sequence.
VERSION CF298148.1 GI:33669909
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SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 15)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .15

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

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/tissue_type="leaf"

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 100.0%; Score 13; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 289

CF298630/c

LOCUS

DEFINITION 7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-B23, mRNA

sequence.

ACCESSION CF298630

VERSION CF298630.1 GI:33670391

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 15)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .15

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="7LEAF--02-B23"

/tissue_type="leaf"

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 100.0%; Score 13; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 290

CF298733/c

LOCUS

DEFINITION 7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-E20, mRNA

sequence.

ACCESSION CF298733

VERSION CF298733.1 GI:33670494

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 15)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .15

/organism="Oryza sativa (japonica cultivar-group)"

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/cultivar="Nackdong"

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/clone="7LEAF--02-E20"

/tissue_type="leaf"

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 100.0%; Score 13; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 291

CF298805/c

LOCUS

DEFINITION 7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-G20, mRNA

sequence.

ACCESSION CF298805


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DEFINITION 7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L04, mRNA
            sequence.
ACCESSION  CF299608
VERSION     CF299608.1 GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE   1 (bases 1 to 15)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     Query Match      0.3%; Score 13; DB 1; Length 15;
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     Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
Db  15 AAAAAAAAAAAAAA 3

RESULT 295
CF300121/c
LOCUS     7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G12, mRNA
            sequence.
ACCESSION  CF300121
VERSION     CF300121.1 GI:33671882
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE   1 (bases 1 to 15)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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     Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
Db  15 AAAAAAAAAAAAAA 3

RESULT 295
CF300121/c
LOCUS     7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G12, mRNA
            sequence.
ACCESSION  CF300121
VERSION     CF300121.1 GI:33671882
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE   1 (bases 1 to 15)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="7LEAF--04-G12"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     Query Match      0.3%; Score 13; DB 1; Length 15;
     Best Local Similarity 100.0%; Pred. No. 1.6e+02;
     Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
Db  15 AAAAAAAAAAAAAA 3

RESULT 296
CF300361/c
LOCUS     7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L16, mRNA
            sequence.
ACCESSION  CF300361
VERSION     CF300361.1 GI:33672122
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE   1 (bases 1 to 15)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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Oy  2576 AAAAAAAAAAAAAA 2588
Db  15 AAAAAAAAAAAAAA 3

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RESULT 297
CF300992/c
LOCUS
DEFINITION
15 bp mRNA linear EST 15-AUG-2003
7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-K19, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 15 AAAAAAAAAAAAAA 3

RESULT 298
CF302034/c
LOCUS
DEFINITION
15 bp mRNA linear EST 15-AUG-2003
7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C24, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
|||||
Db 15 AAAAAAAAAAAAAA 3

RESULT 299
CF302124/c
LOCUS
DEFINITION
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7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-F16, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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/clone="HD-01-G13"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 306

CF316251

LOCUS

DEFINITION HD-05-H15, b1 OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CF316251

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

CONTACT: Nahm B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

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of Bioscience and Bioinformatics, Myongji University
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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .15
/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="HD-05-H15"

/tissue_type="callus"

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/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

0.3%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 307

CF318035/c

LOCUS

DEFINITION HD-07-P06, b1 OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CF318035

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .15
/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD-07-P06"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 308

CF327434/c

LOCUS

DEFINITION NACL--01-018, b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-018, mRNA sequence.

ACCESSION CF327434

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


```
REFERENCE
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-018"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
      |||||
DB   15 AAAAAAAAAAAAAA 3

RESULT 309
CF330195/c
LOCUS    NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
sativa (japonica cultivar-group) cDNA clone NACL--05-N03, mRNA
sequence.
ACCESSION CF330195.1 GI:33808618
VERSION   EST.
KEYWORDS  Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--05-N03"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
      |||||
DB   15 AAAAAAAAAAAAAA 3

RESULT 309
CF330195/c
LOCUS    NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
sativa (japonica cultivar-group) cDNA clone NACL--05-N03, mRNA
sequence.
ACCESSION CF330195.1 GI:33808618
VERSION   EST.
KEYWORDS  Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..15
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
      |||||
DB   15 AAAAAAAAAAAAAA 3

RESULT 311
CF332178/c
LOCUS    NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
sativa (japonica cultivar-group) cDNA clone NACL--08-J10, mRNA
sequence.
ACCESSION CF332178.1 GI:33812580
VERSION   EST.

```

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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
      |||||
DB   15 AAAAAAAAAAAAAA 3

RESULT 310
CF330668/c
LOCUS    NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
sativa (japonica cultivar-group) cDNA clone NACL--06-H16, mRNA
sequence.
ACCESSION CF330668.1 GI:33809572
VERSION   EST.
KEYWORDS  Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
      |||||
DB   15 AAAAAAAAAAAAAA 3

RESULT 311
CF332178/c
LOCUS    NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
sativa (japonica cultivar-group) cDNA clone NACL--08-J10, mRNA
sequence.
ACCESSION CF332178.1 GI:33812580
VERSION   EST.

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KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE    Large-scale Sequencing Analysis of Rice ESTs
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3
RESULT 313
CF336202/c
LOCUS      CF336202
DEFINITION JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--06-C20, mRNA sequence.
ACCESSION  CF336202
VERSION    1
KEYWORDS   Oryza sativa (japonica cultivar-group) cDNA clone
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
REFERENCE  1 (bases 1 to 15)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

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/db_xref="taxon:39947"
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cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3
RESULT 313
CF547282
LOCUS      CF547282
DEFINITION DKFPZ4681112_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
DKFPZ4681112 5', mRNA sequence.
ACCESSION  CR547282
VERSION    1
KEYWORDS   EST.
SOURCE     Pongo pygmaeus (orangutan)
ORGANISM   Pongo pygmaeus
REFERENCE  1 (bases 1 to 15)
AUTHORS    Bloecker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
Osanger,A., Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Bloecker,H., Boecker,M., Brandt,P., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany)
within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFPZ4681112) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.
FEATURES
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/tissue_type="heart"
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/lab_host="DH10B"
/clone_lib="468 (synonym: phrt1)"
/notes="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"
Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13
RESULT 314

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```
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 28 row: F column: 08
Seq primer: SP6r; ATTAGGTGACACTATAGAAGA.

FEATURES
source
Location/Qualifiers
1..16
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:194262"
/db_xref="taxon:161934"
/clones="024-028-F08"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-developing root"
/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 16 AAAAAAAAAAAAAA 4

RESULT 318
BQ592965/c
LOCUS
DEFINITION
S013324-024-028-A01-T7 MPiZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION
BQ592965
VERSION
BQ592965.1 GI:26122548
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
REFERENCE
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 28 row: A column: 01
Seq primer: T7; GTAATACGACTCACTATAGGGC.

PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 28 row: A column: 01
Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES
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Location/Qualifiers
1..16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:194262"
/db_xref="taxon:161934"
/clones="024-028-F08"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-developing root"
/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 16 AAAAAAAAAAAAAA 4

RESULT 318
BQ595717
LOCUS
DEFINITION
E012692-024-022-H07-SP6 MPiZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-022-H07 5-PRIME, mRNA sequence.
ACCESSION
BQ595717
VERSION
BQ595717.1 GI:26125300
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
REFERENCE
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: H column: 07
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
source
Location/Qualifiers
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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191134"
/db_xref="taxon:161934"
/clones="024-022-H07"
/tissue_type="developing root"
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/lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-developing root"
 /note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kwa.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 319
 CF279325/c
 LOCUS
 DEFINITION 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
 mRNA sequence.

ACCESSION CF279325
 VERSION CF279325.1 GI:33656711

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..16
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /tissue_type="leaf"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

RESULT 320

CF311057/c

LOCUS

DEFINITION

ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ABF--06-C03, mRNA sequence.

ACCESSION CF311057

VERSION CF311057.1 GI:33682818

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..16

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--06-C03"

/tissue_type="leaf"

/dev_stages="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.3%; Score 13; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

RESULT 321

CF314377/c

LOCUS

DEFINITION

HD--02-001.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--02-001, mRNA sequence.

ACCESSION CF314377

VERSION CF314377.1 GI:33686138

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--02-001"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

RESULT 322

CF315789/c

LOCUS

DEFINITION HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-N10, mRNA sequence.

ACCESSION

CF315789

VERSION

CF315789.1

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 16)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD--04-N10"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

RESULT 323

CF316056/c

LOCUS

DEFINITION HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-D07, mRNA sequence.

ACCESSION

CF316056

VERSION

CF316056.1

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 16)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="HD--05-D07"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match

0.3%; Score 13; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

RESULT 324

CF317718/c

LOCUS

DEFINITION HD--07-I05.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-I05, mRNA sequence.

ACCESSION

CF317718

LOCUS

CF317718/c

DEFINITION

HD--07-I05.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-I05, mRNA sequence.


```

QY      3598 TTTTITTTTAAAT 3610
Db      15 TTTTITTTTAAAT 3

RESULT 327
LOCUS   CF320356/c
DEFINITION
HD--11-D14_b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--11-D14, mRNA sequence.
CF320356
CF320356.1 GI:33692117
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     /clone="NACL--02-F06"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
     /lab_host="E.coli DH10B"
     /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match          0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      16 AAAAAAAAAAAAAA 4

RESULT 328
LOCUS   CF327722/c
DEFINITION
HD--11-D14_b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA
sequence.
CF327722
CF327722.1 GI:33803695
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

Query Match          0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      16 AAAAAAAAAAAAAA 4

RESULT 328
LOCUS   CF327722/c
DEFINITION
HD--11-D14_b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA
sequence.
CF327722
CF327722.1 GI:33803695
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

```

```

REFERENCE
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 13; DB 1; Length 16;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      16 AAAAAAAAAAAAAA 4

RESULT 329
LOCUS   CF327923/c
DEFINITION
HD--02-J18_g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--02-J18, mRNA
sequence.
CF327923
CF327923.1 GI:33804096
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"

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/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 15 AAAAAAAAAAAAAA 3

RESULT 330
CF328223/c
LOCUS
DEFINITION
NACl--03-A10.g1 Rice callus plasmid cDNA library (NACl) Oryza
sativa (japonica cultivar-group) cDNA clone NACl--03-A10, mRNA
sequence.
CF328223 16 bp mRNA linear EST 18-AUG-2003
NACl--03-A10.g1 Rice callus plasmid cDNA library (NACl) Oryza
sativa (japonica cultivar-group) cDNA clone NACl--03-A10, mRNA
sequence.
CF328223 1 GI:33804692
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACl)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 15 AAAAAAAAAAAAAA 3

RESULT 331
CF333386
LOCUS
DEFINITION
JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-E05, mRNA sequence.
CF333386
JMT--02-E05, mRNA sequence.
CF333386 1 GI:33815044
EST.
Oryza sativa (japonica cultivar-group)

```

```

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="JMT--02-E05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match          0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 1 AAAAAAAAAAAAAA 13

RESULT 332
CR786609
LOCUS
DEFINITION
DKFZp468C2031.r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
DKFZp468C2031.5, mRNA sequence.
CR786609 16 bp mRNA linear EST 01-OCT-2004
CR786609 1 GI:53705606
EST.
Pongo pygmaeus (orangutan)
Pongo pygmaeus
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
1 (bases 1 to 16)
Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; mforaching GmbH in Berlin,
Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp468C2031
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
source
1..16
/organism="Pongo pygmaeus"
/mol_type="mRNA"

```



```
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-M14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTCTTTTAA 2757
|||||
Db 16 TTTTCTTTTAA 4

RESULT 336
CL693164/c
LOCUS
DEFINITION
Prio160a_G09_2 - PRI0160a.BR (21) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
CL693164.1 GI:50215072
VERSION
GSS.
KEYWORDS
Pristionchus pacificus
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 21)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Nucleic Acids Res. 32 (1), D421-D422 (2004)
CONTACT: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..21
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
Query Match 0.3%; Score 13; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1157 TTTTATATATATTTTCTT 1177
|||||
Db 21 TTTTCTTTTATTTTCTT 1

RESULT 338
CW020436/c
LOCUS
DEFINITION
CW0698 TIGEM gene trap library Mus musculus cDNA clone A012.A8,
mRNA sequence.
ACCESSION
CW020436
VERSION
CW020436.1 GI:52789696
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
Cobellis,G., Nicolaus,G., Marra,E., Barbarisi,M., Sardiello,M., Di
Giorgio,F.P., Iovino,N., Zollo,M., Ballabio,A. and Cortese,R.
Tagging genes with cassette-exchange sites
Unpublished (2004)
CONTACT: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
```

Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene Trap.
Location/Qualifiers

FEATURES

source

```
1. .21
/organism="Mus musculus"
/mol_type="mRNA"
/strain="I29 ola"
/db_xref="taxon:10090"
/clone="A012.A8"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"
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Query Match 0.3%; Score 13; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2748 TTTTAAAGGAAAAATA 2768
||||||| |||||
Db 21 TTTTTCCTCCCAAAAAA 1

RESULT 339
BQ590507 16 bp mRNA linear EST 06-DEC-2002
LOCUS E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION Beta vulgaris
ACCESSION BQ590507
VERSION BQ590507.1 GI:26120090
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PubMed 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 19 row: M column: 04
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers

FEATURES

source

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1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189608"
/db_xref="taxon:161934"
/clone="024-019-M04"
/tissue_type="storage root"
/lab_host="EMDH108"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
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cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTA 3279
||||||| |||||
Db 1 TTTTTCCTTTTA 16

RESULT 340
BQ595369 16 bp mRNA linear EST 06-DEC-2002
LOCUS S013317-024-022-P02-T7 MP1Z-ADIS-024-developing root Beta vulgaris
DEFINITION cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION BQ595369
VERSION BQ595369.1 GI:26124952
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PubMed 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: P column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers

FEATURES

source

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1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:191489"
/db_xref="taxon:161934"
/clone="024-022-P02"
/tissue_type="developing root"
/lab_host="EMDH108"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de
```

```
Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTTCCTTTT 3279
      ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTT 16

RESULT 341
CF296130 16 bp mRNA linear EST 14-AUG-2003
LOCUS HD--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA
sequence.
ACCESSION CF296130 GI:33665163
VERSION CF296130
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-F22"
/tissue_type="leaf"
/dev_stages="30 days after germination"
/clone_lib="E.coli DH10B"
/clone_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notice="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTTCCTTTT 3279
      ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTT 16

RESULT 343
CF329320 16 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
sequence.
ACCESSION CF329320 GI:33806877
VERSION CF329320
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-J17"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/clone_lib="E.coli DH10B"
/clone_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notice="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTTCCTTTT 3279
      ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTT 16

RESULT 343
CF329320 16 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
sequence.
ACCESSION CF329320 GI:33806877
VERSION CF329320
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-J17"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/clone_lib="E.coli DH10B"
/clone_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notice="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTTCCTTTT 3279
      ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTT 16

RESULT 342
CF314013 16 bp mRNA linear EST 15-AUG-2003
LOCUS HD--02-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-G01, mRNA sequence.
ACCESSION CF314013 GI:33685774
VERSION CF314013
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
```

/dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTT 3279
 Db 1 TTTTTCCTTTT 16

RESULT 344
 AW246487
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 16)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Other ESTs: 2821557.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 11
 contiguous PHRED high quality bases following vector sequence. Very
 Low Quality Sequence: Trace file contained 16 contiguous distinct
 peaks following vector sequence. Polyadenylation: Based upon the
 presence of a XhoI site followed by a run of 14 or more T residues
 at the beginning of the sequence, this cDNA insert was
 polyadenylated.
 Plate: L1CM7 row: B column: 22
 High quality sequence stop: 11.
 Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821557"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.9kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES

source
 Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821557"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.9kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTTCCTTTT 2761
 Db 1 TTTTTCCTTTT 16

RESULT 345
 AW246487/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 16)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Other ESTs: 2821557.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 11
 contiguous PHRED high quality bases following vector sequence. Very
 Low Quality Sequence: Trace file contained 16 contiguous distinct
 peaks following vector sequence. Polyadenylation: Based upon the
 presence of a XhoI site followed by a run of 14 or more T residues
 at the beginning of the sequence, this cDNA insert was
 polyadenylated.
 Plate: L1CM7 row: B column: 22
 High quality sequence stop: 11.
 Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821557"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2796 TTATCTGAAAAAAA 2811
 Db 16 TTCTGTAATAAAAA 1

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RESULT 346
AW246490/c
LOCUS
DEFINITION
      16 bp      mRNA      linear      EST 07-JAN-2000
      2821591.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821591 3',
      mRNA sequence.
ACCESSION
AW246490
VERSION
AW246490.1 GI:6589483
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Other ESTs: 2821591.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LNCM7 row: D column: 8
High quality sequence stop: 12.
FEATURES
      source
      1..16
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2821591"
      /tissue_type="small cell carcinoma"
      /cell_line="MGC3"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH MGC_7"
      /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
      EcoRI; cDNA made by oligo-dT priming. Directionally
      cloned into EcoRI/XhoI sites using the following 5',
      adaptor: GGCACGAG(G). Size-selected 5500bp for average
      insert size 1.8kb. Library constructed by Ling Hong in
      the laboratory of Gerald M. Rubin (University of
      California, Berkeley) using ZAP-cDNA synthesis kit
      (Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2572 GTTTTAAAAA 2587
      |||||
      16 GTTTGCAAAAAA 1
Db

RESULT 347
AW251049/c
LOCUS
DEFINITION
      16 bp      mRNA      linear      EST 07-JAN-2000
      2821507.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821507 3',
      mRNA sequence.
```

```

ACCESSION
AW251049
VERSION
AW251049.1 GI:6593995
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Other ESTs: 2821507.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LNCM6 row: P column: 20
High quality sequence stop: 10.
FEATURES
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      /tissue_type="small cell carcinoma"
      /cell_line="MGC3"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH MGC_7"
      /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
      EcoRI; cDNA made by oligo-dT priming. Directionally
      cloned into EcoRI/XhoI sites using the following 5',
      adaptor: GGCACGAG(G). Size-selected >500bp for average
      insert size 1.8kb. Library constructed by Ling Hong in
      the laboratory of Gerald M. Rubin (University of
      California, Berkeley) using ZAP-cDNA synthesis kit
      (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3221 CCTGTTTAAACAGAAA 3236
      |||||
      16 CCTGTTTAAAAA 1
Db

RESULT 348
BQ590688
LOCUS
DEFINITION
      16 bp      mRNA      linear      EST 06-DEC-2002
      S013717-024-018-023-T7 MPI2-ADIS-024-storage root Beta vulgaris
      cDNA clone 024-018-023 3-PRIME, mRNA sequence.
ACCESSION
BQ590688
VERSION
BQ590688.1 GI:26120271
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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REFERENCE
AUTHORS
    Caryophyllales; Amaranthaceae; Beta.
    1 (bases 1 to 16)
    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
    Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
    and Radelof,U.
TITLE
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
PUBMED
    22362189
    12472698
COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MPiZ
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@mpiz-koeln.mpg.de
    Insert Length: 16 Std Error: 0.00
    Plate: 18 row: O column: 23
    Seq primer: T7; GTAATACGACTCACTATAGGCG.
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        /clone="024-018-023"
        /tissue_type="storage root"
        /lab_host="EMDH10B"
        /clone_lib="MPiZ-ADIS-024-storage root"
        /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
        cDNA library from sugar beet, library provided by KWS
        Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
        b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
        orientation:
        SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
        Sequencing granted in the context of the GABI-Beet
        project, local PI: Dr. Katharina Schneider, coordinator:
        Prof. Christian Jung; Sequence submission managed by
        RZPD/GABI-Primary database: http://gabi.rzpd.de"
    Query Match 0.3%; Score 12.8; DB 1; Length 16;
    Best Local Similarity 87.5%; Pred. No. 2.7e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 973 CCCCCCCCCCCCCGCC 988
Db 1 CCCCCCCCCCCCCCCC 16

RESULT 349
BQ590128
LOCUS
DEFINITION
    E012843-024-019-E19-T7 MPiZ-ADIS-024-storage root Beta vulgaris
    cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION
BQ590128
VERSION
BQ590128.1 GI:26119711
KEYWORDS
    EST.
SOURCE
    Beta vulgaris
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        Caryophyllales; Amaranthaceae; Beta.
        Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
        Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
        and Radelof,U.
    1 (bases 1 to 17)
REFERENCE
AUTHORS
    Contact: Weisshaar B
    ADIS DNA core facility at MPiZ
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@mpiz-koeln.mpg.de
    Insert Length: 17 Std Error: 0.00
    Plate: 17 row: H column: 16
    Seq primer: T7; GTAATACGACTCACTATAGGCG.
TITLE
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
PUBMED
    22362189
    12472698

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COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MPiZ
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@mpiz-koeln.mpg.de
    Insert Length: 17 Std Error: 0.00
    Plate: 19 row: E column: 19
    Seq primer: T7; GTAATACGACTCACTATAGGCG.
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        /clone="024-019-E19"
        /tissue_type="storage root"
        /lab_host="EMDH10B"
        /clone_lib="MPiZ-ADIS-024-storage root"
        /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
        cDNA library from sugar beet, library provided by KWS
        Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
        b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
        orientation:
        SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
        Sequencing granted in the context of the GABI-Beet
        project, local PI: Dr. Katharina Schneider, coordinator:
        Prof. Christian Jung; Sequence submission managed by
        RZPD/GABI-Primary database: http://gabi.rzpd.de"
    Query Match 0.3%; Score 12.8; DB 1; Length 17;
    Best Local Similarity 87.5%; Pred. No. 3.5e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3264 TTTTTCCTCTTTTA 3279
Db 2 TTTTTCCTCTTTTA 17

RESULT 350
BQ591181
LOCUS
DEFINITION
    E012715-024-017-H16-T7 MPiZ-ADIS-024-storage root Beta vulgaris
    cDNA clone 024-017-H16 3-PRIME, mRNA sequence.
ACCESSION
BQ591181
VERSION
BQ591181.1 GI:26120764
KEYWORDS
    EST.
SOURCE
    Beta vulgaris
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        Caryophyllales; Amaranthaceae; Beta.
        Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
        Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
        and Radelof,U.
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
PUBMED
    22362189
    12472698
COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MPiZ
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@mpiz-koeln.mpg.de
    Insert Length: 17 Std Error: 0.00
    Plate: 17 row: H column: 16
    Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
    Location/Qualifiers

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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188932"
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/clone="024-017-H16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="WPJZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
Best Local Similarity 87.5%; Pred. No. 3.5e+02; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
|||||
Db 1 TTTTTCCTTTT 16

RESULT 351
CF294668 17 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
sequence.
CF294668.1 GI:33663701
CF294668
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="30DGS-06-C17"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 87.5%; Pred. No. 3.5e+02; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
|||||
Db 1 TTTTTCCTTTT 16

RESULT 351
CF294668 17 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
sequence.
CF294668.1 GI:33663701
CF294668
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 87.5%; Pred. No. 3.5e+02; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
|||||
Db 1 TTTTTCCTTTT 16

RESULT 351
CF294668 17 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
sequence.
CF294668.1 GI:33663701
CF294668
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="30DGS-04-E17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 87.5%; Pred. No. 3.5e+02; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
|||||
Db 1 TTTTTCCTTTT 16

RESULT 351
CF294668 17 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
CF295988
CF295988.1 GI:33665021
CF295988
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 87.5%; Pred. No. 3.5e+02; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
|||||
Db 2 TTTTTCCTTTT 17

RESULT 353
CF311499 17 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
CF311499.1 GI:33683260
CF311499
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)

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Best Local Similarity 87.5%; Pred. No. 3.5e+02; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
|||||
Db 2 TTTTTCCTTTT 17

RESULT 352
CF295988 17 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
CF295988
CF295988.1 GI:33665021
CF295988
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 87.5%; Pred. No. 3.5e+02; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
|||||
Db 2 TTTTTCCTTTT 17

RESULT 353
CF311499 17 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
CF311499.1 GI:33683260
CF311499
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)

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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTT 3279
Db 1 TTTTTCCTTTT 16

RESULT 354
CF319075
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"

CF319075 17 bp mRNA linear EST 15-AUG-2003
HD--09-H06.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.

ACCESSION CF319075.1 GI:33690836
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"

CF319075 17 bp mRNA linear EST 18-AUG-2003
JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-D04, mRNA sequence.

ACCESSION CF336950
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-D04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jaominate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTT 3279
Db 2 TTTTTCCTTTT 17

RESULT 356
AW247976
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"

DEFINITION 2820717.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820717 3', mRNA sequence.

ACCESSION AW247976

VERSION AW247976.1 GI:6591064

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 17)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2820717.5prime

Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.biol.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQuality> Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM4 row: 0 column: 22.

FEATURES

Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2820717"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTTCCTTTTATGAT 3613

Db 1 TTTTTCCTTTTACAA 16

RESULT 357

CF308042

LOCUS ABF--01-L07.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

DEFINITION ABF--01-L07, mRNA sequence.

ACCESSION CF308042

VERSION CF308042

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--01-L07"

/tissue_type="leaf"

/dev_stages="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTCTTTTA 3279

Db 1 TTTTTCCTTTTCTTTTA 16

FEATURES

Location/Qualifiers

15 bp

CF295100

LOCUS 30DGS--04-002.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--04-002, mRNA sequence.

DEFINITION CF295100.1 GI:33664133

ACCESSION CF295100

VERSION CF295100

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..15

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

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/clone="30DGS--04-002"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.3%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2743 TCTTTTCTTTTCTTTA 2756
| | | | | | | | | | | | | | |
Db 2 TTTTCTTTTCTTTTCTTTA 15

RESULT 359
LOCUS BQ591588 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012616-024-017-C15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-C15 5-PRIME, mRNA sequence.
ACCESSION BQ591588
VERSION BQ591588.1 GI:26121171
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE
AUTHORS Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stah,D., Wruck,W., Menze,A., O'Brien,J., Leirach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: C column: 15
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
Source
1..17
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188532"
/db_xref="taxon:161934"
/cb_xref="024-017-C15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
0.3%; Score 12.4; DB 1; Length 17;

Best Local Similarity
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3598 TTTTCTTTTCTTTAATGATC 3614
| | | | | | | | | | | | | | |
Db 1 TTTTCTTTTCTTTAATGATC 17

Best Local Similarity 92.9%; Pred. No. 4.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTCTTTTCTTTT 2755
| | | | | | | | | | | | | | |
Db 3 ATTCTTTTCTTTTCTTTT 16

RESULT 360
LOCUS AW246528 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
mRNA sequence.
ACCESSION AW246528
VERSION AW246528.1 GI:6589521
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE (bases 1 to 17)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Other ESTs: 2821879.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross_match from University of Washington Genome Center
PRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality sequence: 13
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 17 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LCM7 row: P column: 8
High quality sequence stop: 13.
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821879"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

RESULT 361
AW246551
LOCUS
DEFINITION
2822090.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822090 3',
mRNA sequence.
ACCESSION
AW246551
VERSION
AW246551.1 GI:6589544
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822090.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html Base Calling / Quality
Scores: PHRED high quality bases following vector sequence. Very
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 15 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM8 row: I column: 3
High quality sequence stop: 14.
FEATURES
source
1..15
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822090"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match
Best Local Similarity 100.0%; Pred.No. 3.6e+02; Length 15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 2746 TTTTITTTTAA 2757
|||||
Db 1 TTTTITTTTAA 12
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RESULT 362
AW245585/c
LOCUS
DEFINITION
2822740.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822740 3',
mRNA sequence.
ACCESSION
AW245585
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```

VERSION
AW245585.1 GI:6588578
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822740.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html Base Calling / Quality
Scores: PHRED high quality bases following vector sequence. Very
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 15 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM10 row: D column: 5
High quality sequence stop: 6.
FEATURES
source
1..15
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822740"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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```

Query Match
Best Local Similarity 100.0%; Pred.No. 3.6e+02; Length 15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2574 TTAATAAAAAAAAA 2585
|||||
Db 12 TTAATAAAAAAAAA 1
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RESULT 363
AW248540
LOCUS
DEFINITION
2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
mRNA sequence.
ACCESSION
AW248540
VERSION
AW248540.1 GI:6591533
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NIH-MGC http://mgc.nci.nih.gov/.
```

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2820844.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DNP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtp/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 15
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LNCM5 row: E column: 5
High quality sequence stop: 15.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820844"
/tissue_type="small cell carcinoma"
/cell_line="WGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. NO. 4.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2746 TTTTITTTTAA 2757 16 bp mRNA linear EST 15-AUG-2003
Db 1 TTTTITTTTAA 12

RESULT 364
CF319827
LOCUS HD-10-H16.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-10-H16, mRNA sequence.
CF319827
CF319827.1 GI:33691588
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 16)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2820844.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DNP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtp/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LNCM6 row: P column: 20
High quality sequence stop: 10.
Location/Qualifiers
1..16
/organism="Homo sapiens"

Query Match 0.3%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. NO. 4.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTTAAAAA 2585 16 bp mRNA linear EST 07-JAN-2000
Db 4 TTTAAAAA 15

RESULT 365
AW251049
LOCUS AW251049.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821507.3',
DEFINITION mRNA sequence.
ACCESSION AW251049
VERSION AW251049.1 GI:6593995
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821507.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtp/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LNCM6 row: P column: 20
High quality sequence stop: 10.
Location/Qualifiers
1..16
/organism="Homo sapiens"

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-10-H16"
/tissue_type="callus"
/dev_host="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source

FEATURES
source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821507"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0;

QY 2746 TTTTTCCTTAA 2757

|||||

Db 1 TTTTTCCTTAA 12

RESULT 366

CF301359

LOCUS

DEFINITION

7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D05, mRNA

sequence.

ACCESSION CF301359

VERSION CF301359.1

KEYWORDS GI:33673120

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--06-D05"

/tissue_type="leaf"

/dev_stages="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.3%; Score 12; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTCT 3275

|||||

Db 7 TTTTTCCTTCT 18

Search completed: February 25, 2005, 09:53:02
Job time : 13 secs


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KEYWORDS      .
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 14)
AUTHORS
TITLE          ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL        EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES       LOCATION/Qualifiers
source         1..14
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACCTACTGTGTG 1232
Db 14 TGCACCTACTGTGTG 1

RESULT 479
A40526/c
LOCUS          A40526      14 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION     Sequence 63 from Patent WO9425578.
ACCESSION      A40526
VERSION        A40526.1 GI:2296561
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS
TITLE          ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL        EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES       LOCATION/Qualifiers
source         1..14
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357
Db 14 CAGATCCTGAGCAA 1

RESULT 480
A40534/c
LOCUS          A40534      14 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION     Sequence 71 from Patent WO9425578.
ACCESSION      A40534
VERSION        A40534.1 GI:2296569
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS
TITLE          ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL        EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES       LOCATION/Qualifiers
source         1..14
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

KEYWORDS      .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS
TITLE          ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL        EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES       LOCATION/Qualifiers
source         1..14
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTAGCCCAAG 1520
Db 14 AGTACTAGCCCAAG 1

RESULT 481
A40537/c
LOCUS          A40537      14 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION     Sequence 74 from Patent WO9425578.
ACCESSION      A40537
VERSION        A40537.1 GI:2296572
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS
TITLE          ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL        EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES       LOCATION/Qualifiers
source         1..14
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574
Db 14 AAAATGCCATCCCG 1

RESULT 482
A40538/c
LOCUS          A40538      14 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION     Sequence 75 from Patent WO9425578.
ACCESSION      A40538
VERSION        A40538.1 GI:2296573
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS
TITLE          ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL        EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES       LOCATION/Qualifiers
source         1..14
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTCTACAG 1588
Db 14 CCCACTTCTACAG 1588
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DEFINITION LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION E53842
VERSION E53842.1 GI:18633612
KEYWORDS JP 2001078772-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Kadoita,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
TITLE LUNX gene and method for detecting micrometastasis of cancer
JOURNAL Patent: JP 2001078772-A 3 27-MAR-2001;
OF SUKA PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 2001078772-A/3
PD 27-MAR-2001
PF 07-SEP-1999 JP 1999253186
PI MORITO KADOTA,YOSHIYUKI FUJIWARA,RYUJI WATANABE,KOICHI OZAKI
PC C12N15/09,C07K14/82,C07K16/32,C12N1/15,C12N1/21, PC
C12N5/10,C12Q1/68,
PC G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC
A61K35/12,A61K35/76,
PC A61K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,
PC C12N15/00,
PC C12N5/00
CC
FH Key Location/Qualifiers
FT source 1..16
FT /organism='Unidentified'.
FEATURES
source 1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.3%; Score 14.2; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2574 TTAAAAAATAAAAAA 2588
DB 16 TBAATAAAAAAATAAAAA 2
RESULT 475
AX406535/C
LOCUS AX406535 17 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 12 from Patent WO222686.
ACCESSION AX406535
VERSION AX406535.1 GI:21439550
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kwak,L.W. and Biragyn,A.
TITLE Defensin-antigen fusion proteins
JOURNAL Patent: WO 022686-A 12 21-MAR-2002;
The Secretary, Dept. of Health and Human services, NIH (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence; Note =
Synthetic Construct"
Query Match 0.3%; Score 14.2; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 3.5e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 974 CCCCCCACCSCCCCC 990
:||||| ||||| |||||

Db 17 SCSCCCCCSCCCCCC 1
RESULT 476
AX721791/C
LOCUS AX721791 17 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 12 from Patent WO03025002.
ACCESSION AX721791
VERSION AX721791.1 GI:30422379
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Biragyn,A. and Kwak,L.W.
TITLE Method and compositions of defensin-antigen fusion proteins and chemokine-antigen fusion proteins as vaccines for tumors and viral infection
JOURNAL Patent: WO 03025002-A 12 27-MAR-2003;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.2; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 3.5e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 974 CCCCCCACCSCCCCC 990
:||||| ||||| |||||
Db 17 SCSCCCCCSCCCCCC 1
RESULT 477
A40172/C
LOCUS A40172 14 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 2 from Patent WO9425588.
ACCESSION A40172
VERSION A40172.1 GI:2296326
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
TITLE EFFECTS OF TRANSFORMING GROWTH FACTOR- beta (TGF- beta)
JOURNAL Patent: WO 9425588-A 2 10-NOV-1994;
BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT Other publication AU 6794594 941121.
FEATURES
source 1..14
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1222 ACTACTGTGTGTGTG 1235
||||| ||||| |||||
Db 14 ACTACTGTGTGTG 1
RESULT 478
A40520/C
LOCUS A40520 14 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 57 from Patent WO9425578.
ACCESSION A40520
VERSION A40520.1 GI:2296555

TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 18 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/18
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
PC C12Q1/68, C12M1/00, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC
G01N33/566.
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
FEATURES source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3
RESULT 469
BD107503/c
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION BD107503
ACCESSION BD107503
VERSION BD107503.1 GI:23202321
KEYWORDS JP 2002000275-A/12.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 12 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/12
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12Q1/34, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
FEATURES source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3
RESULT 471
BD107505/c
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION BD107505
ACCESSION BD107505
VERSION BD107505.1 GI:23202322
KEYWORDS JP 2002000275-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 13 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/13
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12Q1/34, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
FEATURES source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3
RESULT 471
BD107505/c

CC acid. nucleic
CC Key Location/Qualifiers
FH source 1. .18
/organism="Artificial Sequence".
FT source Location/Qualifiers
1. .18
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/db_xref="taxon:32630"
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Location/Qualifiers
1. .18
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/db_xref="taxon:32630"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3
RESULT 470
BD107504/c
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION BD107504
ACCESSION BD107504
VERSION BD107504.1 GI:23202322
KEYWORDS JP 2002000275-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 13 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/13
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12Q1/34, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
FEATURES source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3
RESULT 471
BD107505/c

ATATATATTTTCTT 1177

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/note="Detection oligonucleotide for ELK1"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 935 AAAAAACAAACCTTTC 950
Db 16 AAAAAACAAACCTTTC 1

|||||
16 AAAAAACAAACCTTTC 1

RESULT 464
AX826754
LOCUS
DEFINITION
Sequence 1006 from Patent WO03072821.
ACCESSION
AX826754
VERSION
AX826754.1 GI:39752268
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE
Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL
Patent: WO 03072821-A 1006 04-SEP-2003;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for GPIb beta"

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4130 AGTTTGGTTGAGTTT 4145
Db 3 AGTTTGGTTGAGTTT 18

|||||
3 AGTTTGGTTGAGTTT 18

RESULT 465
BD072876/c
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD072876
VERSION
BD072876.1 GI:22618479
KEYWORDS
JP 2001286300-A/14.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2001286300-A 14 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT
OS Artificial Sequence
PN JP 2001286300-A/14
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53,G01N33/542, PC
G01N33/566,
CC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
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Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pelet,C. and Ziebarth,H.
Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
Patent: WO 02077272-A 652 03-OCT-2002;
Epigenomics AG (DE)
JOURNAL
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950
Db 16 AAAAAACAACCTTC 1

RESULT 458
AX599726/C
LOCUS
DEFINITION
Sequence 1066 from Patent WO02077272.
ACCESSION
AX599726
VERSION
AX599726.1 GI:28399874
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Berlin,K., Braun,A., Disler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pelet,C. and Ziebarth,H.
Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
Patent: WO 02077272-A 1066 03-OCT-2002;
Epigenomics AG (DE)
JOURNAL
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950
Db 16 AAAAAACAACCTTC 1

RESULT 459
AX767728/C
LOCUS
DEFINITION
Sequence 376 from Patent WO03044226.
ACCESSION
AX767728
VERSION
AX767728.1 GI:32436333
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
Nimmrich,I.
Method and nucleic acids for the analysis of a lymphoid cell
proliferative disorder

JOURNAL
FEATURES
source
Patent: WO 03044226-A 376 30-MAY-2003;
Epigenomics AG (DE)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950
Db 16 AAAAAACAACCTTC 1

RESULT 460
AX796166/C
LOCUS
DEFINITION
Sequence 509 from Patent WO03052135.
ACCESSION
AX796166
VERSION
AX796166.1 GI:37516832
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Burger,M., Field,J.K., Genc,B., Lilloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
Method and nucleic acids for the analysis of a lung cell
proliferative disorder
Patent: WO 03052135-A 509 26-JUN-2003;
Epigenomics AG (DE)
JOURNAL
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950
Db 16 AAAAAACAACCTTC 1

RESULT 461
AX822692/C
LOCUS
DEFINITION
Sequence 584 from Patent EP1340818.
ACCESSION
AX822692
VERSION
AX822692.1 GI:39749328
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
Method and nucleic acids for the analysis of a colon cell
proliferative disorder
Patent: EP 1340818-A 584 03-SEP-2003;
Epigenomics AG (DE)
JOURNAL
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
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Db 18 ATATATATTTTTTTT 3

RESULT 453
AR478213/c
LOCUS AR478213 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 16 from patent US 6699661.
ACCESSION AR478213
VERSION AR478213.1 GI:47236861
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 16 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
|||||
Db 18 ATATATATTTTTTTT 3

RESULT 454
AR478214/c
LOCUS AR478214 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 17 from patent US 6699661.
ACCESSION AR478214
VERSION AR478214.1 GI:47236862
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 17 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
|||||
Db 18 ATATATATTTTTTTT 3

RESULT 455
AR478215/c
LOCUS AR478215 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 18 from patent US 6699661.
ACCESSION AR478215
VERSION AR478215.1 GI:47236864
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 19 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
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Db 18 ATATATATTTTTTTT 3

RESULT 456
AX085253/c
LOCUS AX085253 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 7 from Patent WO0112855.
ACCESSION AX085253
VERSION AX085253.1 GI:13275311
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 7 22-FEB-2001;
YALE UNIVERSITY (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAAACA 2816
|||||
Db 18 TGAATAAAAAAAAAAAA 3

RESULT 457
AX599312/c
LOCUS AX599312 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 652 from Patent WO2077272.
ACCESSION AX599312
VERSION AX599312.1 GI:28399454
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Dietler,J., Guetig,D., Howe,A., Mueller,J.,

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VERSION CQ807628.1 GI:47113022
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fockens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
Marx,A.
TITLE Method and nucleic acids for the improved treatment of breast cell
proliferative disorders
JOURNAL Patent: WO 2004035803-A 1078 29-APR-2004;
EpiGenomics AG (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Detection oligonucleotide for GPIIB"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4130 AGTTGGTTGAGTTT 4145
Db 3 AGTTGGTTGGGTTT 18
RESULT 444
CQ814895/c
LOCUS 18 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 18 from Patent WO2004039979.
ACCESSION CQ814895
VERSION CQ814895.1 GI:47604062
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Heils,A. and Haug,K.
TITLE Means and methods for diagnosing and treating idiopathic
generalized epilepsy (ige)
JOURNAL Patent: WO 2004039979-A 18 13-MAY-2004;
Rheinische Friedrich-Wilhelms-Universitaet Bonn (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer for amplifying a fragment of the CLCN-2
nucleotide sequence"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 96 GAGCTCTGGGGCAGGC 111
Db 18 GAGCTCTGGGGCAGGC 3
RESULT 445
AR196692
LOCUS 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1157 from patent US 6350934.
ACCESSION AR196692
VERSION AR196692.1 GI:20246129
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 15 10-DEC-2002;
EpiGenomics AG (DE)
FEATURES
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1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1162 ATATATATTTTCTT 1177
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1157 26-FEB-2002;
EpiGenomics AG (DE)
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 586 CTCCCGCGGCTCGCC 601
Db 2 CTCCCGCGGCTCGCC 17
RESULT 446
AR208427/c
LOCUS 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6383754.
ACCESSION AR208427
VERSION AR208427.1 GI:21509578
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Peng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 7 07-MAY-2002;
EpiGenomics AG (DE)
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2801 TGAATAAAAAAAAAACA 2816
Db 18 TGAATAAAAAAAAAACA 3
RESULT 447
AR264931/c
LOCUS 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 15 from patent US 6492121.
ACCESSION AR264931
VERSION AR264931.1 GI:29693318
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 15 10-DEC-2002;
EpiGenomics AG (DE)
FEATURES
source
1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1162 ATATATATTTTCTT 1177
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PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examinig the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..18
/organism='Artificial Sequence'.
FEATURES
source
1..18 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1162 ATATATATTTTCTT 1177
DB 18 ATATATATTTT 3
RESULT 441
BD166037/C
LOCUS
DEFINITION
18 bp DNA linear PAT 17-JAN-2003
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
VERSION BD166037.1 GI:27871849
KEYWORDS JP 2002191372-A/17.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
JOURNAL
BD166037 18 bp DNA linear PAT 17-JAN-2003
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
VERSION BD166037.1 GI:27871849
KEYWORDS JP 2002191372-A/17.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
examining the
decrease in fluorescence emission of a nucleic acid probe CC
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..18
/organism='Artificial Sequence'.
FEATURES
source
1..18 Location/Qualifiers
/organism='unidentified'

/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1162 ATATATATTTTCTT 1177
DB 18 ATATATATTTT 3
RESULT 442
BD166039/C
LOCUS
DEFINITION
18 bp DNA linear PAT 17-JAN-2003
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
VERSION BD166039.1 GI:27871851
KEYWORDS JP 2002191372-A/19.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
examining the
decrease in fluorescence emission of a nucleic acid probe CC
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..18
/organism='Artificial Sequence'.
FEATURES
source
1..18 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1162 ATATATATTTTCTT 1177
DB 18 ATATATATTTT 3
RESULT 443
CO807628
LOCUS
DEFINITION
18 bp DNA linear PAT 10-MAY-2004
Sequence 1078 from Patent WO2004035803.
ACCESSION
CO807628

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Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 438
BD145039/c
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD145039
VERSION
BD145039.1 GI:27850797
KEYWORDS
JP 2002119291-A/20.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2002119291-A 20 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002119291-A/20
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
53,
PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..18
/organism='Artificial Sequence'.

FEATURES
source
1..18
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 439
BD166035/c
LOCUS
DEFINITION
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166035
VERSION
BD166035.1 GI:27871847
KEYWORDS
JP 2002191372-A/15.
SOURCE
unidentified

QY 1162 ATATATATTTTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 440
BD166036/c
LOCUS
DEFINITION
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166036
VERSION
BD166036.1 GI:27871848
KEYWORDS
JP 2002191372-A/16.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
Patent: JP 2002191372-A 16 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/16
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2138 CTACTGCTTTAGAAAT 2153
Db 17 CTACTGCTTTAGAGAT 2

RESULT 431
AX761129/c
LOCUS AX761129 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 4450 from Patent WO03040369.
ACCESSION AX761129
VERSION AX761129.1 GI:32255745
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 4450 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2649 AATGGCATCTGAGAT 2664
Db 17 AATGGCATCTGAGAT 2

RESULT 432
AX781716
LOCUS AX781716 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 47 from Patent WO03050284.
ACCESSION AX781716
VERSION AX781716.1 GI:32949550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 47 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 CGCGCGCACGCACG 631
Db 1 CGCGCGCACGCACG 631

RESULT 433
AX781717
LOCUS AX781717 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 48 from Patent WO03050284.
ACCESSION AX781717
VERSION AX781717.1 GI:32949551
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 48 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 CGCGCGCACGCACG 631
Db 1 CGCGCGCACGCACG 16

RESULT 434
AR078640
LOCUS AR078640 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 19 from patent US 5962673.
ACCESSION AR078640
VERSION AR078640.1 GI:10005386
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Monia,B.P. and Cowsert,L.M.
TITLE Antisense modulation of inhibitor-kappa B kinase-alpha expression
JOURNAL Patent: US 5962673-A 19 05-OCT-1999;
Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3727 TATTTTATGTATTGTC 3742
Db 1 TATTTTATGTATTATC 16

RESULT 435
BD145035/c
LOCUS BD145035 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145035
VERSION BD145035.1 GI:27850793
KEYWORDS JP 2002119291-A/16.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 388 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 833 GATCAGCCACTCCGCA 848
Db 1 GATCAGCCACCCGCA 16
RESULT 427
AX757780
LOCUS AX757780 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1101 from Patent WO03040369.
ACCESSION AX757780
VERSION AX757780.1 GI:32252396
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 1101 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 821 GATCGGAGTTCAGATC 836
Db 1 GATCTGAGTTCAGATC 16
RESULT 428
AX757892/c
LOCUS AX757892 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1213 from Patent WO03040369.
ACCESSION AX757892
VERSION AX757892.1 GI:32252508
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,

apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 1213 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2803 AAAAAAACAATC 2818
Db 16 AAAAAAACAATC 1
RESULT 429
AX759064/c
LOCUS AX759064 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2385 from Patent WO03040369.
ACCESSION AX759064
VERSION AX759064.1 GI:32253680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 2385 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2422 AGCTTTCCATATGAT 2437
Db 17 AGCTTTCCATATGAT 2
RESULT 430
AX759785/c
LOCUS AX759785 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3106 from Patent WO03040369.
ACCESSION AX759785
VERSION AX759785.1 GI:32254401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3106 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 821 GATCGAGTTCAGATC 836
|||||
Db 1 GATCTGAGTTCAGATC 16

RESULT 422
AX737597/c
LOCUS AX737597 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3187 from Patent WO03025177.
ACCESSION AX737597
VERSION AX737597.1 GI:30516885
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 167 TGGCGAGAGAAGGATC 182
|||||
Db 16 TGGGAGAGAAGGATC 1

RESULT 423
AX738493/c
LOCUS AX738493 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4083 from Patent WO03025177.
ACCESSION AX738493
VERSION AX738493.1 GI:30517781
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 4083 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACATC 2818
|||||
Db 16 AAAAAAAAAAAGATC 1

RESULT 424
AX739553
LOCUS AX739553 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5143 from Patent WO03025177.
ACCESSION AX739553
VERSION AX739553.1 GI:30518850
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5143 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 821 GATCGAGTTCAGATC 836
|||||
Db 1 GATCTGAGTTCAGATC 16

RESULT 425
AX739596/c
LOCUS AX739596 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5186 from Patent WO03025177.
ACCESSION AX739596
VERSION AX739596.1 GI:30518893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5186 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 167 TGGCGAGAGAAGGATC 182
|||||
Db 16 TGAGGAGAGAAGGATC 1

RESULT 426
AX757067
LOCUS AX757067 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 388 from Patent WO03040369.
ACCESSION AX757067
VERSION AX757067.1 GI:32251683
KEYWORDS

<p>AUTHORS TITLE JOURNAL FEATURES</p> <p>source</p> <p>1. .17</p> <p>/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 3.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>QY 2138 CTACTGCTTTAGAAAT 2153 Db 17 CTACTGCTTTAGAGAT 2</p> <p>RESULT 420 AX736066/c LOCUS DEFINITION Sequence 1656 from Patent WO03025177. ACCESSION AX736066 VERSION AX736066.1 GI:30515343 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Telerman,A., Amson,R. and Tuijnder,M. TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments JOURNAL Patent: WO 03025177-A 1656 27-MAR-2003; Molecular Engines Laboratories (FR) FEATURES Location/Qualifiers source</p> <p>1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 3.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>QY 512 CCGGCTCTGTGGATC 527 Db 16 CCGGCTCTGTGGATC 1</p> <p>RESULT 421 AX736332 LOCUS DEFINITION Sequence 1922 from Patent WO03025177. ACCESSION AX736332 VERSION AX736332.1 GI:30515609 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Telerman,A., Amson,R. and Tuijnder,M. TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments JOURNAL Patent: WO 03025177-A 1922 27-MAR-2003; Molecular Engines Laboratories (FR) FEATURES Location/Qualifiers source</p> <p>1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 3.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>QY 1727 GATCCTTAATCCAA 1742 Db 1 GATCCTTAATCCAA 16</p> <p>RESULT 419 AX735212/c LOCUS DEFINITION Sequence 802 from Patent WO03025177. ACCESSION AX735212 VERSION AX735212.1 GI:30514489 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Telerman,A., Amson,R. and Tuijnder,M. TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments JOURNAL Patent: WO 03025177-A 802 27-MAR-2003; Molecular Engines Laboratories (FR) FEATURES Location/Qualifiers source</p> <p>1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 3.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p> <p>QY 1727 GATCCTTAATCCAA 1742 Db 1 GATCCTTAATCCAA 16</p> <p>RESULT 419 AX735212/c LOCUS DEFINITION Sequence 802 from Patent WO03025177. ACCESSION AX735212 VERSION AX735212.1 GI:30514489 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Telerman,A., Amson,R. and Tuijnder,M. 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TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis</p>
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Db          ||||| ||||| ||||| |||||
2 ATCTACCTGCCTGTA 17

RESULT 413
AX674166
LOCUS      AX674166          17 bp    DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 2611 from Patent WO03004526.
ACCESSION AX674166
VERSION    AX674166.1 GI:29332514
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL    Patent: WO 03004526-A 2611 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
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            1. .17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2798 ATGTGAAAAAAGAAA 2813
Db      ||||| ||||| ||||| |||||

RESULT 414
AX676082
LOCUS      AX676082          17 bp    DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 35 from Patent WO02059381.
ACCESSION AX676082
VERSION    AX676082.1 GI:29333766
KEYWORDS
SOURCE     Mus sp.
ORGANISM   Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Slaugenhaupt,S. and Gusella,J.F.
TITLE      Gene for identifying individuals with familial dysautonomia
JOURNAL    Patent: WO 02059381-A 35 01-AUG-2002;
            The General Hospital Corporation (US)
FEATURES   Location/Qualifiers
            source
            1. .17
                /organism="Mus sp."
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Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2745 TTTTCTTTTCTTAAAGGA 2760
Db      TTTTCTTTTCTTAAAGGA 17

RESULT 415
AX724450
LOCUS      AX724450          17 bp    DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2137 from Patent WO03025176.
ACCESSION AX724450
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VERSION
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 2137 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1. .17
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                /db_xref="taxon:10090"

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      821 GATCGGAGTTCAGATC 836
Db      ||||| ||||| ||||| |||||
            1 GATCTGAGTTCAGATC 16

RESULT 416
AX726113
LOCUS      AX726113          17 bp    DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 3800 from Patent WO03025176.
ACCESSION AX726113
VERSION    AX726113.1 GI:30505456
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 3800 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2566 ATCAGTGTTTTAAAAAAA 2581
Db      TTTTCTTTTCTTAAAGGA 17

RESULT 417
AX726611/c
LOCUS      AX726611/c          17 bp    DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 4298 from Patent WO03025176.
ACCESSION AX726611
VERSION    AX726611.1 GI:30505954
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
```

```

Unclassified.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 6425 20-MAY-2003;
FEATURES
Location/Qualifiers
1..17
/mol_type="unknown"
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Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 1 TCTCCTTCGACGTGAC 16

RESULT 409
AX214791
LOCUS
AX214791 17 bp RNA linear PAT 07-SEP-2001
DEFINITION
Sequence 233 from Patent WO0159103.
ACCESSION
AX214791
VERSION
AX214791.1 GI:15524834
KEYWORDS
synthetic construct
SOURCE
synthetic construct; artificial sequences.
ORGANISM
1
REFERENCE
1
AUTHORS
Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 233 16-AUG-2001; Blatt, Lawrence (US) ;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Chowrira, Bharat M. (US)
McSwiggen, James (US) ;
FEATURES
Location/Qualifiers
1..17
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/db_xref="taxon:32630"
/notes="Nucleic Acid"
source

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1587 AGACCCCTACTTCAGAA 1602
Db 2 AGATCCTACTTCAGAA 17

RESULT 410
AX227570
LOCUS
AX227570 17 bp RNA linear PAT 10-SEP-2001
DEFINITION
Sequence 942 from Patent WO0157206.
ACCESSION
AX227570
VERSION
AX227570.1 GI:15556711
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Fattaey,A.R., Jarvis,T., McSwiggen,J., Boehr,R.N. and Holman,P.S.
TITLE
Method and reagent for the inhibition of checkpoint kinase-1 (CHK
1) enzyme
JOURNAL
Patent: WO 0157206-A 942 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
1..17
/mol_type="synthetic construct"
/mol_type="unassigned RNA"
source

Unclassified.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 6425 20-MAY-2003;
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Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 1 TCTCCTTCGACGTGAC 16

RESULT 409
AX214791
LOCUS
AX214791 17 bp RNA linear PAT 07-SEP-2001
DEFINITION
Sequence 233 from Patent WO0159103.
ACCESSION
AX214791
VERSION
AX214791.1 GI:15524834
KEYWORDS
synthetic construct
SOURCE
synthetic construct; artificial sequences.
ORGANISM
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REFERENCE
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AUTHORS
Blatt,L., McSwiggen,J. and Chowrira,B.M.
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nogo gene expression
JOURNAL
Patent: WO 0159103-A 233 16-AUG-2001; Blatt, Lawrence (US) ;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Chowrira, Bharat M. (US)
McSwiggen, James (US) ;
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/db_xref="taxon:32630"
/notes="Nucleic Acid"
source

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1587 AGACCCCTACTTCAGAA 1602
Db 2 AGATCCTACTTCAGAA 17

RESULT 410
AX227570
LOCUS
AX227570 17 bp RNA linear PAT 10-SEP-2001
DEFINITION
Sequence 942 from Patent WO0157206.
ACCESSION
AX227570
VERSION
AX227570.1 GI:15556711
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS
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QY 1813 TCTCCTTCGACGTGAC 1828
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AX214791 17 bp RNA linear PAT 07-SEP-2001
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Sequence 233 from Patent WO0159103.
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SOURCE
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ORGANISM
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ACCESSION
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Location/Qualifiers
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Location/Qualifiers
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Query Match 0.3%; Score 14.4; DB 1; Length 17;
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RESULT 409
AX214791
LOCUS
AX214791 17 bp RNA linear PAT 07-SEP-2001
DEFINITION
Sequence 233 from Patent WO0159103.
ACCESSION
AX214791
VERSION
AX214791.1 GI:15524834
KEYWORDS
synthetic construct
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synthetic construct; artificial sequences.
ORGANISM
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REFERENCE
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AUTHORS
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McSwiggen, James (US) ;
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"
source

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Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1587 AGACCCCTACTTCAGAA 1602
Db 2 AGATCCTACTTCAGAA 17

RESULT 410
AX227570
LOCUS
AX227570 17 bp RNA linear PAT 10-SEP-2001
DEFINITION
Sequence 942 from Patent WO0157206.
ACCESSION
AX227570
VERSION
AX227570.1 GI:15556711
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS
Fattaey,A.R., Jarvis,T., McSwiggen,J., Boehr,R.N. and Holman,P.S.
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RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
1..17
/mol_type="synthetic construct"
/mol_type="unassigned RNA"
source

Unclassified.
REFERENCE
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TITLE
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JOURNAL
Patent: US 6566127-A 6425 20-MAY-2003;
FEATURES
Location/Qualifiers
1..17
/mol_type="unknown"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 1 TCTCCTTCGACGTGAC 16

RESULT 409
AX214791
LOCUS
AX214791 17 bp RNA linear PAT 07-SEP-2001
DEFINITION
Sequence 233 from Patent WO0159103.
ACCESSION
AX214791
VERSION
AX214791.1 GI:15524834
KEYWORDS
synthetic construct
SOURCE
synthetic
```


[illegible]

AUTHORS	Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE	Regulation of repressor genes using nucleic acid molecules
JOURNAL	Patent: JP 2002541795-A 6330 10-DEC-2002;
COMMENT	RIBOZYME PHARMACEUTICALS INC OS Eukaryote PN JP 2002541795-A/6330 PD 10-DEC-2002 PF 11-APR-2000 JP 2000611654 PR 12-APR-1999 US 60/129390 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC C12P21/02, PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC C12R1:91), PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC A61K37/02, PC (C12N5/00,C12R1:91) CC Regulation of repressor genes using nucleic acid molecules FH Key Location/Qualifiers FT source 1..17 Location/Qualifiers /organism='Eukaryote'.
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DEFINITION	Regulation of repressor genes using nucleic acid molecules.
ACCESSION	BD258538
VERSION	BD258538.1 GI:330689308
KEYWORDS	JP 2002541795-A/6331.
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE	Regulation of repressor genes using nucleic acid molecules
JOURNAL	Patent: JP 2002541795-A 6331 10-DEC-2002;
COMMENT	RIBOZYME PHARMACEUTICALS INC OS Eukaryote PN JP 2002541795-A/6331 PD 10-DEC-2002 PF 11-APR-2000 JP 2000611654 PR 12-APR-1999 US 60/129390 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC C12P21/02, PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC C12R1:91), PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC A61K37/02, PC (C12N5/00,C12R1:91) CC Regulation of repressor genes using nucleic acid molecules FH Key Location/Qualifiers FT source 1..17 Location/Qualifiers /organism='Eukaryote'.
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1 (bases 1 to 17)
REFERENCE
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3062 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/3062
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
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LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255585
VERSION BD255585.1 GI:33065355
KEYWORDS JP 2002541795-A/3378.
SOURCE unidentified
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REFERENCE
1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3378 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
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PN JP 2002541795-A/3378
PD 10-DEC-2002
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PR 12-APR-1999 US 60/129390
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AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3062 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
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RESULT 392
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LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255585
VERSION BD255585.1 GI:33065355
KEYWORDS JP 2002541795-A/3378.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3378 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3062 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
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DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD257465
VERSION BD257465.1 GI:33067235
KEYWORDS JP 2002541795-A/5258.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 5258 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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OS Eukaryote
PN JP 2002541795-A/5258
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TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3062 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258537
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REFERENCE 1 (bases 1 to 17)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
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ACCESSION AR029906
VERSION AR029906.1 GI:5943120
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 95 19-JAN-1999;
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ACCESSION AR047360
VERSION AR047360.1 GI:5968825
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 2153 06-OCT-1998;
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ACCESSION AR047366
VERSION AR047366.1 GI:5968831
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 2159 06-OCT-1998;
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DEFINITION Sequence 2161 from patent US 5817796.
ACCESSION AR047368
VERSION AR047368.1 GI:5968833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 2161 06-OCT-1998;
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DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255269
VERSION BD255269.1 GI:33065039
KEYWORDS JP 2002541795-A/3062.
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ORGANISM unidentified
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Db 16 CTCCTACAGACTGGAG 1
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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065915
VERSION BD065915.1 GI:22611518
KEYWORDS JP 2001511000-A/550.
SOURCE unidentified
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REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 550 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/550
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
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PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
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LOCUS BD066595 16 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066595
VERSION BD066595.1 GI:22612198
KEYWORDS JP 2001511000-A/1230.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.

TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1230 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1230
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066607
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KEYWORDS JP 2001511000-A/1242.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1242 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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PN JP 2001511000-A/1242
PD 07-AUG-2001
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ACCESSION AX030145
VERSION AX030145.1 GI:10190362
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 107 14-JUN-2000;
BIOGNOSTIK GES (DE)
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1. .16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2060 CCTGCTAATGTTGTTG 2075
Db 16 CCTGCTAATGTTATTG 1
RESULT 379
AX0316453/c
LOCUS AX0316453 16 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 94 from Patent EP1160319.
ACCESSION AX0316453
VERSION AX0316453.1 GI:17899626
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H., Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 94 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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/note="Description of unknown: unknown"
Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1851 CACCACAAGACAGA 1866
Db 16 CACCATAAGACAGA 1
RESULT 380
AX0316466/c
LOCUS AX0316466 16 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 107 from Patent EP1160319.
ACCESSION AX0316466
VERSION AX0316466.1 GI:17899639
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1

AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H., Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 107 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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/db_xref="taxon:32644"
/note="Description of unknown: unknown"
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Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2060 CCTGCTAATGTTGTTG 2075
Db 16 CCTGCTAATGTTATTG 1
RESULT 381
AX0419943/c
LOCUS AX0419943 16 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 280 from Patent WO0198537.
ACCESSION AX0419943
VERSION AX0419943.1 GI:21524310
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 280 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
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1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 65 TGGGAGAGAAAGACAG 80
Db 16 TGGGAGAGAAACACAG 1
RESULT 382
BD065908/c
LOCUS BD065908 16 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065908
VERSION BD065908.1 GI:22611511
KEYWORDS JP 2001511000-A/543.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 543 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/543
PD 07-AUG-2001
PR 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH

AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 543 05-AUG-1998;
BIOGNOSTIK GES (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2078 CTCTACAGACTGGAG 2093 16 bp DNA linear PAT 22-JAN-2000
Db 16 CTCTACAGACTGGAG 1

RESULT 374
LOCUS A90369/c
DEFINITION Sequence 550 from Patent EP0856579.
ACCESSION A90369
VERSION A90369.1 GI:6738883
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 550 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2245 CTAACCTCTCTGCTGG 2260 16 bp DNA linear PAT 20-DEC-2002
Db 16 CCAACTCTCTGCTGG 1

RESULT 375
LOCUS AR232837/c
DEFINITION Sequence 94 from patent US 6455689.
ACCESSION AR232837
VERSION AR232837.1 GI:27275175
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 94 24-SEP-2002;
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source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1851 CACCACAAAGACAGGA 1866 16 bp DNA linear PAT 20-DEC-2002
Db 16 CACCATAAAGACAGGA 1

RESULT 376
LOCUS AR232850/c
DEFINITION Sequence 107 from patent US 6455689.
ACCESSION AR232850
VERSION AR232850.1 GI:27275188
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 107 24-SEP-2002;
FEATURES
source
1. .16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2060 CCTGCTAAATGTTGTTG 2075 16 bp DNA linear PAT 16-SEP-2000
Db 16 CCTGCTAAATGTTATTG 1

RESULT 377
LOCUS AX030132/c
DEFINITION Sequence 94 from Patent EP1008649.
ACCESSION AX030132
VERSION AX030132.1 GI:10190349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE
JOURNAL Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
Patent: EP 1008649-A 94 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
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1. .16
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/db_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1851 CACCACAAAGACAGGA 1866 16 bp DNA linear PAT 16-SEP-2000
Db 16 CACCATAAAGACAGGA 1

RESULT 378
LOCUS AX030145/c
DEFINITION Sequence 107 from Patent EP1008649.

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Query Match
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  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2060 CCTGCTAATGTTGTTG 2075
Db 16 CCTGCTAATGTTATTG 1

RESULT 369
A88395/c
LOCUS A88395 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 543 from Patent WO9833904.
ACCESSION A88395
VERSION A88395.1 GI:6736965
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 543 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
  source
    Location/Qualifiers
      1..16
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.3%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2078 CTCTACAGACTGGAG 2093
Db 16 CTCTACAGACTTGAG 1

RESULT 370
A88402/c
LOCUS A88402 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 550 from Patent WO9833904.
ACCESSION A88402
VERSION A88402.1 GI:6736972
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 550 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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Query Match
  Best Local Similarity 0.3%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2245 CTAACCTTCTGCTGG 2260
Db 16 CCAACTTCTGCTGTTG 1
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RESULT 371
A89082/c
LOCUS A89082 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1230 from Patent WO9833904.
ACCESSION A89082
VERSION A89082.1 GI:6737652
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 1230 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"
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Query Match
  Best Local Similarity 0.3%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1851 CACCACAAAGACAGGA 1866
Db 16 CACCATAAGACAGGA 1

RESULT 372
A89094/c
LOCUS A89094 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1242 from Patent WO9833904.
ACCESSION A89094
VERSION A89094.1 GI:6737664
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 1242 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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Query Match
  Best Local Similarity 0.3%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2060 CCTGCTAATGTTGTTG 2075
Db 16 CCTGCTAATGTTATTG 1

RESULT 373
A90362/c
LOCUS A90362 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 543 from Patent EP0856579.
ACCESSION A90362
VERSION A90362.1 GI:6738876
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
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Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2914 CTGCAGTGGTGCCCTCC 2931
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Db 18 CTGCAGTAGTGCCCAACC 1

RESULT 365
BD107508/c
LOCUS BD107508 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107508
VERSION BD107508.1 GI:23202326
KEYWORDS JP 200200275-A/17,
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 200200275-A 17 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 200200275-A/17
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
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1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
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Db 18 ATATATATTTTCTTTC 1

RESULT 366
ASE250931/c
LOCUS ASE250931 18 bp RNA linear SYN 17-NOV-1999
DEFINITION Artificial oligonucleotide antisense primer sequence for Homo
sapiens beta3-adrenoceptor.
ACCESSION AJ250931
VERSION AJ250931.1 GI:6453302
KEYWORDS beta3-adrenoceptor; oligonucleotide; primer.
SOURCE synthetic construct
ORGANISM synthetic construct; artificial sequences.
REFERENCE 1
AUTHORS Bardou,M.Y. and Loustalot,C.
TITLE Evidence for a role of beta3-adrenoceptor in inhibition of human

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term myometrium spontaneous contractions
Unpublished
REFERENCE 2 (bases 1 to 18)
AUTHORS Bardou,M.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-1999) Bardou M., Lppce, Faculty of Medicine of
Dijon, 7, bd Jeanne d'Arc BP 87900, 21079 Dijon cedex, FRANCE
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="other RNA"
/db_xref="taxon:32630"
/notes="synthetic oligonucleotide"
misc_feature complement(1..18)
/notes="PCR antisense primer for Homo sapiens
beta3-adrenoceptor"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 723 AGCCCGCGCGAGCCCGG 740
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Db 18 AGCCGAGCGAGCCCGG 1

RESULT 367
A40557/c
LOCUS A40557 16 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 94 from Patent WO9425578.
ACCESSION A40557
VERSION A40557.1 GI:2296592
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1851 CACCACAAAGACAGGA 1866
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Db 16 CACCATAAGACAGGA 1

RESULT 368
A40570/c
LOCUS A40570 16 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 107 from Patent WO9425578.
ACCESSION A40570
VERSION A40570.1 GI:2296605
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS
TITLE
JOURNAL

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/db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2375 ACCATGACCATCTCTCA 2392
DB 18 ACCTTAACCATCTCTCA 1

RESULT 362
BD066632/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066632
VERSION     BD066632.1 GI:22612235
KEYWORDS   JP 2001511000-A/1267.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 1267 07-AUG-2001;
          BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
PN JP 2001511000-A/1267
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
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   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTCTTAC 1179
DB 18 ATATATATTTTCTTCTTAC 1

RESULT 364
BD104178/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION  BD104178
VERSION     BD104178.1 GI:22649752
KEYWORDS   WO 0192572-A/282.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
          Nishida,M.
TITLE      Kit and method for determining HLA type
JOURNAL    Patent: WO 0192572-A 282 06-DEC-2001;
          NISHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
          KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
          NISHIDA
COMMENT    OS Artificial Sequence
PN WO 0192572-A/282
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
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   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      0.3%; Score 14.8; DB 1; Length 18;

/db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2439 GTCAAGTCTTGTAATGC 2456
DB 18 GTAAAGTCTTGCAATGC 1

RESULT 363
BD072881/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
          and method for analyzing data obtained by that method.
ACCESSION  BD072881
VERSION     BD072881.1 GI:22618484
KEYWORDS   JP 2001286300-A/19.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
          Yokomaki,F., Koyama,O. and Furusho,K.
TITLE      Method for assaying nucleic acid, nucleic acid probe used therefor,
          and method for analyzing data obtained by that method
JOURNAL    Patent: JP 2001286300-A 19 16-OCT-2001;
          JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
          NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
          AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT    OS Artificial Sequence
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SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 18)
AUTHORS     Schlingensiepen,K.H. and Brysch,W.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: JP 2001511000-A 1221 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS Unknown
            PN JP 2001511000-A/1221
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC C12N15/11,C07H21/04,A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source 1..18
            FT /organism='Unknown'.

FEATURES    source
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            /db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGACGTATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 359
BD066597/c
LOCUS      18 bp DNA linear
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066597
VERSION    1 GI:22612200
KEYWORDS   JP 2001511000-A/1232.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Schlingensiepen,K.H. and Brysch,W.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: JP 2001511000-A 1232 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS Unknown
            PN JP 2001511000-A/1232
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC C12N15/11,C07H21/04,A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source 1..18
            FT /organism='Unknown'.

FEATURES    source
            Location/Qualifiers
            1..18
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACATGCCC 1897
Db 18 AATAAGCTTACACTGTCC 1

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RESULT 360
BD066615/c
LOCUS      18 bp DNA linear
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066615
VERSION    1 GI:22612218
KEYWORDS   JP 2001511000-A/1250.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Schlingensiepen,K.H. and Brysch,W.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: JP 2001511000-A 1250 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS Unknown
            PN JP 2001511000-A/1250
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC C12N15/11,C07H21/04,A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source 1..18
            FT /organism='Unknown'.

FEATURES    source
            Location/Qualifiers
            1..18
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2175 CGCCCTCTTTACATTGAT 2192
Db 18 CGTCCACTTTACATTGAT 1

RESULT 361
BD066628/c
LOCUS      18 bp DNA linear
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066628
VERSION    1 GI:22612231
KEYWORDS   JP 2001511000-A/1263.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Schlingensiepen,K.H. and Brysch,W.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: JP 2001511000-A 1263 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS Unknown
            PN JP 2001511000-A/1263
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC C12N15/11,C07H21/04,A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source 1..18
            FT /organism='Unknown'.

FEATURES    source
            Location/Qualifiers
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            /organism="unidentified"
            /mol_type="genomic DNA"

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/db_xref="taxon:32630"
/note="Detection oligonucleotide for MSH4"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2808 AAAAAACATCAAAACAA 2825
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Db 18 AAAAACACCAAAACAA 1
RESULT 355
BD064848 18 bp DNA linear PAT 27-AUG-2002
LOCUS Method for detecting the extent of binding of transcriptional
DEFINITION regulatory protein to oligoDNA.
ACCESSION BD064848
VERSION BD064848.1 GI:22610451
KEYWORDS JP 2001275678-A/60.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and Nishikawa,K.
TITLE Method for detecting the extent of binding of transcriptional regulatory protein to oligoDNA
JOURNAL Patent: JP 2001275678-A 60 09-OCT-2001;
SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT OS Artificial Sequence
PN JP 2001275678-A/60
PD 09-OCT-2001
PF 31-MAR-2000 JP 2000096306
PI TOSHIOHKO KISHIMOTO, SHINICHIRO NIWA, YUKO MORI, SACHIYO MI
MINAKI, REI FUKUSHIMA,
PI KAZUKO NISHIKAWA
PC C12N15/09, C12N5/10, C12Q1/00, C12Q1/68, C12N15/00, C12N5/00 CC
SYNTHETIC DNA
FH Key
FT source 1..18
FT Location/Qualifiers
/organism='Artificial Sequence'.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 573 GGGGGCGATCTGCCTCCC 590
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Db 1 GGGGGCGAGCTGCGTCCC 18
RESULT 356
BD066574/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066574
ACCESSION BD066574
VERSION BD066574.1 GI:22612177
KEYWORDS JP 2001511000-A/1209.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingsiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1209 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1209
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1636 ATGCTTCGAATCTGGTGA 1653
||||| |||||
Db 18 ATGCTTCCAATTGGTGA 1
RESULT 358
BD066586/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066586
ACCESSION BD066586
VERSION BD066586.1 GI:22612189
KEYWORDS JP 2001511000-A/1221.
COMMENT OS Unknown

PN JP 2001511000-A/1209
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source 1..18
FT Location/Qualifiers
/organism='Unknown'.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1527 TATAAAATCGACATGCCG 1544
||||| |||||
Db 18 TACAAATAGACATGCCG 1
RESULT 357
BD066580/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066580
ACCESSION BD066580
VERSION BD066580.1 GI:22612183
KEYWORDS JP 2001511000-A/1215.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingsiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1215 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1215
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source 1..18
FT Location/Qualifiers
/organism='Unknown'.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1636 ATGCTTCGAATCTGGTGA 1653
||||| |||||
Db 18 ATGCTTCCAATTGGTGA 1
RESULT 358
BD066586/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066586
ACCESSION BD066586
VERSION BD066586.1 GI:22612189
KEYWORDS JP 2001511000-A/1221.

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544
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Db 18 TACAAATAGACATGCCG 1

RESULT 346
AX316431/c
LOCUS AX316431 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 72 from Patent EP1160319.
ACCESSION AX316431
VERSION AX316431.1 GI:17899604
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 72 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544
||| ||||| ||||| |||||
Db 18 TACAAATAGACATGCCG 1

RESULT 347
AX316438/c
LOCUS AX316438 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 79 from Patent EP1160319.
ACCESSION AX316438
VERSION AX316438.1 GI:17899611
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 79 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGGTGA 1653
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Db 18 ATGCTTCGAATTTGGTGA 1

RESULT 348
AX316444/c
LOCUS AX316444 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 85 from Patent EP1160319.
ACCESSION AX316444
VERSION AX316444.1 GI:17899617
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 85 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACGTATCAGA 1728
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Db 18 GGATTGAGCTATATCAGA 1

RESULT 349
AX316455/c
LOCUS AX316455 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 96 from Patent EP1160319.
ACCESSION AX316455
VERSION AX316455.1 GI:17899628
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 96 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACACTGCC 1897
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Db 18 AATAAGCTTACACTGTC 1

RESULT 350
AX316474/c
LOCUS AX316474 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 115 from Patent EP1160319.
ACCESSION AX316474
VERSION AX316474.1 GI:17899647
KEYWORDS .

TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 131 14-JUN-2000;
BIOGNOSTIK GES (DE)

FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2439 GTCAAGTCTTGTAATGC 2456
Db 18 GTAAAGTCTTGCAATGC 1

RESULT 342
AX047272
LOCUS AX047272 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 22 from Patent WO0068422.
ACCESSION AX047272
VERSION AX047272.1 GI:11876552
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Muehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M., Gumbiowski, K. and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 22 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCACCGCCCC 990
Db 1 CCCCCCCCCCCCCCCCC 18

RESULT 343
AX047274/c
LOCUS AX047274 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 24 from Patent WO0068422.
ACCESSION AX047274
VERSION AX047274.1 GI:11876554
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Muehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M., Gumbiowski, K. and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 24 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCACCGCCCC 990
Db 18 CCCCCCCCCCCCCCCCC 1

RESULT 344
AX191970/c
LOCUS AX191970 18 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 122 from Patent WO0149833.
ACCESSION AX191970
VERSION AX191970.1 GI:15210119
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Lewis, N.G., Davin, L.B., Dinkova-Kostova, A.T., Fujita, M., Gang, D.R., Ford, J.D. and Sarkanen, S.
TITLE Recombinant pinorexinol/laricresinol reductase, recombinant dirigent protein, and methods of use
JOURNAL Patent: WO 0149833-A 122 12-JUL-2001;
Washington State University Research Foundation (US) ; REGENTS OF THE UNIVERSITY OF MINNESOTA (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
misc_feature 1. .18
/note="Linker primer"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAAACTCGAG 1

RESULT 345
AX252494/c
LOCUS AX252494 18 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 4 from Patent WO0168146.
ACCESSION AX252494
VERSION AX252494.1 GI:15985765
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlingensiepen, K.H. and Schlingensiepen, R.
TITLE Mixture comprising an inhibitor or suppressor of a gene and a molecule binding to an expression product of that gene
JOURNAL Patent: WO 0168146-A 4 20-SEP-2001;
Biognostik Gesellschaft fuer biomolekulare Diagnostik mbH (DE)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;

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RESULT 337
AX030123/c
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 85 from Patent EP1008649.
ACCESSION  AX030123
VERSION     AX030123.1  GI:10190340
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 85 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1711 GGATTGAACTGATCAGA 1728
Db 18 GGATTGAGCTATCAGA 1
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 96 from Patent EP1008649.
ACCESSION  AX030134
VERSION     AX030134.1  GI:10190351
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 96 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1880 AATAAGTTTACACTGCC 1897
Db 18 AATAAGCTTACACTGTCC 1
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 115 from Patent EP1008649.
ACCESSION  AX030153
VERSION     AX030153.1  GI:10190370
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 115 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2175 GGCCTCTTTTACATTGAT 2192
Db 18 CGTCCACTTTACATTGAT 1
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 128 from Patent EP1008649.
ACCESSION  AX030166
VERSION     AX030166.1  GI:10190383
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 128 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2375 ACCACTGACCATTTCTCTA 2392
Db 18 ACCTCTAACCATTCTCTA 1
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 131 from Patent EP1008649.
ACCESSION  AX030169
VERSION     AX030169.1  GI:10190386
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
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HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGTTGA 1653
18 ATGCTTCCAATTGTGTA 1

RESULT 333
AX008983/c
LOCUS AX008983 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 16 from Patent WO9963975.
ACCESSION AX008983
VERSION AX008983.1 GI:9996357
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 16 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACTGTATCAGA 1728
18 GGATTGACTATATCAGA 1

RESULT 334
AX009032/c
LOCUS AX009032 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 65 from Patent WO9963975.
ACCESSION AX009032
VERSION AX009032.1 GI:9996406
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 65 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1462 CAAGCCGAGGCGGCGG 1479
18 CGAGCCGAGGCGGCGG 1

RESULT 335
AX030110/c
LOCUS AX030110 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 72 from Patent EP1008649.
ACCESSION AX030110
VERSION AX030110.1 GI:10190327
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 72 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATTAATCGACATGCGG 1544
18 TACAAATAGACATGCGG 1

RESULT 336
AX030117/c
LOCUS AX030117 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 79 from Patent EP1008649.
ACCESSION AX030117
VERSION AX030117.1 GI:10190334
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 79 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGTTGA 1653
18 ATGCTTCCAATTGTGTA 1
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Qy 973 CCCCCCCCCCCCCCCCCC 990
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 18)
TITLE Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
JOURNAL Method for determining a concentration of target nucleic acid
FEATURES molecules, nucleic acid probes for the method, and method for
SOURCE analyzing data obtained by the method
PATENT: US 6699661-A 20 02-MAR-2004;
LOCATION/Qualifiers
1. .18
/organism="unknown"
/mol_type="genomic DNA"

RESULT 328
AR264936/c
LOCUS 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 20 from patent US 6492121.
ACCESSION AR264936
VERSION AR264936.1 GI:29693323
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 18)
TITLE Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
JOURNAL Method for determining a concentration of target nucleic acid
FEATURES molecules, nucleic acid probes for the method, and method for
SOURCE analyzing data obtained by the method
PATENT: US 6492121-A 20 10-DEC-2002;
LOCATION/Qualifiers
1. .18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTTAC 1179
Db 18 ATATATATTTTCTTTC 1

RESULT 331
AX008976/c
LOCUS 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 9 from Patent WO9963975.
ACCESSION AX008976
VERSION AX008976.1 GI:9996350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS 1
TITLE Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
JOURNAL A method for stimulating the immune system
PATENT: WO 9963975-A 9 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
SOURCE 1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATCGCG 1544
Db 18 TACAAAATAGACATCGCG 1

RESULT 332
AX008980/c
LOCUS 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 13 from Patent WO9963975.
ACCESSION AX008980
VERSION AX008980.1 GI:9996354
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS 1
TITLE Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
JOURNAL A method for stimulating the immune system
PATENT: WO 9963975-A 13 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
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Db 18 AATAAGCTTACACTGCC 1
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RESULT 323
AR232858/c
LOCUS AR232858 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 115 from patent US 6455689.
ACCESSION AR232858
VERSION AR232858.1 GI:27275196
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 115 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2175 CGCCCTCTTACATTGAT 2192
||| ||||| ||||| ||||| |||||
Db 18 CGTCCACTTTACATTGAT 1
RESULT 324
AR232871/c
LOCUS AR232871 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 128 from patent US 6455689.
ACCESSION AR232871
VERSION AR232871.1 GI:27275209
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 128 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2375 ACCACTGACCATTTCTTA 2392
||| ||||| ||||| ||||| |||||
Db 18 ACCTTAACCATTTCTTA 1
RESULT 325
AR232875/c
LOCUS AR232875 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 132 from patent US 6455689.
ACCESSION AR232875
VERSION AR232875.1 GI:27275213
KEYWORDS
SOURCE
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 132 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2439 GTCAAGCTTTGTAATGC 2456
||| ||||| ||||| ||||| |||||
Db 18 GTAAAGCTTTGCAATGC 1
RESULT 326
AR262417
LOCUS AR262417 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 42 from patent US 6323185.
ACCESSION AR262417
VERSION AR262417.1 GI:28073848
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Fennewald,S., Zendequi,J.G., Ojwang,J.O. and Hogan,M.E.
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
JOURNAL Patent: US 6323185-A 42 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 973 CCCCCCCCCACCCGCCCCC 990
||||| ||||| ||||| ||||| |||||
Db 1 CCCCCCCCCCCCCCCCCC 18
RESULT 327
AR262418
LOCUS AR262418 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 43 from patent US 6323185.
ACCESSION AR262418
VERSION AR262418.1 GI:28073849
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Fennewald,S., Zendequi,J.G., Ojwang,J.O. and Hogan,M.E.
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
JOURNAL Patent: US 6323185-A 43 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 318
AR200286 LOCUS 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 43 from patent US 6355785.
ACCESSION AR200286
VERSION AR200286.1 GI:20250360
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 973 CCCCCCCCCACCCGCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 319
AR232815/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 72 from patent US 6455689.
ACCESSION AR232815
VERSION AR232815.1 GI:27275153
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1527 TATAAATCGACATGCCG 1544
Db 18 TACAAATAGACATGCCG 1

RESULT 320
AR232822/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 79 from patent US 6455689.
ACCESSION AR232822
VERSION AR232822.1 GI:27275160
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1711 GGATTGAACGTATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 322
AR232839/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 96 from patent US 6455689.
ACCESSION AR232839
VERSION AR232839.1 GI:27275177
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1880 AATAAGTTTACTGCCCC 1897
Db 1880 AATAAGTTTACTGCCCC 1897
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TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 79 24-SEP-2002;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1636 ATGCTTCGAATCTCGTGA 1653
Db 18 ATGCTTCCAATTTCGTGA 1

RESULT 321
AR232828/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 85 from patent US 6455689.
ACCESSION AR232828
VERSION AR232828.1 GI:27275166
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1711 GGATTGAACGTATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 322
AR232839/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 96 from patent US 6455689.
ACCESSION AR232839
VERSION AR232839.1 GI:27275177
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1880 AATAAGTTTACTGCCCC 1897
Db 1880 AATAAGTTTACTGCCCC 1897
```


AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
 TITLE Mammal-derived tissue specific physiologically active protein
 JOURNAL Patent: JP 2000037190-A 18 08-FEB-2000;
 JAPAN TOBACCO INC
 COMMENT OS Artificial Sequence
 PN JP 2000037190-A/18
 PD 08-FEB-2000
 PF 23-JUL-1998 JP 1998225228
 PR JUN NISHIU YUSUKE NAKAMURA TOSHIHIRO TANAKA
 PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
 C12N15/02,
 PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
 PC C12N15/00,
 PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
 CC
 FH Key Location/Qualifiers
 FT primer_bind (1)..(18).
 FEATURES
 source 1..18
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2801 TGAATAAAAAAAAAACATC 2818
 Db 18 TGAATAAAAAAAAAAAAAAC 1
 RESULT 314
 I27810
 LOCUS 18 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 42 from patent US 5567604.
 ACCESSION I27810
 VERSION I27810.1 GI:1818586
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Rando,R.F., Fennelwald,S., Zendequi,J.G. and Ojwang,J.O.
 TITLE Anti-viral guanosine-rich oligonucleotides
 JOURNAL Patent: US 5567604-A 42 22-OCT-1996;
 FEATURES
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 973 CCCCCCCCCCGCCCC 990
 Db 1 CCCCCCCCCCGCCCCC 18
 RESULT 315
 I27811
 LOCUS 18 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 43 from patent US 5567604.
 ACCESSION I27811
 VERSION I27811.1 GI:1818587
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Rando,R.F., Fennelwald,S., Zendequi,J.G. and Ojwang,J.O.

TITLE Anti-viral guanosine-rich oligonucleotides
 JOURNAL Patent: US 5567604-A 43 22-OCT-1996;
 FEATURES
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 973 CCCCCCCCCCGCCCC 990
 Db 1 CCCCCCCCCCGCCCCC 18
 RESULT 316
 I33107/c
 LOCUS 18 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 21 from patent US 5589585.
 ACCESSION I33107
 VERSION I33107.1 GI:1823898
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Mabilat,C. and Pechere,J.-C.
 TITLE DNA fragments, probes and amplification primers of the 65 kd
 antigen of mycobacteria
 JOURNAL Patent: US 5589585-A 21 31-DEC-1996;
 FEATURES
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 359 CTTGGCCCGCTGGAGCA 376
 Db 18 CTTGGCCGACTTGAGCA 1
 RESULT 317
 AR200285
 LOCUS 18 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 42 from patent US 6355785.
 ACCESSION AR200285
 VERSION AR200285.1 GI:20250359
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Rando,R.F., Fennelwald,S., Zendequi,J.G., Ojwang,J.O., Hogan,M.E.,
 Pommier,Y. and Mazumder,A.
 TITLE Guanosine-rich oligonucleotide integrase inhibitors
 JOURNAL Patent: US 6355785-A 42 12-MAR-2002;
 FEATURES
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 973 CCCCCCCCCCGCCCC 990
 Db 1 CCCCCCCCCCGCCCCC 18


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labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
FEATURES
source
1..18
/organism="Artificial Sequence".
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTTAC 1179
Db 18 ATATATATTTTCTTTC 1

RESULT 307
BD234905/c
LOCUS BD234905 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234905
VERSION BD234905.1 GI:33044675
KEYWORDS JP 2002517434-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
AUTHORS A method for stimulating the immune system
TITLE Patent: JP 2002517434-A 9 18-JUN-2002;
JOURNAL BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/9
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
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source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGTGA 1653
Db 18 ATGCTTCGAATCTGTGA 1

RESULT 309
BD234912/c
LOCUS BD234912 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234912
VERSION BD234912.1 GI:33044682
KEYWORDS JP 2002517434-A/16.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
AUTHORS A method for stimulating the immune system
TITLE Patent: JP 2002517434-A 16 18-JUN-2002;
JOURNAL BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/16
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATGACATGCCG 1544
Db 18 TACAAAATGACATGCCG 1

RESULT 308
BD234909/c
LOCUS BD234909 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234909
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RESULT 303
LOCUS AR168816 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 42 from patent US 6288042.
ACCESSION AR168816
VERSION AR168816.1 GI:17904932
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 6288042-A 42 11-SEP-2001;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 973 CCCCCCCCCCGCCCC 990
Db 1 CCCCCCCCCCGCCCC 18

RESULT 304
LOCUS AR168817 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 43 from patent US 6288042.
ACCESSION AR168817
VERSION AR168817.1 GI:17904933
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 6288042-A 43 11-SEP-2001;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 973 CCCCCCCCCCGCCCC 990
Db 1 CCCCCCCCCCGCCCC 18

RESULT 305
LOCUS BD145040/c 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD145040
VERSION BD145040.1 GI:27850798
KEYWORDS JP 2002119291-A/21.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,

and method for analyzing data obtained by that method
Patent: JP 2002119291-A 21 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/21
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/PC
G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
G01N1/28,
G01N1/28,
The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH key Location/Qualifiers
1..18
FT source /organism='Artificial Sequence'.
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1162 ATATATATATTTTCTTAC 1179
Db 18 ATATATATATTTTCTTTC 1

RESULT 306
LOCUS BD166040/c 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.
ACCESSION BD166040
VERSION BD166040.1 GI:27871852
KEYWORDS JP 2002191372-A/20.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method
Patent: JP 2002191372-A 20 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/20
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566,PC
C12N15/00
The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC

Db 18 GTAAAGCTTGGCAATGC 1
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RESULT 298
AR034902 AR034902 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 24 from patent US 5869643.
DEFINITION AR034902
ACCESSION AR034902
VERSION AR034902.1 GI:5950507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a tightly packed bed
JOURNAL Patent: US 5869643-A 24 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 973 CCCCCCCCACCCGCCCC 990
|| |||||
Db 1 CCCCCCCCACCCGCCCC 18
|| |||||
RESULT 299
AR056298/c AR056298 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 21 from patent US 5849901.
DEFINITION AR056298
ACCESSION AR056298
VERSION AR056298.1 GI:5996514
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments of mycobacteria, amplification primers hybridization probes, reagents and method for the detection of mycobacteria
JOURNAL Patent: US 5849901-A 21 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 359 CCTTGGCGCGCTGGAGCA 376
|| |||||
Db 18 CCTTGGCGCGACTTGAGCA 1
|| |||||
RESULT 300
AR084526 AR084526 18 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 15 from patent US 5981185.
DEFINITION AR084526
ACCESSION AR084526
VERSION AR084526.1 GI:10011297
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)

AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 15 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2666 ACAGCAACACACACCA 2683
|| |||||
Db 1 ACAACAACACACACCA 18
|| |||||
RESULT 301
AR084527 AR084527 18 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 16 from patent US 5981185.
DEFINITION AR084527
ACCESSION AR084527
VERSION AR084527.1 GI:10011298
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 16 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2667 CAGCAACACACACCA 2684
|| |||||
Db 1 CAACACACACACACAA 18
|| |||||
RESULT 302
AR144877/c AR144877 18 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 122 from patent US 6210942.
DEFINITION AR144877
ACCESSION AR144877
VERSION AR144877.1 GI:15106744
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lewis,N.G., Davin,D.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R., Sarkanen,S. and Ford,J.D.
TITLE Recombinant pinoreisnol/lariciresinol reductase, recombinant dirigent protein, and methods of use
JOURNAL Patent: US 6210942-A 122 03-APR-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2577 AAAAAAAAAAATGGAG 2594
|| |||||
Db 18 AAAAAAAAAAATCGAG 1
|| |||||

RESULT 293
A89073/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1221 from Patent WO9833904.
ACCESSION A89073
VERSION A89073.1 GI:6737643
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1221 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACTGTATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 294
A89084/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1232 from Patent WO9833904.
ACCESSION A89084
VERSION A89084.1 GI:6737654
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1232 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACACTGCC 1897
Db 18 AATAAGCTTACACTGTCC 1

RESULT 295
A89102/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1250 from Patent WO9833904.
ACCESSION A89102
VERSION A89102.1 GI:6737672
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

JOURNAL Patent: WO 9833904-A 1250 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2175 GGCCTCTTTTACATTGAT 2192
Db 18 CGTCCACTTTTACATTGAT 1

RESULT 296
A89115/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1263 from Patent WO9833904.
ACCESSION A89115
VERSION A89115.1 GI:6737685
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1263 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2375 ACCACTGACCATTTCTCTA 2392
Db 18 ACCTCTAACCATTCTCTA 1

RESULT 297
A89119/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1267 from Patent WO9833904.
ACCESSION A89119
VERSION A89119.1 GI:6737689
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1267 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2439 GTCAAGTCTTGTAAATGC 2456


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FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 359 CCTTGGCGCGCTGGAGCA 376
Db 18 CCTTGGCGCGACTTGAGCA 1

RESULT 284
A40535/c
LOCUS A40535 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 72 from Patent WO9425578.
ACCESSION A40535
VERSION A40535.1 GI:2296570
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
PATENT: WO 9425578-A 72 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544
Db 18 TACAAAATAGACATGCCG 1

RESULT 285
A40542/c
LOCUS A40542 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 79 from Patent WO9425578.
ACCESSION A40542
VERSION A40542.1 GI:2296577
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
PATENT: WO 9425578-A 79 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCCAATCTGGTGA 1653
Db 18 ATGCTTCCAATTTGGTGA 1

RESULT 286
A40548/c
LOCUS A40548 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 85 from Patent WO9425578.
ACCESSION A40548
VERSION A40548.1 GI:2296583
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
PATENT: WO 9425578-A 85 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACTGTATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 287
A40559/c
LOCUS A40559 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 96 from Patent WO9425578.
ACCESSION A40559
VERSION A40559.1 GI:2296594
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
PATENT: WO 9425578-A 96 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
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    Location/Qualifiers
      1..18
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACTGCGCC 1897
Db 18 AATAAGCTTACTGCTCC 1

RESULT 288
A40578/c
LOCUS A40578 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 115 from Patent WO9425578.
ACCESSION A40578
VERSION A40578.1 GI:2296613
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telesman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 743 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3922 CTGTGTCACACAGA 3936
Db 17 CTGTGTCACACAGA 3
RESULT 280
E32456/c
LOCUS E32456 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32456
VERSION E32456.1 GI:13018692
KEYWORDS JP 2000037190-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 16 08-FEB-2000;
JAPAN TORACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/16
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT primer_bind (1)..(18).
Location/Qualifiers
source
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2574 TTAATAAAAAAAAAA 2588
Db 18 TTAATAAAAAAAAAA 4
RESULT 281
A28690 18 bp RNA linear PAT 04-JUN-1995
LOCUS

DEFINITION Oligonucleotide 19 (comp.).
ACCESSION A28690
VERSION A28690.1 GI:1248729
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
JOURNAL Patent: WO 9014090-A 18 29-NOV-1990;
FEATURES Location/Qualifiers
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 970 ATTCCCCCCCCACCCCGC 987
Db 1 ATTCCCCCCCCCCCCCCC 18
RESULT 282
A28695 18 bp RNA linear PAT 04-JUN-1995
LOCUS A28695
DEFINITION Oligonucleotide 17 (comp.).
ACCESSION A28695
VERSION A28695.1 GI:1248734
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
JOURNAL Patent: WO 9014090-A 23 29-NOV-1990;
FEATURES Location/Qualifiers
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 970 ATTCCCCCCCCACCCCGC 987
Db 1 ATTCCCCCCCCCCCCCCC 18
RESULT 283
A36755/c 18 bp DNA linear PAT 05-MAR-1997
LOCUS A36755
DEFINITION Sequence 21 from Patent EP0594023.
ACCESSION A36755
VERSION A36755.1 GI:2294022
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mabilat,C. and Pechere,J.
TITLE Mycobacteria DNA fragments, amplification primers, hybridization
probes, reagents and detection process of mycobacteria
JOURNAL Patent: EP 0584023-A 21 23-FEB-1994;
BIO MERIEUX (FR)
COMMENT Other publication CA 2103933 940213
Other publication FR 2694754 940218.

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macromolecular structures
JOURNAL Patent: US 5571677-A 5 05-NOV-1996;
FEATURES Location/Qualifiers
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1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 276
BD065904/c
LOCUS BD065904 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065904
VERSION BD065904.1 GI:22611507
KEYWORDS JP 2001511000-A/539.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 539 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/539
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1. .15
/organism='Unknown'

FEATURES
source
1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1971 GGTATTGATGCACC 1985
Db 15 GGTATTGATGCACC 1

RESULT 278
BD065953/c
LOCUS BD065953 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065953
VERSION BD065953.1 GI:22611556
KEYWORDS JP 2001511000-A/588.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 588 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/588
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1. .15
/organism='Unknown'

FEATURES
source
1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1968 GCAGGTATTGATGC 1982
Db 15 GCAGGTATTGATGC 1

RESULT 277
BD065905/c
LOCUS BD065905 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065905
VERSION BD065905.1 GI:22611508
KEYWORDS JP 2001511000-A/540.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 540 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/540
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1. .15
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FEATURES
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1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1919 TAATAATTACATCAT 1933
Db 15 TAATAATTACATCAT 1

RESULT 279
AX729109/c
LOCUS AX729109 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 743 from Patent WO03025175.
ACCESSION AX729109
VERSION AX729109.1 GI:30508452
KEYWORDS
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Unclassified.
1 (bases 1 to 15)
Gryaznov,S.M. and Lloyd,D.H.
Oligonucleotide clamps having diagnostic and therapeutic
applications
Patent: US 5817795-A 5 06-OCT-1998;
Location/Qualifiers
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 271
AR051237/c
LOCUS AR051237 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5830658.
ACCESSION AR051237
VERSION AR051237.1 GI:5974601
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 5 03-NOV-1998;
Location/Qualifiers
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 272
AR084519
LOCUS AR084519 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 8 from patent US 5981185.
ACCESSION AR084519
VERSION AR084519.1 GI:10011290
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 8 09-NOV-1999;
Location/Qualifiers
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAAAAAAAAA 2587
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1 TTTAAAAAAAAAAAAA 15

RESULT 273
AR127784/c
LOCUS AR127784 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6180777.
ACCESSION AR127784
VERSION AR127784.1 GI:14114379
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 5 30-JAN-2001;
Location/Qualifiers
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 274
I16031/c
LOCUS I16031 15 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 5 from patent US 5473060.
ACCESSION I16031
VERSION I16031.1 GI:1250939
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic applications
JOURNAL Patent: US 5473060-A 5 05-DEC-1995;
Location/Qualifiers
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 275
I28366/c
LOCUS I28366 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5571677.
ACCESSION I28366
VERSION I28366.1 GI:1819142
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
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AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 983904-A 588 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1. .15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1919 TAATAATTACATCAT 1933
Db 15 TAATAATTACATCAT 1
RESULT 266
A90358/c
LOCUS A90358 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 539 from Patent EP0856579.
ACCESSION A90358
VERSION A90358.1 GI:6738872
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 539 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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1. .15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1968 GCAGGTATTGATGTC 1982
Db 15 GCAGGTATTGATGTC 1
RESULT 267
A90359/c
LOCUS A90359 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 540 from Patent EP0856579.
ACCESSION A90359
VERSION A90359.1 GI:6738873
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 540 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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1. .15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCACC 1985
Db 15 GGTATTGATGGCACC 1
RESULT 268
A90407/c
LOCUS A90407 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 588 from Patent EP0856579.
ACCESSION A90407
VERSION A90407.1 GI:6738921
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 588 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
source
1. .15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1919 TAATAATTACATCAT 1933
Db 15 TAATAATTACATCAT 1
RESULT 269
AR002256/c
LOCUS AR002256 15 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 5 from patent US 5741643.
ACCESSION AR002256
VERSION AR002256.1 GI:3963810
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide Clamps
JOURNAL Patent: US 5741643-A 5 21-APR-1998;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1
RESULT 270
AR045206/c
LOCUS AR045206 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5817795.
ACCESSION AR045206
VERSION AR045206.1 GI:5966671
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdc25 hs ribozyme binding site"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CAGGAGAAAAAACAAC 941
Db 19 CAGGAGAAAAAACAAC 3

RESULT 261
AX132311/c
LOCUS AX132311 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3529 from Patent WO0130362.
ACCESSION AX132311
VERSION AX132311.1 GI:14138616
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
PATENT: WO 0130362-A 3529 03-MAY-2001;
JOURNAL IMMUSOL, INC. (US)
FEATURES
source
1. .19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdc25 hs ribozyme binding site"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAAACA 940
Db 17 CCAGGAGAAAAAACA 1

RESULT 262
AR488890
LOCUS AR488890 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 7 from patent US 6709818.
ACCESSION AR488890
VERSION AR488890.1 GI:47255117
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nelson,W.G., Lin,X., Tchou,J.C. and Bakker,J.
TITLE Methods of diagnosing and treating hepatic cell proliferative
disorders
JOURNAL Patent: US 6709818-A 7 23-MAR-2004;
FEATURES
source
1. .20
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTCTTTTAAAG 2758
Db 4 ATTTTCTTTTCTTTAAAG 20
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RESULT 263
A88391/c
LOCUS A88391 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 539 from Patent WO9833904.
ACCESSION A88391
VERSION A88391.1 GI:6736961
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 539 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1. .15
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1968 GCAGGTATTGATGGC 1982
Db 15 GCAGGTATTGATGGC 1

RESULT 264
A88392/c
LOCUS A88392 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 540 from Patent WO9833904.
ACCESSION A88392
VERSION A88392.1 GI:6736962
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 540 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCACC 1985
Db 15 GGTATTGATGGCACC 1

RESULT 265
A88440/c
LOCUS A88440 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 588 from Patent WO9833904.
ACCESSION A88440
VERSION A88440.1 GI:6737010
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 256
AR241645
LOCUS AR241645 19 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6472141.
ACCESSION AR241645
VERSION AR241645.1 GI:27287419
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Nikiforov,T.T.
TITLE Kinase assays using polycations
JOURNAL Patent: US 6472141-A 3 29-OCT-2002;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 257
AR292884
LOCUS AR292884 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4619 from patent US 6537751.
ACCESSION AR292884
VERSION AR292884.1 GI:31680168
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4619 25-MAR-2003;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3126 GTTGTATTAGACTAAG 3142
Db 2 GTTGTATTAGACTAAG 18

RESULT 258
AR473599
LOCUS AR473599 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6689565.

/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 259
AR478107
LOCUS AR478107 19 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 3 from patent US 6699655.
ACCESSION AR478107
VERSION AR478107.1 GI:47236709
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Nikiforov,T.T.
TITLE Fluorescent polarization assays involving multivalent metal ions
JOURNAL Patent: US 6699655-A 3 02-MAR-2004;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 260
AX132308/c
LOCUS AX132308 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3526 from Patent WO0130362.
ACCESSION AX132308
VERSION AX132308.1 GI:14138613
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 3526 03-MAY-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="Homo sapiens"

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FT source 1. .18 /organism='Artificial Sequence'.
FT Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATATTTTCTT 1

RESULT 252
LOCUS AR167910 19 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6287774.
ACCESSION AR167910
VERSION AR167910.1 GI:17903721
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Nikiforov,T.T.
TITLE Assay methods and system
JOURNAL Patent: US 6287774-A 3 11-SEP-2001;
FEATURES
source
Location/Qualifiers
1. .19
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCT 2139
Db 1 CGCTGTGGATGCTGCT 17

RESULT 253
BD211727 19 bp DNA linear PAT 17-JUL-2003
LOCUS ALG-2LP and ALG-2-like molecules and utilization thereof.
DEFINITION BD211727
ACCESSION BD211727
VERSION BD211727.1 GI:33021497
KEYWORDS JP 2002516335-A/10.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Curtis,R.A.J.
TITLE ALG-2LP and ALG-2-like molecules and utilization thereof
JOURNAL Patent: JP 2002516335-A 10 04-JUN-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2002516335-A/10
PD 04-JUN-2002
PR 13-MAY-1999 JP 2000550863
PF 26-MAY-1998 US 09/084749
PI RORY A J CURTIS
PC A61K45/00,A61P25/28,A61P35/00,A61P37/02,A61P43/00,A61P43/00,
PC C07K14/47,
PC C07K16/18,C07K17/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
,C12N5/10,C12N15/09,
PC C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/574//C12P21/08,
PC C12N5/00,
PC C12N5/00,C12N15/00
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CC Strandedness: Single;
CC Topology: Linear;
CC ALG-2LP and ALG-2-like molecules and utilization thereof FH
CC Location/Qualifiers
FT source 1. .19
PT Location/Qualifiers
/organism='Unidentified'.
FEATURES
source
Location/Qualifiers
1. .19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 158 CAACCCATCTGCGGAGA 174
Db 3 CAACCCATCTGTGAGA 19

RESULT 254
LOCUS CQ808384 19 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 1834 from Patent WO2004035803.
ACCESSION CQ808384
VERSION CQ808384.1 GI:47113778
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,P.,
Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
Marx,A.
TITLE Method and nucleic acids for the improved treatment of breast cell
proliferative disorders
JOURNAL Patent: WO 2004035803-A 1834 29-APR-2004;
Epigenomics AG (DE)
FEATURES
source
Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for BCAR1"

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2959 GTTATTATTGTGTGTT 2975
Db 1 GGTATTATTGTGTGTT 17

RESULT 255
CQ829560 19 bp DNA linear PAT 05-JUL-2004
LOCUS Sequence 3 from Patent EP1418239.
DEFINITION CQ829560
ACCESSION CQ829560
VERSION CQ829560.1 GI:49732871
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Nikiforov,T.T.
TITLE Fluorescence polarization assays involving polyions
JOURNAL Patent: EP 1418239-A 3 12-MAY-2004;
Caliper Life Sciences, Inc. (US)
FEATURES
source
Location/Qualifiers
1. .19
/organism="synthetic construct"
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LOCUS AR264934 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 18 from patent US 6492121.
ACCESSION AR264934
VERSION AR264934.1 GI:29693321
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kuran, R., Kanagawa, T., Kamagata, Y., Kurata, S., Yamada, K., Yokomaku, T., Koyama, O. and Furusho, K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 18 10-DEC-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
||||| |||||||
Db 17 TATATATTTTCTT 1

RESULT 245
LOCUS AR478215/c 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 18 from patent US 6699661.
ACCESSION AR478215
VERSION AR478215.1 GI:47236963
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kuran, R., Kanagawa, T., Kamagata, Y., Kurata, S., Yamada, K., Yokomaku, T., Koyama, O. and Furusho, K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 18 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
||||| |||||||
Db 17 TATATATTTTCTT 1

RESULT 246
LOCUS AX030150/c 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 112 from Patent EP1008649.
ACCESSION AX030150
VERSION AX030150.1 GI:10190367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H.

and Schlingensiepen, R.
Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2 (tgf-b2)
Patent: EP 1008649-A 112 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2136 GCCTACTGCTTTAGAAA 2152
||||| |||||||
Db 17 GCCTATTGCTTTAGAAA 1

RESULT 247
LOCUS AX316471/c 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 112 from Patent EP1160319.
ACCESSION AX316471
VERSION AX316471.1 GI:17899644
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen, G.F., Brysch, W., Schlingensiepen, K.H., Schlingensiepen, R. and Bogdahn, U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 112 05-DEC-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2136 GCCTACTGCTTTAGAAA 2152
||||| |||||||
Db 17 GCCTATTGCTTTAGAAA 1

RESULT 248
LOCUS AX599662/c 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1002 from Patent WO02077272.
ACCESSION AX599662
VERSION AX599662.1 GI:28399810
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
JOURNAL Patent: WO 02077272-A 1002 03-OCT-2002;
FEATURES Epigenomics AG (DE)
Location/Qualifiers

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RESULT 240
BD166038/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 17-JAN-2003
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166038
VERSION
BD166038.1 GI:27871850
KEYWORDS
JP 2002191372-A/18.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Yamane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K., and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
Patent: JP 2002191372-A 18 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/18
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source
1..18
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1161 TATATATATTTTTCIT 1177
Db 17 TATATATTTTTCIT 1
RESULT 241
AR232855/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 20-DEC-2002
Sequence 112 from patent US 6455689.
ACCESSION
AR232855
VERSION
AR232855.1 GI:27275193
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF- beta.)
JOURNAL
Patent: US 6455689-A 112 24-SEP-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1161 TATATATATTTTTCIT 1177
Db 17 TATATATTTTTCIT 1
RESULT 242
AR237465/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 20-DEC-2002
Sequence 3 from patent US 6465628.
ACCESSION
AR237465
VERSION
AR237465.1 GI:27282215
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 3 15-OCT-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 243
AR237467/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 20-DEC-2002
Sequence 5 from patent US 6465628.
ACCESSION
AR237467
VERSION
AR237467.1 GI:27282217
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 5 15-OCT-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 244
AR264934/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 20-DEC-2002
Sequence 112 from patent US 6455689.
ACCESSION
AR232855
VERSION
AR232855.1 GI:27275193
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF- beta.)
JOURNAL
Patent: US 6455689-A 112 24-SEP-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
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source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2136 GCCTACTGCTTTAGAAA 2152
Db 17 GCCTATTGCTTAGAAA 1
RESULT 242
AR237465/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 20-DEC-2002
Sequence 3 from patent US 6465628.
ACCESSION
AR237465
VERSION
AR237465.1 GI:27282215
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 3 15-OCT-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 243
AR237467/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 20-DEC-2002
Sequence 5 from patent US 6465628.
ACCESSION
AR237467
VERSION
AR237467.1 GI:27282217
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 5 15-OCT-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 244
AR264934/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 20-DEC-2002
Sequence 112 from patent US 6455689.
ACCESSION
AR232855
VERSION
AR232855.1 GI:27275193
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF- beta.)
JOURNAL
Patent: US 6455689-A 112 24-SEP-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
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DEFINITION Sequence 1219 from Patent WO03025177.
ACCESSION AX736539
VERSION AX736539.1 GI:30515827
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Telerman,A., Anson,R. and Tuijinder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2129 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
    source
        1..17
            Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTCTTTTAAATGATC 1
RESULT 237
A40575/c
LOCUS A40575 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 112 from Patent WO9425578.
ACCESSION A40575
VERSION A40575.1 GI:2296610
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 112 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
    source
        1..18
            Location/Qualifiers
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2136 GCCTACTGCTTTAGAAA 2152
Db 17 GCCTATTGCTTTAGAAA 1
RESULT 238
A89099/c
LOCUS A89099 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1247 from Patent WO9833904.
ACCESSION A89099
VERSION A89099.1 GI:6737669
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1247 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
        1..18
            Location/Qualifiers
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2136 GCCTACTGCTTTAGAAA 2152
Db 17 GCCTATTGCTTTAGAAA 1
RESULT 239
BD145038/c
LOCUS BD145038 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145038
VERSION BD145038.1 GI:27850796
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,K., Kanagawa,T., Kanagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 19 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/19
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, VOICHI KAWAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28,
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..18
/organism='Artificial Sequence'.
FEATURES
    source
        1..18
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1
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DEFINITION Sequence 2155 from patent US 5646042.
ACCESSION 154414
VERSION 154414.1 GI:2475617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2155 08-JUL-1997;
FEATURES
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Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATAT 1168
Db 1 TTATTTTATATATAT 17

RESULT 232
154416
LOCUS 154416 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 2157 from patent US 5646042.
ACCESSION 154416
VERSION 154416.1 GI:2475619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2157 08-JUL-1997;
FEATURES
    source
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            /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCTTTTATATATAT 1169
Db 1 TTATTTTATATATAT 17

RESULT 233
154416
LOCUS 154416 17 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 579 from patent US 5731295.
ACCESSION 154416
VERSION 154416.1 GI:3938886
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.
TITLE Method of reducing stromelysin RNA via ribozymes
JOURNAL Patent: US 5731295-A 579 24-MAR-1998;
FEATURES
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            /mol_type="unassigned DNA"

DEFINITION Sequence 2155 from patent US 5646042.
ACCESSION 154414
VERSION 154414.1 GI:2475617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2155 08-JUL-1997;
FEATURES
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            /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATAT 1168
Db 1 TTATTTTATATATAT 17

RESULT 232
154416
LOCUS 154416 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 2157 from patent US 5646042.
ACCESSION 154416
VERSION 154416.1 GI:2475619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2157 08-JUL-1997;
FEATURES
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Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCTTTTATATATAT 1169
Db 1 TTATTTTATATATAT 17

RESULT 233
154416
LOCUS 154416 17 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 579 from patent US 5731295.
ACCESSION 154416
VERSION 154416.1 GI:3938886
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.
TITLE Method of reducing stromelysin RNA via ribozymes
JOURNAL Patent: US 5731295-A 579 24-MAR-1998;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTTCTTTTAAAGGA 1048
Db 1 TTTTCATTTTAAAGGA 17

RESULT 234
194417
LOCUS 194417 17 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 580 from patent US 5731295.
ACCESSION 194417
VERSION 194417.1 GI:3938887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.
TITLE Method of reducing stromelysin RNA via ribozymes
JOURNAL Patent: US 5731295-A 580 24-MAR-1998;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTTCTTTTAAAGGAA 1049
Db 1 TTTTCATTTTAAAGGA 17

RESULT 235
AX009039/c
LOCUS AX009039 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 72 from Patent WO9963975.
ACCESSION AX009039
VERSION AX009039.1 GI:9996413
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 72 16-DEC-1999;
BIOLOGICAL INFORMATION: BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
    source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2349 CCTTCTGTGTGTCCCA 2365
Db 17 CCTTCTGTGTGTCCCA 1

RESULT 236
AX736539/c
LOCUS AX736539 17 bp DNA linear PAT 08-MAY-2003
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTTCCTTTTATATATA 1168
DB 1 TTTATTTTATATATA 17

RESULT 227
LOCUS AR047364 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2157 from patent US 5817796.
ACCESSION AR047364
VERSION AR047364.1 GI:5968829
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J., and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 2157 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCTTTTTTATATATAT 1169
DB 1 TTATTTTATATATAT 17

RESULT 228
LOCUS BD234968/c 17 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234968
VERSION BD234968.1 GI:33044738
KEYWORDS JP 2002517434-A/72.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
JOURNAL A method for stimulating the immune system
PATENT: JP 2002517434-A 72 18-JUN-2002;
COMMENT BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/72
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KRL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00.
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2349 CCTGCTGTGTGTCCTCA 2365
DB 17 CCTGCTGCTGTGTCCTCA 1

RESULT 229
LOCUS I37566 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 579 from patent US 5612215.
ACCESSION I37566
VERSION I37566.1 GI:2085526
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
Stinchcomb,D.T.
TITLE Stromelysin targeted ribozymes
JOURNAL Patent: US 5612215-A 579 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTCTTTTTTAAAGGA 1048
DB 1 TTTTCATTTTAAAGGA 17

RESULT 230
LOCUS I37567 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 580 from patent US 5612215.
ACCESSION I37567
VERSION I37567.1 GI:2085527
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
Stinchcomb,D.T.
TITLE Stromelysin targeted ribozymes
JOURNAL Patent: US 5612215-A 580 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTTCTTTTTTAAAGGA 1049
DB 1 TTTTCATTTTAAAGGA 17

RESULT 231
LOCUS I54414 17 bp DNA linear PAT 07-OCT-1997
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TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 528 07-AUG-2001;
COMMENT BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/528
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSC
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..19
FT Location/Qualifiers
1..19 /organism='Unknown'.
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 GGAGGTTTATAAATCGAC 1538
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Db 19 GGAGGTTTACAAAATAGAC 1
RESULT 223
BD065913/c
LOCUS 19 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065913
VERSION BD065913.1 GI:22611516
KEYWORDS JP 2001511000-A/548.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Schlingensiepen K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 548 07-AUG-2001;
COMMENT BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/548
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSC
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..19
FT Location/Qualifiers
1..19 /organism='Unknown'.
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2212 GGAATGGATCCATGAACC 2230
|||||
Db 19 GGAATGGATACACGAACC 1
RESULT 224
AR409919/c
LOCUS 22 bp RNA linear PAT 18-DEC-2003

DEFINITION Sequence 32 from patent US 6635422.
ACCESSION AR409919
VERSION AR409919.1 GI:40161054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Keene, J.D., Tenenbaum, S.A. and Carson, C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein
(mRNP) complexes
JOURNAL Patent: US 6635422-A 32 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..22
/organism='unknown'
/mol_type='unassigned RNA'
Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2578 AAAAAAAATTTGGAGAAAAA 2599
|||||
Db 22 AAAAAACCAATTAAGAAAAA 1
RESULT 225
AX404674/c
LOCUS 22 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 48 from Patent WO224745.
ACCESSION AX404674
VERSION AX404674.1 GI:21437955
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Abken, H. and Schinkoethe, T.
TITLE Method for detecting tumor cells
JOURNAL Patent: WO 0224745-A 48 28-MAR-2002;
FEATURES Abken, Hinrich (DE)
source Location/Qualifiers
1..22
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Sonde'
Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3795 TCTATTTTCCAAAGATAAAAA 3816
|||||
Db 22 TTTTTCCTCAAAAAA 1
RESULT 226
AR047362
LOCUS 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2155 from patent US 5817796.
ACCESSION AR047362
VERSION AR047362.1 GI:5968827
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17).
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myc ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 2155 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..17

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Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
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Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 218
LOCUS AX355314/c
DEFINITION AX355314
ACCESSION AX355314
VERSION AX355314.1 GI:18619982
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 138 11-JUL-2002;
FEATURES
LOCATION/Qualifiers
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CCGCGCGCGCACGCGCGC 634
      |||||
Db 19 CCGCGCGCGCGCGCGCGC 1

RESULT 221
LOCUS AX785856
DEFINITION AX785856
ACCESSION AX785856
VERSION AX785856.1 GI:32953476
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Cullen,P. and Seedorf,U.
TITLE Method for analysing hereditary masculine infertility
JOURNAL Patent: WO 03050299-A 365 19-JUN-2003;
FEATURES
LOCATION/Qualifiers
source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3162 TCAAGAGCCCCGCAAAACAC 3180
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Db 1 TCACTGCCCGCCAGCAAAACAC 19

RESULT 222
LOCUS BD065893/c
DEFINITION BD065893
ACCESSION BD065893
VERSION BD065893.1 GI:22611496
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Schlingenselepen,K.H. and Brysch,W.

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
      |||||
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 220
LOCUS AX546999
DEFINITION AX546999
ACCESSION AX546999
VERSION AX546999.1 GI:25812143
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 138 11-JUL-2002;
FEATURES
LOCATION/Qualifiers
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
      |||||
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 220
LOCUS AX546999/c
DEFINITION AX546999
ACCESSION AX546999
VERSION AX546999.1 GI:25812143
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 138 11-JUL-2002;
FEATURES
LOCATION/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CCGCGCGCGCACGCGCGC 634
      |||||
Db 19 CCGCGCGCGCGCGCGCGC 1

RESULT 221
LOCUS AX785856
DEFINITION AX785856
ACCESSION AX785856
VERSION AX785856.1 GI:32953476
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Cullen,P. and Seedorf,U.
TITLE Method for analysing hereditary masculine infertility
JOURNAL Patent: WO 03050299-A 365 19-JUN-2003;
FEATURES
LOCATION/Qualifiers
source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3162 TCAAGAGCCCCGCAAAACAC 3180
      |||
Db 1 TCACTGCCCGCCAGCAAAACAC 19

RESULT 222
LOCUS BD065893/c
DEFINITION BD065893
ACCESSION BD065893
VERSION BD065893.1 GI:22611496
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Schlingenselepen,K.H. and Brysch,W.

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ACCESSION AX008974
VERSION AX008974.1 GI:9996348
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 7 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAATAGAC 1
RESULT 214
AX103946
LOCUS AX103946 19 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 138 from Patent WO0122972.
ACCESSION AX103946
VERSION AX103946.1 GI:13920143
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
source 1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCACGCGCG 633
Db 1 GCGCGCGCGCGCGCGCG 19
RESULT 215
AX103946/c
LOCUS AX103946/c 19 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 138 from Patent WO0122972.
ACCESSION AX103946
VERSION AX103946.1 GI:13920143
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
source 1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCACGCGCG 633
Db 1 GCGCGCGCGCGCGCGCG 19
RESULT 216
AX103946/c
LOCUS AX103946/c 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 4067 from Patent WO0130362.
ACCESSION AX103946
VERSION AX103946.1 GI:14139159
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 4067 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/Note="PCNA HH ribozyme binding site"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3591 TTTGGACTTTTCTTTTAA 3609
Db 19 TTTGGACTTTATCTTTAA 1
RESULT 217
AX355314
LOCUS AX355314 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 342 from Patent WO0197843.
ACCESSION AX355314
VERSION AX355314.1 GI:18619982
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 342 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
Location/Qualifiers
source 1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="Synthetic oligonucleotide-phosphodiester backbone"
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAAATAGAC 1

RESULT 209
A88400/c
LOCUS
DEFINITION Sequence 548 from Patent WO9833904.
ACCESSION A88400
VERSION A88400.1 GI:6736970
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 548 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
Location/Qualifiers
source
1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2212 GGAATGGATCCATGAACC 2230
Db 19 GGAATGGATACACGAACC 1

RESULT 212
BD234903/c
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234903
VERSION BD234903.1 GI:33044673
KEYWORDS JP 2002517434-A/7.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 7 18-JUN-2002;
BIOGHOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/7
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Homo sapiens (human)'.

FEATURES
source
1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAAATAGAC 1

RESULT 211
A90367/c
LOCUS
DEFINITION Sequence 548 from Patent EP0856579.
ACCESSION A90367
VERSION A90367.1 GI:6738881
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 528 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
Location/Qualifiers
source
1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAAATAGAC 1

RESULT 211
A90367/c
LOCUS
DEFINITION Sequence 548 from Patent EP0856579.
ACCESSION A90367
VERSION A90367.1 GI:6738881
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Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAGAAACATCTTTT TTTT 2754
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Db 24 AAAAAAAGGGGTTT TTTT 1

RESULT 204
I35523/c
LOCUS I35523 24 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 13 from patent US 5599922.
ACCESSION I35523
VERSION I35523.1 GI:2088491
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligonucleotide N3'-p5', phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5599922-A 13 04-FEB-1997;
FEATURES Location/Qualifiers
source 1..24
/mol_type="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAGAAACATCTTTT TTTT 2754
||||| ||||| ||||| ||||| |||||
Db 24 AAAAAAAGGGGTTT TTTT 1

RESULT 205
I43133/c
LOCUS I43133 24 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 13 from patent US 5631135.
ACCESSION I43133
VERSION I43133.1 GI:2468377
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligonucleotide N3'.fwdarw.p5', phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5631135-A 13 20-MAY-1997;
FEATURES Location/Qualifiers
source 1..24
/mol_type="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAGAAACATCTTTT TTTT 2754
||||| ||||| ||||| ||||| |||||
Db 24 AAAAAAAGGGGTTT TTTT 1

RESULT 206
I92011/c
LOCUS I92011 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 13 from patent US 5726297.
ACCESSION I92011
VERSION I92011.1 GI:3936481
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KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3' P5', phosphoramidates
JOURNAL Patent: US 5726297-A 13 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..24
/mol_type="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAAGGGGTTT TTTT 2754
||||| ||||| ||||| ||||| |||||
Db 24 AAAAAAAGGGGTTT TTTT 1

RESULT 207
A05202
LOCUS A05202 19 bp DNA linear PAT 07-MAY-1993
DEFINITION Oligonucleotide primer 1.
ACCESSION A05202
VERSION A05202.1 GI:345043
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Patent: WO 8803807-A 2 02-JUN-1988;
JOURNAL Location/Qualifiers
FEATURES source 1..19
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2268 CCATATCTATGAGTTCAG 2286
||||| ||||| ||||| ||||| |||||
Db 1 CCGTATTATGAGTTCAG 19

RESULT 208
A88380/c
LOCUS A88380 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 528 from Patent WO9833904.
ACCESSION A88380
VERSION A88380.1 GI:6736950
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 528 06-AUG-1998;
FEATURES BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
source 1..19
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
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Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAGAAACATCTTTTTTTTTT 2754
Db 24 AAAAAAGAAAGGGGTTTTTTTTT 1

RESULT 200
LOCUS AR123295/c
DEFINITION Sequence 13 from patent US 6169170.
ACCESSION AR123295
VERSION AR123295.1 GI:14108261
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.N5'.Phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 13 02-JAN-2001;
FEATURES
    Location/Qualifiers
    1..24
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAGAAACATCTTTTTTTTTT 2754
Db 24 AAAAAAGAAAGGGGTTTTTTTTT 1

RESULT 201
LOCUS BD175807/c
DEFINITION 2'-4'-RNA oligonucleotide having N3'-P5' binding.
ACCESSION BD175807
VERSION BD175807.1 GI:29121509
KEYWORDS JP 2002255990-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Imanishi,T. and Kohiga,S.
TITLE 2'-4'-RNA oligonucleotide having N3'-P5' binding
JOURNAL Patent: JP 2002255990-A 10 11-SEP-2002;
COMMENT SANKYO CO LTD
OS Artificial Sequence
PN JP 2002255990-A/10
PD 11-SEP-2002
PF 19-NOV-2001 JP 2001352543
PI TAKESHI IMANISHI,SATOSHI KOHIGA
PC C07H19/06,A61K31/712,A61K48/00,A61P31/18,C07H19/16,C07H21/00,
PC C12N15/09,
PC C12N15/00
CC Description of Artificial Sequence: Synthesized and hairpin-
CC formed
CC oligonucleotide
CC Key Location/Qualifiers
FH Key 1..24
FT source /organism='Artificial Sequence'.
FT Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 2731 AAAAAAGAAACATCTTTTTTTTTT 2754
Db 24 AAAAAAGAAAGGGGTTTTTTTTT 1

RESULT 202
LOCUS BD188897/c
DEFINITION Sequence 13 from patent US 5591607.
ACCESSION BD188897
VERSION BD188897.1 GI:32998636
KEYWORDS JP 2003012688-A/13.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
JOURNAL Patent: JP 2003012688-A 13 15-JAN-2003;
FEATURES
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    /organism="unidentified"
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    /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAGAAACATCTTTTTTTTTT 2754
Db 24 AAAAAAGAAAGGGGTTTTTTTTT 1

RESULT 203
LOCUS I33258/c
DEFINITION Sequence 13 from patent US 5591607.
ACCESSION I33258
VERSION I33258.1 GI:1824049
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3.fwdarw.P5' phosphoramidates: triplex DNA
JOURNAL Patent: US 5591607-A 13 07-JAN-1997;
FEATURES
    Location/Qualifiers
    1..24
    /organism="unknown"
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    source
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DEFINITION Sequence 40 from Patent WO0071747.
ACCESSION AX048441
VERSION AX048441.1 GI:12225605
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 40 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz:Erkennungssystem"
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
RESULT 196
AX048442/c
LOCUS AX048442 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 41 from Patent WO0071747.
ACCESSION AX048442
VERSION AX048442.1 GI:12225606
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 41 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz:Erkennungssystem"
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
RESULT 197
AX048443/c
LOCUS AX048443 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 42 from Patent WO0071747.
ACCESSION AX048443
VERSION AX048443.1 GI:12225607
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 42 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz:Erkennungssystem"
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
RESULT 198
AX058881/c
LOCUS AR058881 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5837835.
ACCESSION AR058881
VERSION AR058881.1 GI:5984458
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 13 17-NOV-1998;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source
1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2731 AAAAGAAAACATCTTTT 2754
Db 24 AAAAGAAAAGGGTTT 1
RESULT 199
AR079586/c
LOCUS AR079586 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 13 from patent US 5965720.
ACCESSION AR079586
VERSION AR079586.1 GI:10006330
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 13 12-OCT-1999;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source
1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2731 AAAAGAAAACATCTTTT 2754
Db 24 AAAAGAAAAGGGTTT 1
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PD 12-FEB-2002
PF 18-FEB-1999 JP 2000532549
PR 20-FEB-1998 US 09/026601
PI JAMES JOSEPH BECK
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: primer JB659 FH key
FT source 1..19
FT Location/Qualifiers
   Location/Qualifiers
   1..19
   /organism='Artificial Sequence'.

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGGACGC 3205
Db 1 GAAGCTTCATGGACGC 16

RESULT 191
AR200636
LOCUS AR200636 19 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 25 from patent US 6358680.
ACCESSION AR200636
VERSION AR200636.1 GI:20251524
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Beck,J.Joseph.
TITLE Detection of wheat and barley fungal pathogens using the polymerase
JOURNAL Chain reaction
FEATURES
   source
   Location/Qualifiers
   1..19
   /organism="unknown"
   /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGGACGC 3205
Db 1 GAAGCTTCATGGACGC 16

RESULT 192
AR116691
LOCUS AR116691 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6133434.
ACCESSION AR116691
VERSION AR116691.1 GI:14097013
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buell,G.Nutter., Surprenant,A. and Kawashima,E.
TITLE Purinergic receptor
JOURNAL Patent: US 6133434-A 4 17-OCT-2000;
FEATURES
   source
   Location/Qualifiers
   1..20
   /organism="unknown"
   /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCCGCGGGAAG 2117
Db 1 GTCCAGCCGCGGGAAG 16

RESULT 193
AR275649
LOCUS AR275649 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 4 from patent US 6509163.
ACCESSION AR275649
VERSION AR275649.1 GI:29709100
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buell,G.N., Surprenant,A. and Kawashima,E.
TITLE Methods of screening modulators of mammalian P2X7 purinergic
JOURNAL Patent: US 6509163-A 4 21-JAN-2003;
FEATURES
   source
   Location/Qualifiers
   1..20
   /organism="unknown"
   /mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCCGCGGGAAG 2117
Db 1 GTCCAGCCGCGGGAAG 16

RESULT 194
AX048440/C
LOCUS AX048440 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 39 from Patent WO0071747.
ACCESSION AX048440
VERSION AX048440.1 GI:12225604
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
JOURNAL production and use of the same
FEATURES
   source
   Location/Qualifiers
   1..20
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Beschreibung der kunstlichen
   Sequenz:Erkennungssystem"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTTAAAAA 2588
Db 16 TTTTAAAAA 1

RESULT 195
AX048441/C
LOCUS AX048441 20 bp DNA linear PAT 12-JAN-2001

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thioredoxin reductase genes and methods of using same to modulate cell growth
Patent: US 6566514-A 2 20-MAY-2003;
JOURNAL Location/Qualifiers
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1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2209 GATGGAATGGATCCA 2224
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Db 1 GATGGAATGGATCCA 16

RESULT 187
AX009027/c
LOCUS 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 60 from Patent WO9963975.
ACCESSION AX009027
VERSION AX009027.1 GI:9996401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R.
AUTHORS A method for stimulating the immune system
TITLE Patent: WO 9963975-A 60 16-DEC-1999;
JOURNAL BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
LOCATION/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1806 GAATGGCTCTCCTTCG 1821
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Db 16 GAATGGCTCTCCTTCG 1

RESULT 188
BD131940
LOCUS 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Oligonucleotide sequence complementary to thioredoxin gene or
thioredoxin reductase gene and utilization thereof for controlling
cell proliferation.
ACCESSION BD131940
VERSION BD131940.1 GI:23226885
KEYWORDS JP 2002501743-A/2.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 17)
AUTHORS Wright, J.A., Young, A.H. and Lee, Y.S.
TITLE Oligonucleotide sequence complementary to thioredoxin gene or
thioredoxin reductase gene and utilization thereof for controlling
JOURNAL Patent: JP 2002501743-A 2 22-JAN-2002;
GENESENSE TECHNOLOGIES INC
COMMENT OS Homo sapiens (human)
PN JP 2002501743-A/2
PD 22-JAN-2002
PF 29-JAN-1999 JP 2000529423
PR 30-JAN-1998 US 60/073196

PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09, A61K31/711, A61K48/00, A61P35/00, A61P35/04, C07H21/04//
PC (A61K31/711, A61K45/00), (A61K48/00, A61K45/00), C12N15/00 CC
Oligonucleotide sequence complementary to thioredoxin gene or CC
thioredoxin
CC reductase gene and utilization thereof for controlling cell
proliferation
FH Key Location/Qualifiers
FT source 1. .17
/organism="Homo sapiens (human)"
/db_xref="taxon:9606"

FEATURES
source
1. .17
Location/Qualifiers
Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2209 GATGGAATGGATCCA 2224
|||||
Db 1 GATGGAATGGATCCA 16

RESULT 189
I73187/c
LOCUS 18 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 1 from patent US 5686242.
ACCESSION I73187
VERSION I73187.1 GI:3009326
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bruice, T.W. and Lima, W.F.
TITLE Determination of oligonucleotides for therapeutics, diagnostics and
research reagents
JOURNAL Patent: US 5686242-A 1 11-NOV-1997;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACATC 2818
|||||
Db 17 AAAAAAAAAAACATC 2

RESULT 190
BD137911
LOCUS 19 bp DNA linear PAT 18-SEP-2002
DEFINITION Detection of wheat and barley fungal pathogens using the polymerase
chain reaction.
ACCESSION BD137911
VERSION BD137911.1 GI:23232856
KEYWORDS JP 2002504347-A/25.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Beck, J.J.
TITLE Detection of wheat and barley fungal pathogens using the polymerase
chain reaction
JOURNAL Patent: JP 2002504347-A 25 12-FEB-2002;
NOVARTIS AG
COMMENT OS Artificial Sequence
PN JP 2002504347-A/25

QY 2156 GCAGGATAATTGCTGC 2171
Db 16 GCAGGATAATTGCTGC 1

RESULT 183
BD066606/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066606
VERSION BD066606.1 GI:22612209
KEYWORDS JP 2001511000-A/1241.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1241 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1241
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PR KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..16
FT /organism='Unknown'.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAA 2035
Db 16 AGTCCACTAGGAAAA 1

RESULT 184
BD066613/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066613
VERSION BD066613.1 GI:22612216
KEYWORDS JP 2001511000-A/1248.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1248 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1248
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PR KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..16
FT /organism='Unknown'.
FEATURES
source
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

QY 2156 GCAGGATAATTGCTGC 2171
Db 16 GCAGGATAATTGCTGC 1

RESULT 183
BD066606/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066606
VERSION BD066606.1 GI:22612209
KEYWORDS JP 2001511000-A/1241.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1241 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1241
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PR KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..16
FT /organism='Unknown'.
FEATURES
source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

QY 2020 AGTCCACTAGGAAAA 2035
Db 16 AGTCCACTAGGAAAA 1

RESULT 184
BD066613/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066613
VERSION BD066613.1 GI:22612216
KEYWORDS JP 2001511000-A/1248.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1248 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1248
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PR KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..16
FT /organism='Unknown'.
FEATURES
source
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/db_xref="taxon:32644"

QY 2153 TGTGCAGGATAATTGC 2168
Db 16 TGTGCAGGATAATTGC 1

RESULT 185
BD234956/c
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234956
VERSION BD234956.1 GI:33044726
KEYWORDS JP 2002517434-A/60.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schlengensiepen,K.H., Schlengensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 60 18-JUN-2002;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/60
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PI 10-JUN-1998 EP 98110709.7.25-JUL-1998 EP 98113974.4 PI
PR KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1806 GAATGGCTCTCCTTCG 1821
Db 16 GAATGGCTCTCCTTCG 1

RESULT 186
AR337667
LOCUS
DEFINITION Sequence 2 from patent US 6566514.
ACCESSION AR337667
VERSION AR337667.1 GI:33724235
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE Oligonucleotide sequences complementary to thioredoxin or

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
  0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2020 AGTCCACTAGGAAAA 2035
Db 16 AGTCCACTAGGAAAA 1

RESULT 179
AX30151/c
LOCUS
DEFINITION Sequence 113 from Patent EP1008649.
ACCESSION AX30151
VERSION AX30151.1 GI:10190368
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 113 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source
1. .16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
  0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 TGTGCAGGATAATGC 2168
Db 16 TGTGCAGGATAATGC 1

RESULT 180
AX316464/c
LOCUS
DEFINITION Sequence 105 from Patent EP1160319.
ACCESSION AX316464
VERSION AX316464.1 GI:17899637
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 105 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source
1. .16
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match
  0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2020 AGTCCACTAGGAAAA 2035
Db 16 AGTCCACTAGGAAAA 1

RESULT 181
AX316472/c
LOCUS
DEFINITION Sequence 113 from Patent EP1160319.
ACCESSION AX316472
VERSION AX316472.1 GI:17899645
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 113 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source
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Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match
  0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 TGTGCAGGATAATGC 2168
Db 16 TGTGCAGGATAATGC 1

RESULT 182
BD065911/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065911
VERSION BD065911.1 GI:22611514
KEYWORDS JP 2001511000-A/546.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 546 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/546
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 JP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source
1. .16
/organism='Unknown'.
Location/Qualifiers
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/organism="unidentified"
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Query Match
  0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 174
AR367888
LOCUS AR367888 16 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 17 from patent US 6376199.
ACCESSION AR367888
VERSION AR367888.1 GI:34601344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Caniggia,I., Post,M. and Lye,S.
TITLE Methods to diagnose a required regulation of trophoblast invasion
JOURNAL Patent: US 6376199-A 17 23-APR-2002;
FEATURES
source Location/Qualifiers
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACTACTGTGTG 1232
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Db 1 CATGCACTACTGTGTG 16

RESULT 175
AX008985/c
LOCUS AX008985 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 18 from Patent WO9963975.
ACCESSION AX008985
VERSION AX008985.1 GI:9996359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 18 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAAA 2035
|||||
Db 16 AGTCCACTAGGAAAAA 1

RESULT 176
AX008987/c
LOCUS AX008987 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 20 from Patent WO9963975.
ACCESSION AX008987
VERSION AX008987.1 GI:9996361
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 20 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTGC 2168
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Db 16 TGTGCAGGATAATTGC 1

RESULT 177
AX008988/c
LOCUS AX008988 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 21 from Patent WO9963975.
ACCESSION AX008988
VERSION AX008988.1 GI:9996362
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 21 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2156 GCAGGATAATTGCTGC 2171
|||||
Db 16 GCAGGATAATTGCTGC 1

RESULT 178
AX030143/c
LOCUS AX030143 16 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 105 from Patent EP1008649.
ACCESSION AX030143
VERSION AX030143.1 GI:10190360
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
JOURNAL effects of transforming growth factor-b2(tgf-b2)
Patent: EP 1008649-A 105 14-JUN-2000;
BIOGOSTIK GES (DE)
FEATURES
source Location/Qualifiers
1..16
/organism="Homo sapiens"

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source
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/mol_type="genomic DNA"
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Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTGC 2168
Db 16 TGTGCAGGATAATTGC 1

RESULT 170
BD234917/c
LOCUS BD234917 16 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234917
VERSION BD234917.1 GI:33044687
KEYWORDS JP 2002517434-A/21.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 21 18-JUN-2002;
BIOGENOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/21
PD 18-JUN-2002
PP 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00.
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..16
/organism='Homo sapiens (human)'.

FEATURES
source
1..16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2156 GCAGGATAATTGCTGC 2171
Db 16 GCAGGATAATTGCTGC 1

RESULT 171
AR232848/c
LOCUS AR232848 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 105 from patent US 6455689.
ACCESSION AR232848
VERSION AR232848.1 GI:27275186
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 16)
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
Antisense-oligonucleotides for transforming growth factor-.beta.

REFERENCE
1 (bases 1 to 16)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
JOURNAL (TGF-.beta.)
COMMENT Patent: US 6455689-A 113 24-SEP-2002;
Location/Qualifiers
source
1..16
/organism="genomic DNA"

JOURNAL (TGF-.beta.)
Patent: US 6455689-A 105 24-SEP-2002;
Location/Qualifiers
source
1..16
/organism="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAA 2035
Db 16 AGTCCACTAGGAAAA 1

RESULT 172
AR232856/c
LOCUS AR232856 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 113 from patent US 6455689.
ACCESSION AR232856
VERSION AR232856.1 GI:27275194
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 16)
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
Antisense-oligonucleotides for transforming growth factor-.beta.

REFERENCE
1 (bases 1 to 16)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
JOURNAL (TGF-.beta.)
COMMENT Patent: US 6455689-A 113 24-SEP-2002;
Location/Qualifiers
source
1..16
/organism="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTGC 2168
Db 16 TGTGCAGGATAATTGC 1

RESULT 173
AR367887/c
LOCUS AR367887 16 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 16 from patent US 6376199.
ACCESSION AR367887
VERSION AR367887.1 GI:34601343
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 16)
Caniggia,I., Post,M. and Lye,S.
Methods to diagnose a required regulation of trophoblast invasion

REFERENCE
1 (bases 1 to 16)
AUTHORS Caniggia,I., Post,M. and Lye,S.
TITLE Methods to diagnose a required regulation of trophoblast invasion
JOURNAL Patent: US 6376199-A 16 23-APR-2002;
Location/Qualifiers
source
1..16
/organism="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACACTACTGTGTG 1232
Db 16 CATGCACACTACTGTGTG 1

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Query Match	0.4%;	Score 16;	DB 1;	Length 16;	
Best Local Similarity	100.0%;	Pred. No. 1.4e+02;			
Matches	16;	Conservative	0;	Mismatches	0;
Indels			0;	Gaps	0;
QY	2020	AGTCCACTAGGAAAA	2035		
DB	16	AGTCCACTAGGAAAA	1		
RESULT 166					
A89100/c					
LOCUS	A89100	16 bp	DNA	linear	PAT 22-JAN-2000
DEFINITION	Sequence 1248 from Patent WO9833904.				
ACCESSION	A89100				
KEYWORDS	A89100.1	GI:6737670			
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1	(bases 1 to 16)			
AUTHORS	Brysch,W. and Schlingensiepen,K.				
TITLE	AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD				
JOURNAL	PATENT: WO 9833904-A 1248 06-AUG-1998;				
FEATURES	BIONOSTIK GES (DE); BRYSCH WOLFGANG (DE)				
source	Location/Qualifiers				
	1..16				
	/organism="unidentified"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32644"				
Query Match	0.4%;	Score 16;	DB 1;	Length 16;	
Best Local Similarity	100.0%;	Pred. No. 1.4e+02;			
Matches	16;	Conservative	0;	Mismatches	0;
Indels			0;	Gaps	0;
QY	2153	TGTGCAGGTAATTGC	2168		
DB	16	TGTGCAGGTAATTGC	1		
RESULT 167					
A90365/c					
LOCUS	A90365	16 bp	DNA	linear	PAT 22-JAN-2000
DEFINITION	Sequence 546 from Patent EP0856579.				
ACCESSION	A90365				
KEYWORDS	A90365.1	GI:6738879			
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1	(bases 1 to 16)			
AUTHORS	Brysch,W.D. and Schlingensiepen,K.D.				
TITLE	An antisense oligonucleotide preparation method				
JOURNAL	PATENT: EP 0856579-A 546 05-AUG-1998;				
FEATURES	BIONOSTIK GES (DE)				
source	Location/Qualifiers				
	1..16				
	/organism="unidentified"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32644"				
Query Match	0.4%;	Score 16;	DB 1;	Length 16;	
Best Local Similarity	100.0%;	Pred. No. 1.4e+02;			
Matches	16;	Conservative	0;	Mismatches	0;
Indels			0;	Gaps	0;
QY	2156	GCAGGTAATTGCTGC	2171		
DB	16	GCAGGTAATTGCTGC	1		
RESULT 168					
BD234914/c					
LOCUS	BD234914	16 bp	DNA	linear	PAT 17-JUL-2003

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Db          2 GCCAGGGACGTTTCTTA 19

RESULT 161
AX613450
LOCUS      AX613450                20 bp    DNA          linear    PAT 17-FEB-2003
DEFINITION Sequence 4475 from Patent WO02072882.
ACCESSION  AX613450
VERSION     AX613450.1  GI:28408879
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4475 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES    Location/Qualifiers
            source            1..20
                                /organism="Homo sapiens"
                                /mol_type="unassigned DNA"
                                /db_xref="taxon:9606"

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  935 AAAAAACAACCTTCTT 952
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Db   3 AAAAAAAAACCTTCTT 20

RESULT 162
A40568/c
LOCUS      A40568                16 bp    DNA          linear    PAT 05-MAR-1997
DEFINITION Sequence 105 from Patent WO9425578.
ACCESSION  A40568
VERSION     A40568.1  GI:2296603
KEYWORDS
SOURCE      unidentified
            unclassified
            ORGANISM      unclassified
            unclassified
            unclassified
REFERENCE   1 (bases 1 to 16)
  AUTHORS
  TITLE     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
  JOURNAL   Patent: WO 9425578-A 105 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source            1..16
                                /organism="unidentified"
                                /mol_type="unassigned DNA"
                                /db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2020 AGTCCACTAGGAAAAA 2035
      ||||| ||||| ||||| |||||
Db   16 AGTCCACTAGGAAAAA 1

RESULT 163
A40576/c
LOCUS      A40576                16 bp    DNA          linear    PAT 05-MAR-1997
DEFINITION Sequence 113 from Patent WO9425578.
ACCESSION  A40576
VERSION     A40576.1  GI:2296611
KEYWORDS
SOURCE      unidentified
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ORGANISM    unidentified
            unclassified
REFERENCE   1 (bases 1 to 16)
  AUTHORS
  TITLE     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
  JOURNAL   Patent: WO 9425578-A 113 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source            1..16
                                /organism="unidentified"
                                /mol_type="unassigned DNA"
                                /db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2153 TGTGCAGGATAATTGC 2168
      ||||| ||||| ||||| |||||
Db   16 TGTGCAGGATAATTGC 1

RESULT 164
A88398/c
LOCUS      A88398                16 bp    DNA          linear    PAT 22-JAN-2000
DEFINITION Sequence 546 from Patent WO9833904.
ACCESSION  A88398
VERSION     A88398.1  GI:6736968
KEYWORDS
SOURCE      unidentified
            unclassified
            ORGANISM      unclassified
            unclassified
            unclassified
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 546 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
            source            1..16
                                /organism="unidentified"
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                                /db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2156 GCAGGATAATTGCTGC 2171
      ||||| ||||| ||||| |||||
Db   16 GCAGGATAATTGCTGC 1

RESULT 165
A89093/c
LOCUS      A89093                16 bp    DNA          linear    PAT 22-JAN-2000
DEFINITION Sequence 1241 from Patent WO9833904.
ACCESSION  A89093
VERSION     A89093.1  GI:6737663
KEYWORDS
SOURCE      unidentified
            unclassified
            ORGANISM      unclassified
            unclassified
            unclassified
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 1241 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
            source            1..16
                                /organism="unidentified"
                                /mol_type="unassigned DNA"
                                /db_xref="taxon:32644"
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REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 76 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1589 ACCTACTTCAGAAATCGT 1606
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Db 18 ACCCTACTTCAGAAATGTT 1
RESULT 153
AX316492/c
LOCUS AX316492 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 133 from Patent EP1160319.
ACCESSION AX316492
VERSION AX316492.1 GI:17899665
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 133 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2446 CTTGTAATGCAGCTAAA 2463
|||||
Db 18 CTTGCAATGCAGCTAAA 1
RESULT 154
BD066577/c
LOCUS BD066577 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066577
VERSION BD066577.1 GI:22612180
KEYWORDS JP 2001511000-A/1212.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1212 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1212

PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT Location/Qualifiers
source 1..18
/organism="Unknown".
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1589 ACCTACTTCAGAAATCGT 1606
|||||
Db 18 ACCCTACTTCAGAAATGTT 1
RESULT 155
BD066633/c
LOCUS BD066633 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066633
VERSION BD066633.1 GI:22612236
KEYWORDS JP 2001511000-A/1268.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1268 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1268
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT Location/Qualifiers
source 1..18
/organism="Unknown".
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2446 CTTGTAATGCAGCTAAA 2463
|||||
Db 18 CTTGCAATGCAGCTAAA 1
RESULT 156
CQ808226
LOCUS CQ808226 19 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 1676 from Patent WO2004035803.
ACCESSION CQ808226
VERSION CQ808226.1 GI:47113620
KEYWORDS synthetic construct
SOURCE

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QY 1589 ACCCTACTTCAGAAATCGT 1606
    |||||
Db 18 ACCCTACTTCAGAAATGTT 1

RESULT 148
AX008993/c
LOCUS AX008993 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 26 from Patent WO9963975.
ACCESSION AX008993
VERSION AX008993.1 GI:9996367
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 26 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
    source
    Location/Qualifiers
        1..18
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAAATGCAGCTAAA 2463
    |||||
Db 18 CTTGCAATGCAGCTAAA 1

RESULT 149
AX009037/c
LOCUS AX009037 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 70 from Patent WO9963975.
ACCESSION AX009037
VERSION AX009037.1 GI:9996411
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 70 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
    source
    Location/Qualifiers
        1..18
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2237 GTACATGCTAACTTCTG 2254
    |||||
Db 18 GTACAATGCCAACTTCTG 1

RESULT 150
AX030114/c
LOCUS AX030114 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 76 from Patent EP1008649.
ACCESSION AX030114
VERSION AX030114.1 GI:10190331
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 76 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
    source
    Location/Qualifiers
        1..18
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGAAATCGT 1606
    |||||
Db 18 ACCCTACTTCAGAAATGTT 1

RESULT 151
AX030171/c
LOCUS AX030171 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 133 from Patent EP1008649.
ACCESSION AX030171
VERSION AX030171.1 GI:10190388
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 133 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
    source
    Location/Qualifiers
        1..18
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAAATGCAGCTAAA 2463
    |||||
Db 18 CTTGCAATGCAGCTAAA 1

RESULT 152
AX316435/c
LOCUS AX316435 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 76 from Patent EP160319.
ACCESSION AX316435
VERSION AX316435.1 GI:17899608
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified
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[illegible]

/db_xref="taxon:32644"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
DB 18 CTTGCAATGCAGCTAAA 1

RESULT 140
A89064/c

LOCUS A89064 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1212 from Patent WO9833904.
ACCESSION A89064
VERSION A89064.1 GI:6737634
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1212 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGATCGT 1606
DB 18 ACCCTACTTCAGATTTGT 1

RESULT 141
A89120/c

LOCUS A89120 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1268 from Patent WO9833904.
ACCESSION A89120
VERSION A89120.1 GI:6737690
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1268 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
DB 18 CTTGCAATGCAGCTAAA 1

RESULT 142
BD234908/c

LOCUS BD234908 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234908
VERSION BD234908.1 GI:33044678
KEYWORDS JP 2002517434-A/12.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 12 18-JUN-2002;
BIOGHOSTIK GSELSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/12
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709, 7.25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
BRYSCH
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/
PC 00, A61P35/00,
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..18
/organism='Homo sapiens (human)'.
/db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGATCGT 1606
DB 18 ACCCTACTTCAGATTTGT 1

RESULT 143
BD234922/c

LOCUS BD234922 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234922
VERSION BD234922.1 GI:33044692
KEYWORDS JP 2002517434-A/26.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 26 18-JUN-2002;
BIOGHOSTIK GSELSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/26
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709, 7.25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
BRYSCH
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/
PC 00, A61P35/00,
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..18
/organism='Homo sapiens (human)'.
/db_xref="taxon:9606"

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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 629 ACGCGGCACACACACACAC 648
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Db 21 ACGCGGCACACACACACACAC 2

RESULT 136
ATH523738/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 21 bp DNA linear PLN 29-MAR-2003
ACCESSION AJ523738
VERSION AJ523738.1 GI:26791974
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M., and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 21)
AUTHORS Balzerque, S.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
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Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
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/clone="060H10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1..21
Location/Qualifiers
/note="T-DNA flanking sequence
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Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2808 AAAAAACATCAAAACAAA 2827
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Db 21 AAACAACATCAAAACAGA 2

RESULT 137
AR306126/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 24 bp DNA linear PAT 12-JUN-2003
ACCESSION AR306126
VERSION AR306126.1 GI:31695813
KEYWORDS Sequence 67 from patent US 6548251.

QY 2732 AAAAGAAAACATCTTTTTTTTTT 2754
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Db 24 AAAAAAAAAGTGTGTGTGTGT 2

RESULT 138
A40539/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION Sequence 76 from Patent WO9425578.
ACCESSION A40539
VERSION A40539.1 GI:2296574
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 76 10-NOV-1994;
BIOGNOSTIK GBS (DE)
FEATURES
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1..18
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGATCGT 1606
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Db 18 ACCCTACTTCAGATTTGT 1

RESULT 139
A40596/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION Sequence 133 from Patent WO9425578.
ACCESSION A40596
VERSION A40596.1 GI:2296631
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 133 10-NOV-1994;
BIOGNOSTIK GBS (DE)
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Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"

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PR	31-JAN-1997 EP	97101531.8
PI	KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCHE	
PC	C12N15/11.C07H21/04.A61K31/70	
CC	An antisense oligonucleotide preparation method FH Key	
FT	source	1..20
FT	Location/Qualifiers	/organism='Unknown'.
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		/db_xref="taxon:32644"
Query Match	0.4%; Score 16.8; DB 1; Length 20;	
Best Local Similarity	90.0%; Pred. No. 1.6e+02;	
Matches 18; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
QY	1928 CATCATCCCGAATAAAAGCG 1947	
Dd	20 CATCATCCCCAAATAAAAGTG 1	
RESULT 133		
BD069970		
LOCUS	20 bp DNA linear PAT 27-AUG-2002	
DEFINITION	Use of nucleic acids containing unethylated CPG dinucleotide in the treatment of LPS-associated disorders.	
ACCESSION	BD069970	
VERSION	BD069970.1 GI:22615573	
KEYWORDS	JP 2001513776-A/59.	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Schwartz,D.A. and Krieg,A.M.	
TITLE	Use of nucleic acids containing unethylated CPG dinucleotide in the treatment of LPS-associated disorders	
JOURNAL	Patent: JP 2001513776-A 59 04-SEP-2001;	
	UNIVERSITY OF IOWA RESEARCH FOUNDATION	
COMMENT	OS Artificial Sequence	
	PN JP 2001513776-A/59	
	PD 04-SEP-2001	
	PF 25-FEB-1998 JP 1998537810	
	PR 28-FEB-1997 US 60/039405	
	PI DAVID A SCHWARTZ,ARTHUR M KRIEG	
	PC A61K49/00.C07H21/02.C07H21/04.A01N43/04	
	CC synthetic oligonucleotide	
FH	Key	Location/Qualifiers
FT	source	1..20
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Query Match	0.4%; Score 16.8; DB 1; Length 20;	
Best Local Similarity	90.0%; Pred. No. 1.6e+02;	
Matches 18; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
QY	616 CGCGCGCGCACGACGCGCG 635	
Dd	1 CGCGCGCGCGCGCGCGCG 20	
RESULT 134		
BD069970/c		
LOCUS	20 bp DNA linear PAT 27-AUG-2002	
DEFINITION	Use of nucleic acids containing unethylated CPG dinucleotide in the treatment of LPS-associated disorders.	
ACCESSION	BD069970	
VERSION	BD069970.1 GI:22615573	
KEYWORDS	JP 2001513776-A/59.	

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 520 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGG 635
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Db 20 CGCGCGCGCGCGCGCGG 1

RESULT 129
AX547630
LOCUS AX547630 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 769 from Patent WO02053141.
ACCESSION AX547630
VERSION AX547630.1 GI:25812774
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 769 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
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/note="Synthetic Sequence"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGG 635
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Db 1 CGCGCGCGCGCGCGCGG 20

RESULT 130
AX547630/c
LOCUS AX547630 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 769 from Patent WO02053141.
ACCESSION AX547630
VERSION AX547630.1 GI:25812774
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 769 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGG 635
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Db 20 CGCGCGCGCGCGCGCGG 1

RESULT 131
BD065894/c
LOCUS BD065894 20 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065894
VERSION BD065894.1 GI:22611497
KEYWORDS JP 2001511000-A/529.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 529 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/529
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..20
/organism='Unknown'.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1523 GGTATTATAAATCGACATGC 1542
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Db 20 GGTATTATAAATAGACATGC 1

RESULT 132
BD066600/c
LOCUS BD066600 20 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066600
VERSION BD066600.1 GI:22612203
KEYWORDS JP 2001511000-A/1235.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1235 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1235
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533

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/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
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Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 124
AX355165/c
LOCUS AX355165 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 193 from Patent WO0197843.
ACCESSION AX355165
VERSION AX355165.1 GI:18619832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 193 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
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Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 125
AX441509
LOCUS AX441509 20 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 13 from Patent WO0206531.
ACCESSION AX441509
VERSION AX441509.1 GI:21690470
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Datta Gupta, N.
TITLE Nucleic acid hairpin probes and uses thereof
JOURNAL Patent: WO 0206531-A 13 24-JAN-2002;
Applied Gene Technologies, Inc. (US)
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/db_xref="taxon:32630"
/note="Oligo AGT02020"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTTGAGAAAAA 2599
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Db 1 AAAAAAATTTGAGAAAAA 20
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RESULT 126
AX441510
LOCUS AX441510 20 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 14 from Patent WO0206531.
ACCESSION AX441510
VERSION AX441510.1 GI:21690471
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Datta Gupta, N.
TITLE Nucleic acid hairpin probes and uses thereof
JOURNAL Patent: WO 0206531-A 14 24-JAN-2002;
Applied Gene Technologies, Inc. (US)
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/note="Oligo AGT02021"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTTGAGAAAAA 2599
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Db 1 AAAAAAATTTGAGAAAAA 20

RESULT 127
AX547381
LOCUS AX547381 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 520 from Patent WO02053141.
ACCESSION AX547381
VERSION AX547381.1 GI:25812525
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler, R. L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 520 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
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/organism="synthetic construct"
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Query Match 0.4%; Score 16.8; DB 1; Length 20;
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QY 616 CGCGCGCGCACGCGCGCG 635
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Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 128
AX547381/c
LOCUS AX547381 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 520 from Patent WO02053141.
ACCESSION AX547381
VERSION AX547381.1 GI:25812525
KEYWORDS

LOCUS AX104577 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 769 from Patent WO0122972.
ACCESSION AX104577
VERSION AX104577.1 GI:13920774
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 769 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
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Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1
RESULT 120
AX316458/c
LOCUS AX316458 20 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 99 from Patent EP1160319.
ACCESSION AX316458
VERSION AX316458.1 GI:17899631
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 99 05-DEC-2001;
BIOGNOSTIK GESSELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
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/db_xref="taxon:32644"
/note="Description of unknown: unknown"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1928 CATCATCCCGAATAAAGCG 1947
Db 20 CATCATCCCAATAAAGTG 1
RESULT 121
AX355164
LOCUS AX355164 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 192 from Patent WO0197843.
ACCESSION AX355164
VERSION AX355164.1 GI:18619831
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 193 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
1. .20

AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 192 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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source
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/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20
RESULT 122
AX355164/c
LOCUS AX355164 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 192 from Patent WO0197843.
ACCESSION AX355164
VERSION AX355164.1 GI:18619831
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 192 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1
RESULT 123
AX355165
LOCUS AX355165 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 193 from Patent WO0197843.
ACCESSION AX355165
VERSION AX355165.1 GI:18619832
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 193 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
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JOURNAL Patent: WO 9963975-A 8 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSTIEPEN KARL
HERMANN (DE); SCHLINGENSTIEPEN REIMAR (DE)
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1523 GGTATTATAAATCGACATGC 1542
DB 20 GGTTTACAAATAGACATGC 1

RESULT 115
AX030137/c
LOCUS AX030137 20 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 99 from Patent EP1008649.
ACCESSION AX030137
VERSION AX030137.1 GI:10190354
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,K.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 99 14-JUN-2000;
BIOGOSTIK GES (DE)
FEATURES
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            /mol_type="unassigned DNA"
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Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAAGCG 1947
DB 20 CATCATCCCAATAAAAGTG 1

RESULT 116
AX104328
LOCUS AX104328 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 520 from Patent WO0122972.
ACCESSION AX104328
VERSION AX104328.1 GI:13920525
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 520 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 117
AX104328/c
LOCUS AX104328 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 520 from Patent WO0122972.
ACCESSION AX104328
VERSION AX104328.1 GI:13920525
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 520 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 118
AX104577
LOCUS AX104577 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 769 from Patent WO0122972.
ACCESSION AX104577
VERSION AX104577.1 GI:13920774
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 769 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
    source
        Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 119
AX104577/c
LOCUS AX104577 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 769 from Patent WO0122972.
ACCESSION AX104577
VERSION AX104577.1 GI:13920774
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 769 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 119
AX104577/c
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TITLE      Methods and compositions for analyzing nucleotide sequence
JOURNAL    mismatches using RNase H
PATENT     Patent: US 6596489-A 14 22-JUL-2003;
FEATURES   Location/Qualifiers
SOURCE     1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
      |||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 110
AR360425
LOCUS     AR360425          20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 13 from patent US 6596490.
ACCESSION AR360425
VERSION   AR360425.1 GI:33767455
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Dattagupta,N.
TITLE     Nucleic acid hairpin probes and uses thereof
JOURNAL   Patent: US 6596490-A 13 22-JUL-2003;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
      |||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 111
AR360426
LOCUS     AR360426          20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6596490.
ACCESSION AR360426
VERSION   AR360426.1 GI:33767456
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Dattagupta,N.
TITLE     Nucleic acid hairpin probes and uses thereof
JOURNAL   Patent: US 6596490-A 14 22-JUL-2003;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
      |||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 112
AR363652
LOCUS     AR363652          20 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION Sequence 13 from patent US 5221620.
ACCESSION AR363652
VERSION   AR363652.1 GI:34425532
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Purchio,A.F., Madisen,L. and Webb,N.
TITLE     Cloning and expression of transforming growth factor .beta.2
JOURNAL   Patent: US 5221620-A 13 22-JUN-1993;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2211 TCGAATGGATCCATGAACC 2230
      |||||
Db 20 TCGAATGGATACACGAACC 1

RESULT 113
AR478239/c
LOCUS     AR478239          20 bp      DNA      linear      PAT 14-MAY-2004
DEFINITION Sequence 42 from patent US 6699661.
ACCESSION AR478239
VERSION   AR478239.1 GI:47236887
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanagawa,T., Kanagata,Y., Kurata,S., Yamada,K.,
           Yokomaki,T., Koyama,O. and Furusho,K.
TITLE     Method for determining a concentration of target nucleic acid
           molecules, nucleic acid probes for the method, and method for
           analyzing data obtained by the method
JOURNAL   Patent: US 6699661-A 42 02-MAR-2004;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATATATTT 1171
      |||||
Db 20 TTTTATATATATATATATAT 1

RESULT 114
AX008975/c
LOCUS     AX008975          20 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 8 from Patent WO9963975.
ACCESSION AX008975
VERSION   AX008975.1 GI:9996349
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE     A method for stimulating the immune system
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TITLE      Vectors and methods for immunization or therapeutic protocols
JOURNAL    Patent: US 6339068-A 76 15-JAN-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
Db 1 GCGCGCGCGCGCGCGCGC 20

RESULT 105
AR182904/c
LOCUS      AR182904      20 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 76 from patent US 6339068.
ACCESSION  AR182904
VERSION     AR182904.1  GI:20226111
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE     Vectors and methods for immunization or therapeutic protocols
JOURNAL   Patent: US 6339068-A 76 15-JAN-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
Db 1 GCGCGCGCGCGCGCGCGC 20

RESULT 106
AR232842/c
LOCUS      AR232842      20 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 99 from patent US 6455689.
ACCESSION  AR232842
VERSION     AR232842.1  GI:27275180
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE     Antisense-oligonucleotides for transforming growth factor-.beta.
            (TGF-.beta.)
JOURNAL   Patent: US 6455689-A 99 24-SEP-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAAGCG 1947
Db 20 CATCATCCCGAATAAAAGTG 1
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RESULT 107
AR264958/c
LOCUS      AR264958      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 42 from patent US 6492121.
ACCESSION  AR264958
VERSION     AR264958.1  GI:29693345
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanagawa,T., Kanagata,Y., Kurata,S., Yamada,K.,
            Yokomaki,T., Koyama,O. and Furusho,K.
TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
JOURNAL   Patent: US 6492121-A 42 10-DEC-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTTTATATATATTT 1171
Db 20 TTTTTTTTTATATATATAT 1

RESULT 108
AR360398
LOCUS      AR360398      20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 13 from patent US 6596489.
ACCESSION  AR360398
VERSION     AR360398.1  GI:33767428
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dattagupta,N. and Tseng,T.-C.
TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
JOURNAL   Patent: US 6596489-A 13 22-JUL-2003;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAAATTGGAGAAAAA 20

RESULT 109
AR360399
LOCUS      AR360399      20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6596489.
ACCESSION  AR360399
VERSION     AR360399.1  GI:33767429
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dattagupta,N. and Tseng,T.-C.
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QY	1523	GGTTTATAAATCGACATGC	1542
Db	20	GGTTTAAAAATAGACATGC	1
RESULT 102			
ARL82850			PAT 20-APR-2002
LOCUS	ARL82850	20 bp	DNA
DEFINITION	Sequence 22 from patent US 6339068.		
ACCESSION	ARL82850		
VERSION	ARL82850.1	GI:20226057	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.		
TITLE	Vectors and methods for immunization or therapeutic protocols		
JOURNAL	Patent: US 6339068-A 22 15-JAN-2002;		
FEATURES	Location/Qualifiers		
source	1..20		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	0.4%; Score 16.8; DB 1; Length 20;		
Best Local Similarity	90.0%; Pred. No. 1.6e+02;		
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	616	CGCGCGCGCACGACGCGG	635
Db	1	CGCGCGCGCGCGCGCGG	20
RESULT 103			
ARL82850/c			PAT 20-APR-2002
LOCUS	ARL82850	20 bp	DNA
DEFINITION	Sequence 22 from patent US 6339068.		
ACCESSION	ARL82850		
VERSION	ARL82850.1	GI:20226057	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.		
TITLE	Vectors and methods for immunization or therapeutic protocols		
JOURNAL	Patent: US 6339068-A 22 15-JAN-2002;		
FEATURES	Location/Qualifiers		
source	1..20		
	/organism="unknown"		
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Query Match	0.4%; Score 16.8; DB 1; Length 20;		
Best Local Similarity	90.0%; Pred. No. 1.6e+02;		
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	616	CGCGCGCGCACGACGCGG	635
Db	20	CGCGCGCGCGCGCGCGG	1
RESULT 104			
ARL82904			PAT 20-APR-2002
LOCUS	ARL82904	20 bp	DNA
DEFINITION	Sequence 76 from patent US 6339068.		
ACCESSION	ARL82904		
VERSION	ARL82904.1	GI:20226111	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.		

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QY 1928 CATCATCCCGAATAAAAGCG 1947
Db 20 CATCATCCCAATAAAAGTG 1

RESULT 95
A88381/c
LOCUS Sequence 529 from Patent WO9833904. 20 bp DNA linear PAT 22-JAN-2000
DEFINITION A88381
ACCESSION A88381
VERSION A88381.1 GI:6736951
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Brysch,W.D. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 529 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1523 GGTTTATAAAATCGACATGC 1542
Db 20 GGTTTACAAAATAGACATGC 1

RESULT 98
A8030495
LOCUS AR030495 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 68 from patent US 5861273.
ACCESSION AR030495
VERSION AR030495.1 GI:5943709
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Olson,P.S. and Mascarenhas,D.
TITLE Chromosomal expression of heterologous genes in bacterial cells
JOURNAL Patent: US 5861273-A 68 19-JAN-1999;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2212 GGAATGGATCCATGAACCC 2231
Db 1 GGAATGGATACACGACCC 20

RESULT 99
AR084562
LOCUS AR084562 20 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 51 from patent US 5981185.
ACCESSION AR084562
VERSION AR084562.1 GI:10011333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 51 09-NOV-1999;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAAGCG 1947
Db 20 CATCATCCCAATAAAAGTG 1

RESULT 97
A90348/c
LOCUS A90348 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 529 from Patent EP0856579.
ACCESSION A90348
VERSION A90348.1 GI:6738862
KEYWORDS
SOURCE unidentified
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JOURNAL Patent: WO 9963975-A 3 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1343 GCAGATCCTTGAGCAAGC 1359
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Db 17 GCAGATCCTTGAGCAAGC 1
RESULT 91
AX009035/c
LOCUS 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 68 from Patent WO9963975.
ACCESSION AX009035
VERSION AX009035.1 GI:9996409
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 68 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1509 TACTACGCCAAGGAGGT 1525
|||||
Db 17 TACTACGCCAAGGAGGT 1
RESULT 92
BD065887/c
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065887
VERSION BD065887.1 GI:22611490
KEYWORDS JP 2001511000-A/522.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 522 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/522
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key

FEATURES Location/Qualifiers
FT source 1..17
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FT Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1343 GCAGATCCTTGAGCAAGC 1359
|||||
Db 17 GCAGATCCTTGAGCAAGC 1
RESULT 93
AR488890/c
LOCUS 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 7 from patent US 6709818.
ACCESSION AR488890
VERSION AR488890.1 GI:47255117
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nelson,W.G., Lin,X., Tchou,J.C. and Bakker,J.
TITLE Methods of diagnosing and treating hepatic cell proliferative disorders
JOURNAL Patent: US 6709818-A 7 23-MAR-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2574 TTAAAAAATAAAATTT 2590
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Db 19 TTAAAAAATAAAATTT 3
RESULT 94
A40562/c
LOCUS 20 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 99 from Patent WO9425578.
ACCESSION A40562
VERSION A40562.1 GI:2296597
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 99 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1343 GCAGATCTCTGACGACG 1359
Db 17 GCAGATCTCTGACGACG 1

RESULT 87
BD234899/c
LOCUS BD234899 17 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234899
VERSION BD234899.1 GI:33044669
KEYWORDS JP 2002517434-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 3 18-JUN-2002;
BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/3
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.

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Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 TACTACGCCAAGGAGGT 1525
Db 17 TACTACGCCAAGGAGGT 1

RESULT 89
CO778290
LOCUS CO778290 17 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 1976 from Patent EP1394274.
ACCESSION CO778290
VERSION CO778290.1 GI:45381008
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuwara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 1976 03-MAR-2004;
Genox Research, Inc. (JP)
FEATURES
source 1..17
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='an artificially synthesized TagMan probe sequence'

misc_feature 1
/note='Label FAM(6-carboxy-fluorescein)'

misc_feature 17
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TAMRA(6-carboxy-N,N,N#,NH-tetramethylrhodamine)''

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 CGCAGCCCAACGCGCCA 308
Db 1 CGCAGCCCAACGCGCCA 17

RESULT 90
AX008970/c
LOCUS AX008970 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9963975.
ACCESSION AX008970
VERSION AX008970.1 GI:9996344
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system

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source 1. .21
/organism="unknown"
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Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 588 CCCCGGGCTCGCAGGCTCG 608
Db 21 CCCCGGGCTCYCCAGGCTCG 1

RESULT 83
AX096770/c
LOCUS AX096770 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1948 from Patent WO0118250.
ACCESSION AX096770
VERSION AX096770.1 GI:13513024
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and
McCarthy, J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1948 15-MAR-2001;
WHITHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1. .21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 588 CCCCGGGCTCGCAGGCTCG 608
Db 21 CCCCGGGCTCYCCAGGCTCG 1

RESULT 84
BD129806
LOCUS BD129806 21 bp DNA linear PAT 18-SEP-2002
DEFINITION Asthma-associated gene.
ACCESSION BD129806
VERSION BD129806.1 GI:23224751
KEYWORDS JP 2002500895-A/96.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Wilson, A.R.B., Buckler, A., Cardon, L., Carey, A.H., Galvin, M.,
Miller, A. and North, M.
TITLE Asthma-associated gene
JOURNAL Patent: JP 2002500895-A 96 15-JAN-2002;
AXYS PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2002500895-A/96
PD 15-JAN-2002
PF 21-JAN-1998 JP 2000528715
PI ANGELA R BROOKS WILSON, ALAN BUCKLER, LON
CARDON, ALI SOUN H CAREY,
PI MARGARET GALVIN, ANDREW MILLER, MICHAEL NORTH
PC C12Q1/68, A01K67/027, C07K14/47, C12N15/09, C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Asthma-associated gene
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Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTTCCTTAAGGAAAAA 2765
Db 2 TTTTTCCTTAAGGAAAAA 21

RESULT 85
A88374/c
LOCUS A88374 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 522 from Patent WO9833904.
ACCESSION A88374
VERSION A88374.1 GI:6736944
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 522 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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/mol_type="unassigned DNA"
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Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1343 GCAGATCCTGAGCAAGC 1359
Db 17 GCAGATCCTGAGCAAGC 1

RESULT 86
A90341/c
LOCUS A90341 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 522 from Patent EP0856579.
ACCESSION A90341
VERSION A90341.1 GI:6738855
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brysch, W.D. and Schlingensiepen, K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 522 05-AUG-1998;
BIOGNOSTIK GES (DE)
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source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AUTHORS Brysch,W.D. and Schlingensiefen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 555 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2383 CCATTCTCTATTACATTGG 2401
Db 19 CCATTCTCTACTACATTGG 1

RESULT 79
BD065899/c
LOCUS BD065899 19 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065899
VERSION BD065899.1 GI:22611502
KEYWORDS JP 2001511000-A/534.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Schlingensiefen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 534 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
  OS Unknown
  PN JP 2001511000-A/534
  PD 07-AUG-2001
  PF 30-JAN-1998 JP 1998532533
  PR 31-JAN-1997 EP 97101531.8
  PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
  PC C12N15/11,C07H21/04,A61K31/70
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2383 CCATTCTCTATTACATTGG 2401
Db 19 CCATTCTCTACTACATTGG 1

RESULT 81
AR103576
LOCUS AR103576 21 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 100 from patent US 6087485.
ACCESSION AR103576
VERSION AR103576.1 GI:12815164
KEYWORDS
  SOURCE Unknown.
  ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
  Miller,A. and North,M.
TITLE Asthma related genes
JOURNAL Patent: US 6087485-A 100 11-JUL-2000;
FEATURES
  source
    Location/Qualifiers
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      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTITTTTTTAAGGAAAAA 2765
Db 2 TTTTITTTTTTAAGGAAAAA 21

RESULT 82
AR530745/c
LOCUS AR530745 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1948 from patent US 6727063.
ACCESSION AR530745
VERSION AR530745.1 GI:53919182
KEYWORDS
  SOURCE Unknown.
  ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
  McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: US 6727063-A 1948 27-APR-2004;
FEATURES
  Location/Qualifiers
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source 1. .18
/organism="unidentified"
/mol_type="genomic DNA"
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Query Match 0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1

RESULT 74
AX404674 22 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 48 from Patent WO224745.
ACCESSION AX404674
VERSION AX404674.1 GI:21437955
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Abken,H. and Schinkoethe,T.
TITLE Method for detecting tumor cells
JOURNAL Patent: WO 0224745-A 48 28-MAR-2002;
FEATURES Location/Qualifiers
source 1. .22
/organism="synthetic construct"
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/noe="Sonde"

Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTCTTTTAAAGGAAAAA 2766
Db 1 TTTTCTTTTAAAGGAAAAA 21

RESULT 75
A88386/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 534 from Patent WO9833904.
ACCESSION A88386
VERSION A88386.1 GI:6736956
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 534 06-AUG-1998;
FEATURES Location/Qualifiers
source 1. .19
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCAAGACTTAACATCTCC 1756
Db 19 CCAAGACTTAACATCTCC 1

RESULT 76
A88407/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 555 from Patent WO9833904.
ACCESSION A88407
VERSION A88407.1 GI:6736977
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 555 06-AUG-1998;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2383 CCATTCTCTATTACATTGG 2401
Db 19 CCATTCTCTATTACATTGG 1

RESULT 77
A90353/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 534 from Patent EP0856579.
ACCESSION A90353
VERSION A90353.1 GI:6738867
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 534 05-AUG-1998;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCAAGACTTAACATCTCC 1756
Db 19 CCAAGACTTAACATCTCC 1

RESULT 78
A90374/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 555 from Patent EP0856579.
ACCESSION A90374
VERSION A90374.1 GI:6738888
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
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Db 18 AGGTGATTCCCATCTACA 1
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RESULT 70
AX316463/c
LOCUS AX316463 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 104 from Patent EP1160319.
ACCESSION AX316463
VERSION AX316463.1 GI:17899636
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
AUTHORS Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 104 05-DEC-2001;
BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1
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RESULT 71
BD065907/c
LOCUS BD065907 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065907
VERSION BD065907.1 GI:22611510
KEYWORDS JP 2001511000-A/542.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 542 07-AUG-2001;
BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/542
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1
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RESULT 72
BD066569/c
LOCUS BD066569 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066569
VERSION BD066569.1 GI:22612172
KEYWORDS JP 2001511000-A/1204.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1204 07-AUG-2001;
BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1204
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 73;
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QY 1414 AGGTGATTCCCATCTACA 1431
Db 18 AGGTGATTCCCATCTACA 1
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RESULT 73
BD066605/c
LOCUS BD066605 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066605
VERSION BD066605.1 GI:22612208
KEYWORDS JP 2001511000-A/1240.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1240 07-AUG-2001;
BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1240
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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RESULT 72
BD066569/c
LOCUS BD066569 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066569
VERSION BD066569.1 GI:22612172
KEYWORDS JP 2001511000-A/1204.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1204 07-AUG-2001;
BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1204
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
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Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1414 AGGTGATTCCCATCTACA 1431
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RESULT 73
BD066605/c
LOCUS BD066605 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066605
VERSION BD066605.1 GI:22612208
KEYWORDS JP 2001511000-A/1240.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1240 07-AUG-2001;
BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1240
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
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Unclassified.
1 (bases 1 to 18)
Caniggia,I., Post,M. and Lye,S.
Methods to diagnose a required regulation of trophoblast invasion
Patent: US 6376199-A 9 23-APR-2002;
JOURNAL
FEATURES
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Query Match
Best Local Similarity 0.4%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 CCTACTTCCAGATCGTC 1607
Db 18 CCTACTTCCAGATCGTC 1

RESULT 66
AX008984/c
LOCUS AX008984 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 17 from Patent WO9963975.
ACCESSION AX008984
VERSION AX008984.1 GI:9996358
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Bogdahn,U., Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
A method for stimulating the immune system
Patent: WO 9963975-A 17 16-DEC-1999;
JOURNAL BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSTIEPEN KARL
HERMANN (DE); SCHLINGENSTIEPEN REIMAR (DE)
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Best Local Similarity 0.4%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAAGTCCACTAGGA 2031
Db 18 CTATAAAGTCCACTAGGA 1

RESULT 67
AX030105/c
LOCUS AX030105 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 67 from Patent EP1008649.
ACCESSION AX030105
VERSION AX030105.1 GI:10190322
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
Patent: EP 1008649-A 67 14-JUN-2000;
JOURNAL BIOGNOSTIK GES (DE)
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            /mol_type="unassigned DNA"

Unclassified.
1 (bases 1 to 18)
Caniggia,I., Post,M. and Lye,S.
Methods to diagnose a required regulation of trophoblast invasion
Patent: US 6376199-A 9 23-APR-2002;
JOURNAL
FEATURES
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                /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCTCATCTACA 1431
Db 18 AGGTGATTTCCTCATCTACA 1

RESULT 68
AX030142/c
LOCUS AX030142 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 104 from Patent EP1008649.
ACCESSION AX030142
VERSION AX030142.1 GI:10190359
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
Patent: EP 1008649-A 104 14-JUN-2000;
JOURNAL BIOGNOSTIK GES (DE)
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Best Local Similarity 0.4%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAAGTCCACTAGGA 2031
Db 18 CTATAAAGTCCACTAGGA 1

RESULT 69
AX316426/c
LOCUS AX316426 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 67 from Patent EP1160319.
ACCESSION AX316426
VERSION AX316426.1 GI:17899599
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
Patent: EP 1160319-A 67 05-DEC-2001;
JOURNAL BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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QY 1414 AGGTGATTTCCTCATCTACA 1431
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RESULT 61
A90361/c
LOCUS
Sequence 542 from Patent EP0856579.
A90361
ACCESSION
A90361.1 GI:6738875
VERSION
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Brysch,W.D. and Schlingensiepen,K.D.
TITLE
An antisense oligonucleotide preparation method
JOURNAL
Patent: EP 0856579-A 542 05-AUG-1998;
BIOGNOSTIK GES (DE)
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Location/Qualifiers
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QY 2007 CAGAAAACCTATAAGTCC 2024
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DB 18 CAGAAAACCTATAAGTCC 1
RESULT 62
BD234913/c
LOCUS
A method for stimulating the immune system.
BD234913
DEFINITION
BD234913.1 GI:33044683
ACCESSION
JP 2002517434-A/17.
VERSION
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE
A method for stimulating the immune system
JOURNAL
Patent: JP 2002517434-A 17 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Homo sapiens (human)
PN JP 2002517434-A/17
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709 7.25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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QY 2014 CTATAAGTCCACTAGGA 2031
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DB 18 CTATAAGTCCACTAGGA 1
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RESULT 63
AR232810/c
LOCUS
Sequence 67 from patent US 6455689.
AR232810
DEFINITION
AR232810
ACCESSION
AR232810.1 GI:27275148
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL
Patent: US 6455689-A 67 24-SEP-2002;
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Location/Qualifiers
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Query Match 0.4%; Score 18; DB 1; Length 18;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1414 AGGTGATTTCCTCATCA 1431
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DB 18 AGGTGATTTCCTCATCA 1
RESULT 64
AR232847/c
LOCUS
Sequence 104 from patent US 6455689.
AR232847
DEFINITION
AR232847
ACCESSION
AR232847.1 GI:27275185
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL
Patent: US 6455689-A 104 24-SEP-2002;
FEATURES
Location/Qualifiers
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Query Match 0.4%; Score 18; DB 1; Length 18;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2014 CTATAAGTCCACTAGGA 2031
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DB 18 CTATAAGTCCACTAGGA 1
RESULT 65
AR367880/c
LOCUS
Sequence 9 from patent US 6376199.
AR367880
DEFINITION
AR367880
ACCESSION
AR367880.1 GI:34601336
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.

FEATURES	source	Location/Qualifiers	
ACCESSION	A40530		
VERSION	A40530.1	GI:2296565	
KEYWORDS	.		
SOURCE	unidentified		
ORGANISM	unclassified		
REFERENCE	1 (bases 1 to 18)		
AUTHORS	.		
TITLE	ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE		
JOURNAL	EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))		
Patent:	WO 9425578-A 67 10-NOV-1994;		
BIOGNOSTIK	GES (DE)		
FEATURES	Location/Qualifiers		
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Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1414 AGGTGATTTCCATCTACA 1431		
Db	18 AGGTGATTTCCATCTACA 1		
RESULT 57			
LOCUS	A40567/c	18 bp DNA	PAT 05-MAR-1997
DEFINITION	Sequence 104 from Patent WO9425578.		
ACCESSION	A40567		
VERSION	A40567.1	GI:2296602	
KEYWORDS	.		
SOURCE	unidentified		
ORGANISM	unclassified		
REFERENCE	1 (bases 1 to 18)		
AUTHORS	.		
TITLE	ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE		
JOURNAL	EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))		
Patent:	WO 9425578-A 104 10-NOV-1994;		
BIOGNOSTIK	GES (DE)		
FEATURES	Location/Qualifiers		
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Best Local Similarity	100.0%; Pred. No. 73;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1414 AGGTGATTTCCATCTACA 1431		
Db	18 AGGTGATTTCCATCTACA 1		
RESULT 58			
LOCUS	A88394/c	18 bp DNA	PAT 22-JAN-2000
DEFINITION	Sequence 542 from Patent WO9833904.		
ACCESSION	A88394		
VERSION	A88394.1	GI:6736964	
KEYWORDS	.		
SOURCE	unidentified		
ORGANISM	unclassified		
REFERENCE	1 (bases 1 to 18)		
AUTHORS	Brysch, W. and Schlingensiepen, K.		
TITLE	AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD		
JOURNAL	Patent: WO 9833904-A 542 06-AUG-1998;		
BIOGNOSTIK	GES (DE); BRYSCH WOLFGANG (DE)		
FEATURES	Location/Qualifiers		
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Query Match	0.4%; Score 18; DB 1; Length 18;		
Best Local Similarity	100.0%; Pred. No. 73;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2014 CTATAAAGTCCACTAGGA 2031		
Db	18 CTATAAAGTCCACTAGGA 1		
RESULT 59			
LOCUS	A89056/c	18 bp DNA	PAT 22-JAN-2000
DEFINITION	Sequence 1204 from Patent WO9833904.		
ACCESSION	A89056		
VERSION	A89056.1	GI:6737626	
KEYWORDS	.		
SOURCE	unidentified		
ORGANISM	unclassified		
REFERENCE	1 (bases 1 to 18)		
AUTHORS	Brysch, W. and Schlingensiepen, K.		
TITLE	AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD		
JOURNAL	Patent: WO 9833904-A 1204 06-AUG-1998;		
BIOGNOSTIK	GES (DE); BRYSCH WOLFGANG (DE)		
FEATURES	Location/Qualifiers		
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Best Local Similarity	100.0%; Pred. No. 73;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1414 AGGTGATTTCCATCTACA 1431		
Db	18 AGGTGATTTCCATCTACA 1		
RESULT 60			
LOCUS	A89092/c	18 bp DNA	PAT 22-JAN-2000
DEFINITION	Sequence 1240 from Patent WO9833904.		
ACCESSION	A89092		
VERSION	A89092.1	GI:6737662	
KEYWORDS	.		
SOURCE	unidentified		
ORGANISM	unclassified		
REFERENCE	1 (bases 1 to 18)		
AUTHORS	Brysch, W. and Schlingensiepen, K.		
TITLE	AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD		
JOURNAL	Patent: WO 9833904-A 1240 06-AUG-1998;		
BIOGNOSTIK	GES (DE); BRYSCH WOLFGANG (DE)		
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Best Local Similarity	100.0%; Pred. No. 73;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2014 CTATAAAGTCCACTAGGA 2031		
Db	18 CTATAAAGTCCACTAGGA 1		
RESULT 61			
LOCUS	A89092/c	18 bp DNA	PAT 22-JAN-2000
DEFINITION	Sequence 1240 from Patent WO9833904.		
ACCESSION	A89092		

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RESULT 52
BD065901/c
LOCUS      BD065901                20 bp    DNA        linear        PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065901
VERSION    BD065901.1 GI:22611504
KEYWORDS   JP 2001511000-A/536.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Schlingensiepen,K.H. and Brysch,W.
TITLE     An antisense oligonucleotide preparation method
JOURNAL   Patent: JP 2001511000-A 536 07-AUG-2001;
          BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
          PN JP 2001511000-A/536
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533
          PR 31-JAN-1997 EP 97101531.8
          PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
          PC C12N15/11,C07H21/04,A61K31/70
          CC An antisense oligonucleotide preparation method FH Key
          Location/Qualifiers
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Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1853 CCACAAGACAGGACCTGG 1872
Db 20 CCATAAAGACAGGACCTGG 1

RESULT 53
A87861/c
LOCUS      A87861                23 bp    DNA        linear        PAT 22-JAN-2000
DEFINITION Sequence 9 from Patent WO9833904.
ACCESSION  A87861
VERSION    A87861.1 GI:6736431
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 23)
AUTHORS   Brysch,W. and Schlingensiepen,K.
TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL   Patent: WO 9833904-A 9 06-AUG-1998;
          BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
Db 23 CCATCGCGGGCAGATCCTG 4

RESULT 54
A89828/c
LOCUS      A89828                23 bp    DNA        linear        PAT 05-MAR-1997
DEFINITION Sequence 9 from Patent EP0856579.
ACCESSION  A89828
VERSION    A89828.1 GI:6738342
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 23)
AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
TITLE     An antisense oligonucleotide preparation method
JOURNAL   Patent: EP 0856579-A 9 05-AUG-1998;
          BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
Db 23 CCATCGCGGGCAGATCCTG 4

RESULT 56
A40530/c
LOCUS      A40530                18 bp    DNA        linear        PAT 05-MAR-1997
DEFINITION Sequence 67 from Patent WO9425578.
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LOCUS      A89828                23 bp    DNA        linear        PAT 22-JAN-2000
DEFINITION Sequence 9 from Patent EP0856579.
ACCESSION  A89828
VERSION    A89828.1 GI:6738342
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 23)
AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
TITLE     An antisense oligonucleotide preparation method
JOURNAL   Patent: EP 0856579-A 9 05-AUG-1998;
          BIOGNOSTIK GES (DE)
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Query Match      0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
Db 23 CCATCGCGGGCAGATCCTG 4

RESULT 55
BD065374/c
LOCUS      BD065374                23 bp    DNA        linear        PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065374
VERSION    BD065374.1 GI:22610977
KEYWORDS   JP 2001511000-A/9.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 23)
AUTHORS   Schlingensiepen,K.H. and Brysch,W.
TITLE     An antisense oligonucleotide preparation method
JOURNAL   Patent: JP 2001511000-A 9 07-AUG-2001;
          BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
          PN JP 2001511000-A/9
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533
          PR 31-JAN-1997 EP 97101531.8
          PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
          PC C12N15/11,C07H21/04,A61K31/70
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Query Match      0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
Db 23 CCATCGCGGGCAGATCCTG 4

RESULT 56
A40530/c
LOCUS      A40530                18 bp    DNA        linear        PAT 05-MAR-1997
DEFINITION Sequence 67 from Patent WO9425578.
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A88388 20 bp DNA linear PAT 22-JAN-2000					
LOCUS Sequence 536 from Patent WO9833904.					
DEFINITION A88388					
ACCESSION A88388.1 GI:6736958					
VERSION .					
KEYWORDS unidentified					
SOURCE unclassified.					
ORGANISM .					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Brysch,W. and Schlingsienstepen,K.					
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD					
JOURNAL Patent: WO 9833904-A 536 06-AUG-1998; DE)					
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)					
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Best Local Similarity 95.0%; Pred. No. 79;					
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy 1853 CCACAAAGACAGGAACCTGG 1872					
Db 20 CCATAAAGACAGGAACCTGG 1					
RESULT 48					
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LOCUS Sequence 536 from Patent EP0856579.					
DEFINITION A90355					
ACCESSION A90355					
VERSION A90355.1 GI:6738869					
KEYWORDS .					
SOURCE unidentified					
ORGANISM unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.					
TITLE An antisense oligonucleotide preparation method					
JOURNAL Patent: EP 0856579-A 536 05-AUG-1998;					
BIOGHOSTIK GES (DE)					
FEATURES					
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/db_xref="taxon:32644"					
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Best Local Similarity 95.0%; Pred. No. 79;					
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy 1853 CCACAAAGACAGGAACCTGG 1872					
Db 20 CCATAAAGACAGGAACCTGG 1					
RESULT 49					
AR360400					
LOCUS Sequence 15 from patent US 6596489.					
DEFINITION AR360400					
ACCESSION AR360400					
VERSION AR360400.1 GI:33767430					
KEYWORDS .					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Dattagupta,N. and Tseng,T.-C.					
TITLE Methods and compositions for analyzing nucleotide sequence					
JOURNAL mismatches using RNase H					
Patent: US 6596489-A 15 22-JUL-2003;					
FEATURES					
source Location/Qualifiers					
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Query Match 0.4%; Score 18.4; DB 1; Length 20;					
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy 2580 AAAAAAAAATTGGAGAAAAA 2599					
Db 1 AAAAAAAAATTGGAGAAAAA 20					
RESULT 50					
AR360427					
LOCUS Sequence 15 from patent US 6596490.					
DEFINITION AR360427					
ACCESSION AR360427					
VERSION AR360427.1 GI:33767457					
KEYWORDS .					
SOURCE Unknown.					
ORGANISM Unknown.					
REFERENCE 1 (bases 1 to 20)					
AUTHORS Dattagupta,N.					
TITLE Nucleic acid hairpin probes and uses thereof					
JOURNAL Patent: US 6596490-A 15 22-JUL-2003;					
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Query Match 0.4%; Score 18.4; DB 1; Length 20;					
Best Local Similarity 95.0%; Pred. No. 79;					
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy 2580 AAAAAAAAATTGGAGAAAAA 2599					
Db 1 AAAAAAAAATTGGAGAAAAA 20					
RESULT 51					
AX441511					
LOCUS Sequence 15 from Patent WO0206531.					
DEFINITION AX441511					
ACCESSION AX441511					
VERSION AX441511.1 GI:21690472					
KEYWORDS .					
SOURCE synthetic construct					
ORGANISM other sequences; artificial sequences.					
REFERENCE 1					
AUTHORS Dattagupta,N.					
TITLE Nucleic acid hairpin probes and uses thereof					
JOURNAL Patent: WO 0206531-A 15 24-JAN-2002;					
Applied Gene Technologies, Inc. (US)					
FEATURES					
source Location/Qualifiers					
1..20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="Oligo AGT02022"					
Query Match 0.4%; Score 18.4; DB 1; Length 20;					
Best Local Similarity 95.0%; Pred. No. 79;					
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy 2580 AAAAAAAAATTGGAGAAAAA 2599					
Db 1 AAAAAAAAATTGGAGAAAAA 20					
PAT 02-JUL-2002					
PAT 17-AUG-2003					

AR123404
LOCUS AR123404 22 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6171584.
ACCESSION AR123404
VERSION AR123404.1 GI:14108765
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hotten,G., Neidhardt,H., Bechtold,R., Pohl,J. and Paulista,M.
TITLE Method of treatment with growth/differentiation factors of the TGF-beta family
JOURNAL Patent: US 6171584-A 17 09-JAN-2001;
FEATURES Location/Qualifiers
source
1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
||||| ||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

RESULT 43
AR137687
LOCUS AR137687 22 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 38 from patent US 6197550.
ACCESSION AR137687
VERSION AR137687.1 GI:14479196
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
TITLE DNA sequences encoding growth/differentiation
JOURNAL Patent: US 6197550-A 38 06-MAR-2001;
FEATURES Location/Qualifiers
source
1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
||||| ||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

AR123404
LOCUS AR123404 22 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6171584.
ACCESSION AR123404
VERSION AR123404.1 GI:14108765
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hotten,G., Neidhardt,H., Bechtold,R., Pohl,J. and Paulista,M.
TITLE Method of treatment with growth/differentiation factors of the TGF-beta family
JOURNAL Patent: US 6171584-A 17 09-JAN-2001;
FEATURES Location/Qualifiers
source
1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
||||| ||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

RESULT 44
AR564998
LOCUS AR564998 22 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 25 from patent US 6764994.
ACCESSION AR564998
VERSION AR564998.1 GI:53980610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hotten,G., Neidhardt,H. and Paulista,M.
TITLE Growth/differential factor of the TGF-B family
JOURNAL Patent: US 6764994-A 25 20-JUL-2004;
FEATURES Location/Qualifiers
source
1..22
/organism="unknown"

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
||||| ||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

/mol_type="genomic DNA"

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
||||| ||| ||||| |||||
Db 1 GGGATCTAGGTGGAAATGGAT 22

RESULT 45
AX030592
LOCUS AX030592 22 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 19 from Patent EP1013284.
ACCESSION AX030592
VERSION AX030592.1 GI:10278118
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Frenz,J., Shire,S. and Sliwowski,M.B.
TITLE Purified forms of dnase
JOURNAL Patent: EP 1013284-A 19 28-JUN-2000;
FEATURES Location/Qualifiers
source
1..22
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCAGCGCGCGCGC 636
||||| ||| ||||| |||||
Db 1 GCGCGCGCGCGCGCGCGCGC 22

RESULT 46
AX030592/c
LOCUS AX030592/c 22 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 19 from Patent EP1013284.
ACCESSION AX030592
VERSION AX030592.1 GI:10278118
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Frenz,J., Shire,S. and Sliwowski,M.B.
TITLE Purified forms of dnase
JOURNAL Patent: EP 1013284-A 19 28-JUN-2000;
FEATURES Location/Qualifiers
source
1..22
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCAGCGCGCGCGC 636
||||| ||| ||||| |||||
Db 22 GCGCGCGCGCGCGCGCGCGC 1

RESULT 47
A88388/c

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ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 545 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/545
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
C Location/Qualifiers
FT source 1..19
FT Location/Qualifiers
/organism='Unknown'.
FEATURES
source
1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2149 GAAATGTCAGGATAATTG 2167
Db |||||
19 GAAATGTCAGGATAATTG 1
RESULT 38
AR019469
LOCUS AR019469 22 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 18 from patent US 5783433.
ACCESSION AR019469
VERSION AR019469.1 GI:3974583
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Frenz,J. and Sliwowski,M.B.
TITLE Purified forms of DNase
JOURNAL Patent: US 5783433-A 18 21-JUL-1998;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCACGCGCGC 636
Db |||||
1 GCGCGCGCGCGCGCGCGC 22
RESULT 39
AR019469/c
LOCUS AR019469 22 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 18 from patent US 5783433.
ACCESSION AR019469
VERSION AR019469.1 GI:3974583
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Frenz,J. and Sliwowski,M.B.
TITLE Purified forms of DNase
JOURNAL Patent: US 5783433-A 18 21-JUL-1998;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCACGCGCGC 636
Db |||||
1 GCGCGCGCGCGCGCGCGC 22
TITLE Purified forms of DNase
JOURNAL Patent: US 5783433-A 18 21-JUL-1998;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCACGCGCGC 636
Db |||||
22 GCGCGCGCGCGCGCGCGC 1
RESULT 40
AR038951
LOCUS AR038951 22 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 34 from patent US 5807713.
ACCESSION AR038951
VERSION AR038951.1 GI:5958314
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
TITLE DNA encoding growth/differentiation factor
JOURNAL Patent: US 5807713-A 34 15-SEP-1998;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCACGCGCGC 636
Db |||||
22 GCGCGCGCGCGCGCGCGC 1
TITLE Purified forms of DNase
JOURNAL Patent: US 5783433-A 18 21-JUL-1998;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2200 GGGATCTTGGATGGAATGGAT 2221
Db |||||
1 GGGATCTAGGTGGGAATGGAT 22
RESULT 41
AR091306
LOCUS AR091306 22 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 25 from patent US 5994094.
ACCESSION AR091306
VERSION AR091306.1 GI:10018061
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hotten,G., Neidhardt,H. and Paulista,M.
TITLE Growth/differentiation factor of the TGF-.beta. family
JOURNAL Patent: US 5994094-A 25 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2200 GGGATCTTGGATGGAATGGAT 2221
Db |||||
1 GGGATCTAGGTGGGAATGGAT 22
RESULT 42
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RESULT 33	A88397/c	LOCUS	A88397	Sequence 545 from Patent WO9833904.	19 bp	DNA	linear	PAT 22-JAN-2000	
DEFINITION		ACCESSION	A88397						
VERSION		KEYWORDS	A88397.1	GI:6736967					
SOURCE		ORGANISM		unidentified					
				unclassified.					
REFERENCE				1 (bases 1 to 19)					
AUTHORS				Brysch,W. and Schlingensiepen,K.					
TITLE				AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD					
JOURNAL				Patent: WO 9833904-A 545 06-AUG-1998;					
FEATURES				BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)					
source				1..19					
				/organism="unidentified"					
				/mol_type="unassigned DNA"					
				/db_xref="taxon:32644"					
Query Match				0.4%;	Score 19;	DB 1;	Length 19;		
Best Local Similarity				100.0%;	Pred. No. 53;				
Matches				19;	Conservative	0;	Mismatches	0;	Indels
Qy	2149	GAATGTGCAGGATAATTG	2167						
Db	19	GAATGTGCAGGATAATTG	1						
RESULT 34	A90364/c	LOCUS	A90364	Sequence 545 from Patent EP0856579.	19 bp	DNA	linear	PAT 22-JAN-2000	
DEFINITION		ACCESSION	A90364						
VERSION		KEYWORDS	A90364.1	GI:6738878					
SOURCE				unidentified					
ORGANISM				unclassified.					
REFERENCE				1 (bases 1 to 19)					
AUTHORS				Brysch,W.D. and Schlingensiepen,K.D.					
TITLE				An antisense oligonucleotide preparation method					
JOURNAL				Patent: EP 0856579-A 545 05-AUG-1998;					
FEATURES				BIOGNOSTIK GES (DE)					
source				1..19					
				/organism="unidentified"					
				/mol_type="unassigned DNA"					
				/db_xref="taxon:32644"					
Query Match				0.4%;	Score 19;	DB 1;	Length 19;		
Best Local Similarity				100.0%;	Pred. No. 53;				
Matches				19;	Conservative	0;	Mismatches	0;	Indels
Qy	2149	GAATGTGCAGGATAATTG	2167						
Db	19	GAATGTGCAGGATAATTG	1						
RESULT 35	BD234915/c	LOCUS	BD234915	A method for stimulating the immune system.	19 bp	DNA	linear	PAT 17-JUL-2003	
DEFINITION		ACCESSION	BD234915						
VERSION		KEYWORDS	BD234915.1	GI:33044685					
SOURCE				JP 2002517434-A/19.					
ORGANISM				Homo sapiens					
REFERENCE				1 (bases 1 to 19)					
				Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS				Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.					
TITLE				A method for stimulating the immune system					
JOURNAL				Patent: JP 2002517434-A 19 18-JUN-2002;					
COMMENT				BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH					
				OS Homo sapiens (human)					
				PN JP 2002517434-A/19					
				PD 18-JUN-2002					
				PF 10-JUN-1999 JP 2000553044					
				PR 10-JUN-1998 EP 98110709.7.25-JUL-1998 EP 98113974.4 PI					
				KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI					
				BRYSCH					
				PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/					
				PC 00,A61P35/00,					
				PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A					
				method for stimulating the immune system					
				FH Key					
				Location/Qualifiers					
				FT source					
				1..19					
				/organism='Homo sapiens (human)'					
FEATURES				Location/Qualifiers					
source				1..19					
				/organism="Homo sapiens"					
				/mol_type="genomic DNA"					
				/db_xref="taxon:9606"					
Query Match				0.4%;	Score 19;	DB 1;	Length 19;		
Best Local Similarity				100.0%;	Pred. No. 53;				
Matches				19;	Conservative	0;	Mismatches	0;	Indels
Qy	2149	GAATGTGCAGGATAATTG	2167						
Db	19	GAATGTGCAGGATAATTG	1						
RESULT 36	AX008986/c	LOCUS	AX008986	Sequence 19 from Patent WO9963975.	19 bp	DNA	linear	PAT 06-SEP-2000	
DEFINITION		ACCESSION	AX008986						
VERSION		KEYWORDS	AX008986.1	GI:9996360					
SOURCE				Homo sapiens (human)					
ORGANISM				Homo sapiens					
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE				1					
AUTHORS				Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.					
TITLE				A method for stimulating the immune system					
JOURNAL				Patent: WO 9963975-A 19 16-DEC-1999;					
FEATURES				BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL					
source				HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)					
				Location/Qualifiers					
				1..19					
				/organism="Homo sapiens"					
				/mol_type="unassigned DNA"					
				/db_xref="taxon:9606"					
Query Match				0.4%;	Score 19;	DB 1;	Length 19;		
Best Local Similarity				100.0%;	Pred. No. 53;				
Matches				19;	Conservative	0;	Mismatches	0;	Indels
Qy	2149	GAATGTGCAGGATAATTG	2167						
Db	19	GAATGTGCAGGATAATTG	1						
RESULT 37	BD065910/c	LOCUS	BD065910	An antisense oligonucleotide preparation method.	19 bp	DNA	linear	PAT 27-AUG-2002	
DEFINITION		ACCESSION	BD065910						
VERSION		KEYWORDS	BD065910.1	GI:22611513					
SOURCE				JP 2001511000-A/545.					
ORGANISM				unidentified					

RESULT 28
LOCUS I43133 24 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 13 from patent US 5631135.
ACCESSION I43133
VERSION I43133.1 GI:2468377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligonucleotide N3'.fwdarw.P5'. phosphoramidates: hybridization and nuclease resistance properties
JOURNAL Patent: US 5631135-A 13 20-MAY-1997;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2731 AAAAAGAAACATCTTTT TTTT 2754
||||| ||||| ||||| |||||
Db 1 AAAAAAAACCCTTTT TTTT 24
RESULT 29
LOCUS I92011 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 13 from patent US 5726297.
ACCESSION I92011
VERSION I92011.1 GI:3936481
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3'. P5'. phosphoramidates
JOURNAL Patent: US 5726297-A 13 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2731 AAAAAGAAACATCTTTT TTTT 2754
||||| ||||| ||||| |||||
Db 1 AAAAAAAACCCTTTT TTTT 24
RESULT 30
LOCUS AR306126 24 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 67 from patent US 6548251.
ACCESSION AR306126
VERSION AR306126.1 GI:31695813
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kozayavkin,S.A., Malykh,A.G., Polouchine,N.N. and Slesarev,A.I.
TITLE Inhibition of molecular and biological processes using modified oligonucleotides

JOURNAL Patent: US 6548251-A 67 15-APR-2003;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2730 CAAAAGAAACATCTTTT TTTT 2753
||||| ||||| ||||| |||||
Db 1 CAAAAAAACACTTTT TTTT 24

RESULT 31
LOCUS AR473409 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 22 from patent US 6686516.
ACCESSION AR473409
VERSION AR473409.1 GI:42708866
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lebel,E.G., Heifetz,P.B. and Goff,S.A.
TITLE Expression of trehalose 6-phosphate synthase in plant plastids
JOURNAL Patent: US 6686516-A 22 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCCGCCCGCCGCCCCCA 991
||||| ||||| ||||| |||||
Db 1 AGCTTCCCGCCCGCCGCCCCCA 24

RESULT 32
LOCUS AX278211 24 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 22 from Patent WO0177353.
ACCESSION AX278211
VERSION AX278211.1 GI:16605262
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Heifetz,P.B., Goff,S.A., Tuttle,A.B. and Griot-Wenk,M.E.
TITLE Expression of pollen allergens in plastids
JOURNAL Patent: WO 0177353-A 22 18-OCT-2001;
Syngenta Participations AG (CH)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCCGCCCGCCGCCCCCA 991
||||| ||||| ||||| |||||
Db 1 AGCTTCCCGCCCGCCGCCCCCA 24

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VERSION BD188897.1 GI:32998636
KEYWORDS JP 2003012688-A/13.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
hybridization and nuclease tolerant characteristics
JOURNAL Patent: JP 2003012688-A 13 15-JAN-2003;
COMMENT LYNX THERAPEUTICS INC
OS Unidentified
PN JP 2003012688-A/13
PD 15-JAN-2003
PF 12-JUN-2002 JP 2002171743
PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 P1
SERGEI M GRVYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02.C12Q1/68
CC Strandedness: Both;
CC Topology: Linear;
CC Oligonucleotide N3' to P5' phosphoramidate: synthesis and CC
compound;
CC hybridization and nuclease tolerant characteristics FH Key
Location/Qualifiers
FT source
FT 1. .24
Location/Qualifiers
/organism='Unidentified'.
1. .24
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT TTTT 2754
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Db 1 AAAAAAAAACCCCTTTT TTTT 24

RESULT 25
BD237693 24 bp DNA linear PAT 17-JUL-2003
LOCUS Therapeutically active proteins in plants.
DEFINITION BD237693
ACCESSION BD237693
VERSION BD237693.1 GI:33047463
KEYWORDS JP 2002526116-A/22.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Heifetz,P.B., Goff,S.A., Tuttle,A.B. and Wenk,M.E.G.
TITLE Therapeutically active proteins in plants
JOURNAL Patent: JP 2002526116-A 22 20-AUG-2002;
SYNGENTA PARTICIPATIONS AG
OS Artificial Sequence
PN JP 2002526116-A/22
PD 20-AUG-2002
PF 05-OCT-1999 JP 2000574707
PR 07-OCT-1998 US 09/167362,07-OCT-1998 US 09/168231 P1
PETER BERNARD HEIFETZ,STEPHEN ARTHUR GOFF,ANNMARIE BLOOM PI
TUTTLE,
P1 MONIKA ELSE GRIOT WENK
PC A01H5/00,A23L1/30,A23L3/30,A61K38/00,A61K38/16,A61K38/22, PC
A61K38/28,
PC A61K38/43,A61K39/00,A61K39/35,A61P29/00,A61P37/00,A61P37/06,
PC A61P37/08,
PC C12N5/10.C12N15/09//C12N5/10.C12R1:91,C12N15/00,C12N5/00, PC
A61K37/02,
PC A61K37/26,A61K37/48,A61K37/04,A61K37/24,(C12N5/00,C12R1:91) CC
Description of Artificial Sequence: oligonucleotide FH Key
Location/Qualifiers

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Location/Qualifiers
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/mol_type='genomic DNA'
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Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCCCCCCCACCCGCCCA 991
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Db 1 AGCTTCCCCCCCCCCCCCCCCCA 24

RESULT 26
I33258 24 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 13 from patent US 5591607.
DEFINITION I33258
ACCESSION I33258
VERSION I33258.1 GI:1824049
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3.fwdarw.P5' phosphoramidates: triplex DNA
formation
JOURNAL Patent: US 5591607-A 13 07-JAN-1997;
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Location/Qualifiers
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Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT TTTT 2754
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Db 1 AAAAAAAAACCCCTTTT TTTT 24

RESULT 27
I35523 24 bp DNA linear PAT 13-MAY-1997
LOCUS Sequence 13 from patent US 5599922.
DEFINITION I35523
ACCESSION I35523
VERSION I35523.1 GI:2088491
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5599922-A 13 04-FEB-1997;
FEATURES
source
FT source
FT 1. .24
Location/Qualifiers
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Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT TTTT 2754
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Db 1 AAAAAAAAACCCCTTTT TTTT 24
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DEFINITION Sequence 13 from patent US 5965720.
ACCESSION AR079586
VERSION AR079586.1 GI:10006330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.p5' phosphoramidates
JOURNAL Patent: US 5965720-A 13 12-OCT-1999;
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QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAAAAAAACCCCTTTTITTT 24

RESULT 21
LOCUS AR123295 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 13 from patent US 6169170.
ACCESSION AR123295
VERSION AR123295.1 GI:14108261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.N5'Phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 13 02-JAN-2001;
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QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAAAAAAACCCCTTTTITTT 24

RESULT 22
LOCUS BD138045 24 bp DNA linear PAT 18-SEP-2002
DEFINITION Expression of trehalose biosynthetic genes in plants.
ACCESSION BD138045
VERSION BD138045.1 GI:23232990
KEYWORDS JP 2002505875-A/23.
SOURCE synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1 (bases 1 to 24)
AUTHORS Lebel,E.G., Heifetz,P.B. and Goff,S.A.
TITLE Expression of trehalose biosynthetic genes in plants
JOURNAL Patent: JP 2002505875-A 22 26-FEB-2002;
COMMENT NOVARTIS AG
  OS Artificial Sequence
  PN JP 2002505875-A/22
  PD 26-FEB-2002
  PF 09-MAR-1999 JP 2000535737
  PR 11-MAR-1998 US 60/077665

PI EDOUARD GUILLAUME LEBEL, PETER BERNARD HEIFETZ, STEPHEN ARTHUR
PI GOFF
PC A01H5/00,C12N5/10,C12N9/10,C12N15/09,C12P19/12,C12N5/
PC 00,C12N15/00
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CC Location/Qualifiers
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      /db_xref="taxon:32630"
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  Best Local Similarity 87.5%; Pred.No.86;
  Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 968 AGATTCCCCCCCCACCCGCCCA 991
Db 1 AGCTTCCCCCCCCCCCCCCCCCA 24

RESULT 23
LOCUS BD175807 24 bp DNA linear PAT 18-MAR-2003
DEFINITION 2'-4'-BNA oligonucleotide having N3'-p5' binding.
ACCESSION BD175807
VERSION BD175807.1 GI:29121509
KEYWORDS JP 2002255990-A/10.
SOURCE synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1 (bases 1 to 24)
AUTHORS Imanishi,T. and Kohiga,S.
TITLE 2'-4'-BNA oligonucleotide having N3'-p5' binding
JOURNAL Patent: JP 2002255990-A 10 11-SEP-2002;
COMMENT SANKYO CO LTD
  OS Artificial Sequence
  PN JP 2002255990-A/10
  PD 11-SEP-2002
  PF 19-NOV-2001 JP 2001352543
  PI TAKESHI IMANISHI,SATOSHI KOHIGA
  PC C07H19/06,A61K31/712,A61K48/00,A61P31/18,C07H19/16,C07H21/00,
  PC C12N15/09,
  PC C12N15/00
  CC Description of Artificial Sequence: Synthesized and hairpin-
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  CC oligonucleotide
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  Best Local Similarity 87.5%; Pred.No.86;
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QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAAAAAAACCCCTTTTITTT 24

RESULT 24
LOCUS BD188897 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide N3' to p5' phosphoramidate: synthesis and compound;
ACCESSION hybridization and nuclease tolerant characteristics.
  BD188897
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VERSION AX043186.1 GI:11341794
SOURCE .
KEYWORDS synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 005088-A 752 02-NOV-2000;
Amer sham Pharmacia Biotech AB (SE)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="DPB1 Heterozygote Primer Sequence"
Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 918 TCCTTCCAGGAGAAAAAACA 942
Db 25 TCCTCTCCAGGAGAAAAA 1
RESULT 16
LOCUS AR367879 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 8 from patent US 6376199.
ACCESSION AR367879
VERSION AR367879.1 GI:34601335
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Caniggia,I., Post,M. and Lye,S.
TITLE Methods to diagnose a required regulation of trophoblast invasion
JOURNAL Patent: US 6376199-A 8 23-APR-2002;
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Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1254 CATCTGTCCTCCGTCGCT 1273
Db 1 CATCTGTCCTCCGTCGCT 20
RESULT 17
LOCUS A23914 21 bp DNA linear PAT 25-JAN-1995
DEFINITION TGF-beta hybrid PCR primer.
ACCESSION A23914
VERSION A23914.1 GI:833308
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 20 19-MAY-1993;
CIBA-GEIGY AG
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Best Local Similarity 95.2%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2234 AGGTACAAATGCTAACTTCTG 2254
Db 1 AGGTACAAATGCCAACTTCTG 21
/db_xref="taxon:32630"
RESULT 18
LOCUS A23915/c 21 bp DNA linear PAT 25-JAN-1995
DEFINITION TGF-beta hybrid PCR primer.
ACCESSION A23915
VERSION A23915.1 GI:833309
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 21 19-MAY-1993;
CIBA-GEIGY AG
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Location/Qualifiers
/organism="synthetic construct"
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Best Local Similarity 95.2%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2234 AGGTACAAATGCTAACTTCTG 2254
Db 21 AGGTACAAATGCCAACTTCTG 1
RESULT 19
LOCUS AR058881 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5837835.
ACCESSION AR058881
VERSION AR058881.1 GI:5984458
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 13 17-NOV-1998;
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source
1..24
Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2731 AAAAGAAACATCTTTTTTTT 2754
Db 1 AAAAAAAAAACCCCTTTTTTTT 24
RESULT 20
LOCUS AR079586 24 bp DNA linear PAT 31-AUG-2000
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Query Match	0.5%; Score 22.2; DB 1; Length 27;
Best Local Similarity	88.9%; Pred. No. 29;
Matches	24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1520 GGAGGTTTATAAAATCGACATGCGGTC 1546
Db	27 GGAGGTTTACAAAATAGACATGCCGC 1
RESULT 11	
CQ778291/c	
LOCUS	CQ778291
DEFINITION	Sequence 1977 from Patent EP1394274.
ACCESSION	CQ778291
VERSION	CQ778291.1 GI:45381009
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhashi, K.
TITLE	Methods of testing for bronchial asthma or chronic obstructive pulmonary disease
JOURNAL	Patent: EP 1394274-A 1977 03-MAR-2004;
Genex Research, Inc. (JP)	
FEATURES	Location/Qualifiers
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	/note="an artificially synthesized primer sequence"
Query Match	0.5%; Score 22; DB 1; Length 22;
Best Local Similarity	100.0%; Pred. No. 19;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	317 TGTGTTCACAGGGGTTAAGG 338
Db	22 TGTGTTCACAGGGGTTAAGG 1
RESULT 12	
AR409919	
LOCUS	AR409919
DEFINITION	Sequence 32 from patent US 6635422.
ACCESSION	AR409919
VERSION	AR409919.1 GI:40161054
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 22)
AUTHORS	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.
TITLE	Methods for isolating and characterizing endogenous mRNA-protein (mRNP) complexes
JOURNAL	Patent: US 6635422-A 32 21-OCT-2003;
Genex Research, Inc. (JP)	
FEATURES	Location/Qualifiers
source	1..22
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Query Match	0.5%; Score 22; DB 1; Length 22;
Best Local Similarity	100.0%; Pred. No. 19;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	4078 TTTTCTTTAATGTTTTTTT 4099
Db	1 TTTTCTTTAATGTTTTTTT 22
RESULT 13	
AX043186/c	
LOCUS	AX043186
DEFINITION	Sequence 752 from Patent WO0065088.
ACCESSION	AX043186

CQ778188	
LOCUS	CQ778188
DEFINITION	Sequence 1874 from Patent EP1394274.
ACCESSION	CQ778188
VERSION	CQ778188.1 GI:45380906
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhashi, K.
TITLE	Methods of testing for bronchial asthma or chronic obstructive pulmonary disease
JOURNAL	Patent: EP 1394274-A 1874 03-MAR-2004;
Genex Research, Inc. (JP)	
FEATURES	Location/Qualifiers
source	1..25
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	/db_xref="taxon:32630"
	/note="an artificially synthesized TagMan probe sequence"
misc_feature	1
	/note="Label FAM(6-carboxy-fluorescein)"
misc_feature	25
	/note="Label
	TAMRA(6-carboxy-N,N,NH-tetramethylrhodamine)"
Query Match	0.5%; Score 21.8; DB 1; Length 25;
Best Local Similarity	92.0%; Pred. No. 28;
Matches	23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1759 CCCAGCGCTACATCGATGCAAGGT 1783
Db	1 CCCAGCGCTACATCGACAGCAAGT 25
RESULT 14	
AX113804	
LOCUS	AX113804
DEFINITION	Sequence 50 from Patent WO0127256.
ACCESSION	AX113804
VERSION	AX113804.1 GI:13939970
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Wu, L., Carey, M.F. and Belleggrun, A.S.
TITLE	Chimeric transcriptional regulatory element and methods for prostate-targeted gene expression
JOURNAL	Patent: WO 0127256-A 50 19-APR-2001;
The Regents of the University of California System (US)	
FEATURES	Location/Qualifiers
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Query Match	0.5%; Score 21.4; DB 1; Length 24;
Best Local Similarity	95.7%; Pred. No. 31;
Matches	22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1278 CTGTCTACCTGCAGCACCTCGA 1300
Db	2 CTGTCTACCTGCAGCACCTCGA 24
RESULT 15	
AX043186/c	
LOCUS	AX043186
DEFINITION	Sequence 752 from Patent WO0065088.
ACCESSION	AX043186

Db 1 TTTTTCCTTTAAATGTAATGGTCTTT 33
RESULT 6
LOCUS AR409918 25 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 31 from patent US 6635422.
ACCESSION AR409918
VERSION AR409918.1 GI:40161053
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein (mRNP) complexes
JOURNAL Patent: US 6635422-A 31 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3693 TTCAATTTTTTTTATATACTACTCTT 3717
Db 1 TTCAATTTTTTTTATATACTACTT 25
RESULT 7
LOCUS CQ778289 23 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 1975 from Patent EP1394274.
ACCESSION CQ778289
VERSION CQ778289.1 GI:45381007
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuohara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive pulmonary disease
JOURNAL Patent: EP 1394274-A 1975 03-MAR-2004;
Genox Research, Inc. (JP)
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="an artificially synthesized primer sequence"
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 217 TTACCCTAAGCGAAGAAAGTGCAA 239
Db 1 TTACCCTAAGCGAAGAAAGTGCAA 23
RESULT 8
LOCUS A23924 26 bp DNA linear PAT 25-JAN-1995
DEFINITION TGF-beta hybrid PCR primer.
ACCESSION A23924
VERSION A23924.1 GI:833318
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 30 19-MAY-1993;
CIBA-GEIGY AG
FEATURES Location/Qualifiers
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Best Local Similarity 92.3%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2265 TGCCCATATCTATGGAGTTCAGACAC 2290
Db 1 TGCCCGTATTATTGAGTTCAGACAC 26
RESULT 9
LOCUS A23925/c 26 bp DNA linear PAT 25-JAN-1995
DEFINITION TGF-beta hybrid PCR primer.
ACCESSION A23925
VERSION A23925.1 GI:833319
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 31 19-MAY-1993;
CIBA-GEIGY AG
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 0.5%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2265 TGCCCATATCTATGGAGTTCAGACAC 2290
Db 26 TGCCCGTATTATTGAGTTCAGACAC 1
RESULT 10
LOCUS AX113805/c 27 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 51 from Patent WO0127256.
ACCESSION AX113805
VERSION AX113805.1 GI:13939971
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wu,L., Carey,M.F. and Belldegrun,A.S.
TITLE Chimeric transcriptional regulatory element and methods for prostate-targeted gene expression
JOURNAL Patent: WO 0127256-A 51 19-APR-2001;
The Regents of the University of California System (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"

RESULT 1
A18285
LOCUS A18285 39 bp DNA linear PAT 17-MAY-1994
DEFINITION oligonucleotide.
ACCESSION A18285
VERSION A18285.1 GI:513245
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 39)
AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for the production of biologically active protein (e.g. TGF)
JOURNAL Patent: EP 0433225-A 12 19-JUN-1991;
CIBA-GEIGY AG
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
Query Match 0.8%; Score 35.8; DB 1; Length 39;
Best Local Similarity 94.9%; Pred. No. 0.12;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2124 GCTTTGGATGCGCCCTACTGCTTTAGAAATGTCAGGAT 2162
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Db 1 GCTTTGGATGCGCCCTATTGCTTTAGAAATGTCAGGAT 39
RESULT 2
I56859
LOCUS I56859 39 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5650494.
ACCESSION I56859
VERSION I56859.1 GI:2477272
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Cerletti,N., McMaster,G.Kent., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for refolding recombinantly produced TGF-.beta.-like proteins
JOURNAL Patent: US 5650494-A 6 22-JUL-1997;
FEATURES
source Location/Qualifiers
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RESULT 3
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DEFINITION oligonucleotide.
ACCESSION A18286
VERSION A18286.1 GI:513246
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 39)
AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.

TITLE Process for the production of biologically active protein (e.g. TGF)
JOURNAL Patent: EP 0433225-A 13 19-JUN-1991;
CIBA-GEIGY AG
FEATURES
source Location/Qualifiers
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I56860/c
LOCUS I56860 39 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5650494.
ACCESSION I56860
VERSION I56860.1 GI:2477273
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Cerletti,N., McMaster,G.Kent., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for refolding recombinantly produced TGF-.beta.-like proteins
JOURNAL Patent: US 5650494-A 7 22-JUL-1997;
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ACCESSION AR409916
VERSION AR409916.1 GI:40161051
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein (mRNP) complexes
JOURNAL Patent: US 6635422-A 29 21-OCT-2003;
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601	14	0.3	17	1	AX738493	ACCESSION:AX738493	C 674	13.8	0.3	17	1	AR186698	ACCESSION:AR186698
602	14	0.3	17	1	AX757892	ACCESSION:AX757892	C 675	13.8	0.3	17	1	AR186927	ACCESSION:AR186927
C 603	14	0.3	17	1	BD142808	ACCESSION:BD142808	C 676	13.8	0.3	17	1	AR187056	ACCESSION:AR187056
C 604	14	0.3	17	1	BD143834	ACCESSION:BD143834	C 677	13.8	0.3	17	1	AR187057	ACCESSION:AR187057
C 605	14	0.3	17	1	BD167835	ACCESSION:BD167835	C 678	13.8	0.3	17	1	AR187058	ACCESSION:AR187058
C 606	14	0.3	17	1	BD167907	ACCESSION:BD167907	C 679	13.8	0.3	17	1	AR187059	ACCESSION:AR187059
C 607	14	0.3	17	1	BD168111	ACCESSION:BD168111	C 680	13.8	0.3	17	1	AR187063	ACCESSION:AR187063
C 608	14	0.3	17	1	BD171177	ACCESSION:BD171177	C 681	13.8	0.3	17	1	AR187064	ACCESSION:AR187064
C 609	14	0.3	17	1	E02988	ACCESSION:E02988	C 682	13.8	0.3	17	1	AR187068	ACCESSION:AR187068
C 610	14	0.3	17	1	E34258	ACCESSION:E34258	683	13.8	0.3	17	1	AR187239	ACCESSION:AR187239
C 611	14	0.3	17	1	AR266625	ACCESSION:AR266625	684	13.8	0.3	17	1	AR188317	ACCESSION:AR188317
C 612	14	0.3	17	1	AX215415	ACCESSION:AX215415	C 685	13.8	0.3	17	1	AR188526	ACCESSION:AR188526
C 613	14	0.3	17	1	AX216957	ACCESSION:AX216957	686	13.8	0.3	17	1	AR188812	ACCESSION:AR188812
C 614	14	0.3	17	1	AX216958	ACCESSION:AX216958	687	13.8	0.3	17	1	AR190075	ACCESSION:AR190075
C 615	14	0.3	17	1	AX532502	ACCESSION:AX532502	688	13.8	0.3	17	1	AR190475	ACCESSION:AR190475
C 616	14	0.3	17	1	AX532503	ACCESSION:AX532503	C 689	13.8	0.3	17	1	AR192138	ACCESSION:AR192138
C 617	14	0.3	17	1	AX532504	ACCESSION:AX532504	C 690	13.8	0.3	17	1	AR196413	ACCESSION:AR196413

399	14.4	0.3	17	1	I54412	ACCESSION:I54412	C 472	14.4	0.3	18	1	BD107507	ACCESSION:BD107507
400	14.4	0.3	17	1	I54418	ACCESSION:I54418	C 473	14.2	0.3	16	1	E52143	ACCESSION:E52143
401	14.4	0.3	17	1	I54420	ACCESSION:I54420	C 474	14.2	0.3	16	1	E53842	ACCESSION:E53842
402	14.4	0.3	17	1	I94415	ACCESSION:I94415	C 475	14.2	0.3	17	1	AX406535	ACCESSION:AX406535
403	14.4	0.3	17	1	I94418	ACCESSION:I94418	C 476	14.2	0.3	17	1	AX721791	ACCESSION:AX721791
404	14.4	0.3	17	1	AR188518	ACCESSION:AR188518	C 477	14	0.3	14	1	A40172	ACCESSION:A40172
405	14.4	0.3	17	1	AR192340	ACCESSION:AR192340	C 478	14	0.3	14	1	A40520	ACCESSION:A40520
406	14.4	0.3	17	1	AR324371	ACCESSION:AR324371	C 479	14	0.3	14	1	A40526	ACCESSION:A40526
407	14.4	0.3	17	1	AR326210	ACCESSION:AR326210	C 480	14	0.3	14	1	A40534	ACCESSION:A40534
408	14.4	0.3	17	1	AR329023	ACCESSION:AR329023	C 481	14	0.3	14	1	A40537	ACCESSION:A40537
409	14.4	0.3	17	1	AX214791	ACCESSION:AX214791	C 482	14	0.3	14	1	A40538	ACCESSION:A40538
410	14.4	0.3	17	1	AX227570	ACCESSION:AX227570	C 483	14	0.3	14	1	A40554	ACCESSION:A40554
411	14.4	0.3	17	1	AX671893	ACCESSION:AX671893	C 484	14	0.3	14	1	A40564	ACCESSION:A40564
412	14.4	0.3	17	1	AX673880	ACCESSION:AX673880	C 485	14	0.3	14	1	A40566	ACCESSION:A40566
413	14.4	0.3	17	1	AX674166	ACCESSION:AX674166	C 486	14	0.3	14	1	A40569	ACCESSION:A40569
414	14.4	0.3	17	1	AX676082	ACCESSION:AX676082	C 487	14	0.3	14	1	A40585	ACCESSION:A40585
415	14.4	0.3	17	1	AX724450	ACCESSION:AX724450	C 488	14	0.3	14	1	A40599	ACCESSION:A40599
416	14.4	0.3	17	1	AX726113	ACCESSION:AX726113	C 489	14	0.3	14	1	A88371	ACCESSION:A88371
417	14.4	0.3	17	1	AX726611	ACCESSION:AX726611	C 490	14	0.3	14	1	A88399	ACCESSION:A88399
418	14.4	0.3	17	1	AX733221	ACCESSION:AX733221	C 491	14	0.3	14	1	A88439	ACCESSION:A88439
419	14.4	0.3	17	1	AX735212	ACCESSION:AX735212	C 492	14	0.3	14	1	A89047	ACCESSION:A89047
420	14.4	0.3	17	1	AX736066	ACCESSION:AX736066	C 493	14	0.3	14	1	A89053	ACCESSION:A89053
421	14.4	0.3	17	1	AX736332	ACCESSION:AX736332	C 494	14	0.3	14	1	A89060	ACCESSION:A89060
422	14.4	0.3	17	1	AX737597	ACCESSION:AX737597	C 495	14	0.3	14	1	A89062	ACCESSION:A89062
423	14.4	0.3	17	1	AX738493	ACCESSION:AX738493	C 496	14	0.3	14	1	A89063	ACCESSION:A89063
424	14.4	0.3	17	1	AX739553	ACCESSION:AX739553	C 497	14	0.3	14	1	A89079	ACCESSION:A89079
425	14.4	0.3	17	1	AX739596	ACCESSION:AX739596	C 498	14	0.3	14	1	A89089	ACCESSION:A89089
426	14.4	0.3	17	1	AX757067	ACCESSION:AX757067	C 499	14	0.3	14	1	A89091	ACCESSION:A89091
427	14.4	0.3	17	1	AX757780	ACCESSION:AX757780	C 500	14	0.3	14	1	A89109	ACCESSION:A89109
428	14.4	0.3	17	1	AX757892	ACCESSION:AX757892	C 501	14	0.3	14	1	A89123	ACCESSION:A89123
429	14.4	0.3	17	1	AX759064	ACCESSION:AX759064	C 502	14	0.3	14	1	A90338	ACCESSION:A90338
430	14.4	0.3	17	1	AX759785	ACCESSION:AX759785	C 503	14	0.3	14	1	A90366	ACCESSION:A90366
431	14.4	0.3	17	1	AX761129	ACCESSION:AX761129	C 504	14	0.3	14	1	A90406	ACCESSION:A90406
432	14.4	0.3	17	1	AX761716	ACCESSION:AX761716	C 505	14	0.3	14	1	AR174027	ACCESSION:AR174027
433	14.4	0.3	17	1	AX761717	ACCESSION:AX761717	C 506	14	0.3	14	1	AR174031	ACCESSION:AR174031
434	14.4	0.3	18	1	AR078640	ACCESSION:AR078640	C 507	14	0.3	14	1	BD176798	ACCESSION:BD176798
435	14.4	0.3	18	1	BD145035	ACCESSION:BD145035	C 508	14	0.3	14	1	BD176799	ACCESSION:BD176799
436	14.4	0.3	18	1	BD145036	ACCESSION:BD145036	C 509	14	0.3	14	1	BD176801	ACCESSION:BD176801
437	14.4	0.3	18	1	BD145037	ACCESSION:BD145037	C 510	14	0.3	14	1	BD234897	ACCESSION:BD234897
438	14.4	0.3	18	1	BD145039	ACCESSION:BD145039	C 511	14	0.3	14	1	BD234898	ACCESSION:BD234898
439	14.4	0.3	18	1	BD166035	ACCESSION:BD166035	C 512	14	0.3	14	1	BD234901	ACCESSION:BD234901
440	14.4	0.3	18	1	BD166036	ACCESSION:BD166036	C 513	14	0.3	14	1	BD234907	ACCESSION:BD234907
441	14.4	0.3	18	1	BD166037	ACCESSION:BD166037	C 514	14	0.3	14	1	BD234955	ACCESSION:BD234955
442	14.4	0.3	18	1	BD166039	ACCESSION:BD166039	C 515	14	0.3	14	1	BD234960	ACCESSION:BD234960
443	14.4	0.3	18	1	CQ807628	ACCESSION:CQ807628	C 516	14	0.3	14	1	BD234986	ACCESSION:BD234986
444	14.4	0.3	18	1	CQ814895	ACCESSION:CQ814895	C 517	14	0.3	14	1	AR232800	ACCESSION:AR232800
445	14.4	0.3	18	1	AR196692	ACCESSION:AR196692	C 518	14	0.3	14	1	AR232806	ACCESSION:AR232806
446	14.4	0.3	18	1	AR208427	ACCESSION:AR208427	C 519	14	0.3	14	1	AR232814	ACCESSION:AR232814
447	14.4	0.3	18	1	AR264931	ACCESSION:AR264931	C 520	14	0.3	14	1	AR232817	ACCESSION:AR232817
448	14.4	0.3	18	1	AR264932	ACCESSION:AR264932	C 521	14	0.3	14	1	AR232818	ACCESSION:AR232818
449	14.4	0.3	18	1	AR264933	ACCESSION:AR264933	C 522	14	0.3	14	1	AR232834	ACCESSION:AR232834
450	14.4	0.3	18	1	AR264935	ACCESSION:AR264935	C 523	14	0.3	14	1	AR232844	ACCESSION:AR232844
451	14.4	0.3	18	1	AR371952	ACCESSION:AR371952	C 524	14	0.3	14	1	AR232846	ACCESSION:AR232846
452	14.4	0.3	18	1	AR478212	ACCESSION:AR478212	C 525	14	0.3	14	1	AR232849	ACCESSION:AR232849
453	14.4	0.3	18	1	AR478213	ACCESSION:AR478213	C 526	14	0.3	14	1	AR232865	ACCESSION:AR232865
454	14.4	0.3	18	1	AR478214	ACCESSION:AR478214	C 527	14	0.3	14	1	AR232879	ACCESSION:AR232879
455	14.4	0.3	18	1	AR478216	ACCESSION:AR478216	C 528	14	0.3	14	1	AR242022	ACCESSION:AR242022
456	14.4	0.3	18	1	AX085253	ACCESSION:AX085253	C 529	14	0.3	14	1	AX008968	ACCESSION:AX008968
457	14.4	0.3	18	1	AX599312	ACCESSION:AX599312	C 530	14	0.3	14	1	AX008969	ACCESSION:AX008969
458	14.4	0.3	18	1	AX599726	ACCESSION:AX599726	C 531	14	0.3	14	1	AX008972	ACCESSION:AX008972
459	14.4	0.3	18	1	AX767728	ACCESSION:AX767728	C 532	14	0.3	14	1	AX008978	ACCESSION:AX008978
460	14.4	0.3	18	1	AX796166	ACCESSION:AX796166	C 533	14	0.3	14	1	AX009026	ACCESSION:AX009026
461	14.4	0.3	18	1	AX822692	ACCESSION:AX822692	C 534	14	0.3	14	1	AX009031	ACCESSION:AX009031
462	14.4	0.3	18	1	AX823114	ACCESSION:AX823114	C 535	14	0.3	14	1	AX009057	ACCESSION:AX009057
463	14.4	0.3	18	1	AX826332	ACCESSION:AX826332	C 536	14	0.3	14	1	AX030095	ACCESSION:AX030095
464	14.4	0.3	18	1	AX826754	ACCESSION:AX826754	C 537	14	0.3	14	1	AX030101	ACCESSION:AX030101
465	14.4	0.3	18	1	BD072876	ACCESSION:BD072876	C 538	14	0.3	14	1	AX030109	ACCESSION:AX030109
466	14.4	0.3	18	1	BD072877	ACCESSION:BD072877	C 539	14	0.3	14	1	AX030112	ACCESSION:AX030112
467	14.4	0.3	18	1	BD072878	ACCESSION:BD072878	C 540	14	0.3	14	1	AX030113	ACCESSION:AX030113
468	14.4	0.3	18	1	BD072880	ACCESSION:BD072880	C 541	14	0.3	14	1	AX030129	ACCESSION:AX030129
469	14.4	0.3	18	1	BD107503	ACCESSION:BD107503	C 542	14	0.3	14	1	AX030139	ACCESSION:AX030139
470	14.4	0.3	18	1	BD107504	ACCESSION:BD107504	C 543	14	0.3	14	1	AX030141	ACCESSION:AX030141
471	14.4	0.3	18	1	BD107505	ACCESSION:BD107505	C 544	14	0.3	14	1	AX030144	ACCESSION:AX030144

C 253	15.4	0.4	19	1	BD211727	ACCESSION:BD211727	326	14.8	0.3	18	1	AR262417	ACCESSION:AR262417
C 254	15.4	0.4	19	1	CQ080384	ACCESSION:CQ080384	327	14.8	0.3	18	1	AR262418	ACCESSION:AR262418
C 255	15.4	0.4	19	1	CQ829560	ACCESSION:CQ829560	C 328	14.8	0.3	18	1	AR264936	ACCESSION:AR264936
C 256	15.4	0.4	19	1	AR241645	ACCESSION:AR241645	C 329	14.8	0.3	18	1	AR410329	ACCESSION:AR410329
C 257	15.4	0.4	19	1	AR292884	ACCESSION:AR292884	C 330	14.8	0.3	18	1	AR478217	ACCESSION:AR478217
C 258	15.4	0.4	19	1	AR473599	ACCESSION:AR473599	C 331	14.8	0.3	18	1	AX008976	ACCESSION:AX008976
C 259	15.4	0.4	19	1	AR478107	ACCESSION:AR478107	C 332	14.8	0.3	18	1	AX008980	ACCESSION:AX008980
C 260	15.4	0.4	19	1	AX132308	ACCESSION:AX132308	C 333	14.8	0.3	18	1	AX008983	ACCESSION:AX008983
C 261	15.4	0.4	19	1	AX132311	ACCESSION:AX132311	C 334	14.8	0.3	18	1	AX009032	ACCESSION:AX009032
C 262	15.4	0.4	20	1	AR488890	ACCESSION:AR488890	C 335	14.8	0.3	18	1	AX030110	ACCESSION:AX030110
C 263	15	0.4	15	1	A88391	ACCESSION:A88391	C 336	14.8	0.3	18	1	AX030117	ACCESSION:AX030117
C 264	15	0.4	15	1	A88392	ACCESSION:A88392	C 337	14.8	0.3	18	1	AX030123	ACCESSION:AX030123
C 265	15	0.4	15	1	A88440	ACCESSION:A88440	C 338	14.8	0.3	18	1	AX030134	ACCESSION:AX030134
C 266	15	0.4	15	1	A90358	ACCESSION:A90358	C 339	14.8	0.3	18	1	AX030153	ACCESSION:AX030153
C 267	15	0.4	15	1	A90359	ACCESSION:A90359	C 340	14.8	0.3	18	1	AX030166	ACCESSION:AX030166
C 268	15	0.4	15	1	A90407	ACCESSION:A90407	C 341	14.8	0.3	18	1	AX030169	ACCESSION:AX030169
C 269	15	0.4	15	1	AR002256	ACCESSION:AR002256	C 342	14.8	0.3	18	1	AX047272	ACCESSION:AX047272
C 270	15	0.4	15	1	AR045206	ACCESSION:AR045206	C 343	14.8	0.3	18	1	AX047274	ACCESSION:AX047274
C 271	15	0.4	15	1	AR051237	ACCESSION:AR051237	C 344	14.8	0.3	18	1	AX191970	ACCESSION:AX191970
C 272	15	0.4	15	1	AR084519	ACCESSION:AR084519	C 345	14.8	0.3	18	1	AX252494	ACCESSION:AX252494
C 273	15	0.4	15	1	AR127784	ACCESSION:AR127784	C 346	14.8	0.3	18	1	AX316431	ACCESSION:AX316431
C 274	15	0.4	15	1	I16031	ACCESSION:I16031	C 347	14.8	0.3	18	1	AX316438	ACCESSION:AX316438
C 275	15	0.4	15	1	I28366	ACCESSION:I28366	C 348	14.8	0.3	18	1	AX316444	ACCESSION:AX316444
C 276	15	0.4	15	1	BD065904	ACCESSION:BD065904	C 349	14.8	0.3	18	1	AX316455	ACCESSION:AX316455
C 277	15	0.4	15	1	BD065905	ACCESSION:BD065905	C 350	14.8	0.3	18	1	AX316474	ACCESSION:AX316474
C 278	15	0.4	15	1	BD065953	ACCESSION:BD065953	C 351	14.8	0.3	18	1	AX316487	ACCESSION:AX316487
C 279	15	0.4	17	1	AX729109	ACCESSION:AX729109	C 352	14.8	0.3	18	1	AX316491	ACCESSION:AX316491
C 280	15	0.4	18	1	E32456	ACCESSION:E32456	C 353	14.8	0.3	18	1	AX822988	ACCESSION:AX822988
C 281	14.8	0.3	18	1	A28690	ACCESSION:A28690	C 354	14.8	0.3	18	1	AX826628	ACCESSION:AX826628
C 282	14.8	0.3	18	1	A28695	ACCESSION:A28695	C 355	14.8	0.3	18	1	BD064848	ACCESSION:BD064848
C 283	14.8	0.3	18	1	A36755	ACCESSION:A36755	C 356	14.8	0.3	18	1	BD066574	ACCESSION:BD066574
C 284	14.8	0.3	18	1	A40535	ACCESSION:A40535	C 357	14.8	0.3	18	1	BD066580	ACCESSION:BD066580
C 285	14.8	0.3	18	1	A40542	ACCESSION:A40542	C 358	14.8	0.3	18	1	BD066586	ACCESSION:BD066586
C 286	14.8	0.3	18	1	A40548	ACCESSION:A40548	C 359	14.8	0.3	18	1	BD066597	ACCESSION:BD066597
C 287	14.8	0.3	18	1	A40559	ACCESSION:A40559	C 360	14.8	0.3	18	1	BD066615	ACCESSION:BD066615
C 288	14.8	0.3	18	1	A40578	ACCESSION:A40578	C 361	14.8	0.3	18	1	BD066628	ACCESSION:BD066628
C 289	14.8	0.3	18	1	A40591	ACCESSION:A40591	C 362	14.8	0.3	18	1	BD066632	ACCESSION:BD066632
C 290	14.8	0.3	18	1	A40595	ACCESSION:A40595	C 363	14.8	0.3	18	1	BD072881	ACCESSION:BD072881
C 291	14.8	0.3	18	1	A89061	ACCESSION:A89061	C 364	14.8	0.3	18	1	BD104178	ACCESSION:BD104178
C 292	14.8	0.3	18	1	A89067	ACCESSION:A89067	C 365	14.8	0.3	18	1	BD107508	ACCESSION:BD107508
C 293	14.8	0.3	18	1	A89073	ACCESSION:A89073	C 366	14.8	0.3	18	1	ASE250931	ACCESSION:AJ250931
C 294	14.8	0.3	18	1	A89084	ACCESSION:A89084	C 367	14.4	0.3	16	1	A40557	ACCESSION:A40557
C 295	14.8	0.3	18	1	A89102	ACCESSION:A89102	C 368	14.4	0.3	16	1	A40570	ACCESSION:A40570
C 296	14.8	0.3	18	1	A89115	ACCESSION:A89115	C 369	14.4	0.3	16	1	A88395	ACCESSION:A88395
C 297	14.8	0.3	18	1	A89119	ACCESSION:A89119	C 370	14.4	0.3	16	1	A88402	ACCESSION:A88402
C 298	14.8	0.3	18	1	AR034902	ACCESSION:AR034902	C 371	14.4	0.3	16	1	A89082	ACCESSION:A89082
C 299	14.8	0.3	18	1	AR066298	ACCESSION:AR066298	C 372	14.4	0.3	16	1	A89094	ACCESSION:A89094
C 300	14.8	0.3	18	1	AR084526	ACCESSION:AR084526	C 373	14.4	0.3	16	1	A90362	ACCESSION:A90362
C 301	14.8	0.3	18	1	AR084527	ACCESSION:AR084527	C 374	14.4	0.3	16	1	A90369	ACCESSION:A90369
C 302	14.8	0.3	18	1	AR144877	ACCESSION:AR144877	C 375	14.4	0.3	16	1	AR232837	ACCESSION:AR232837
C 303	14.8	0.3	18	1	AR168816	ACCESSION:AR168816	C 376	14.4	0.3	16	1	AR232850	ACCESSION:AR232850
C 304	14.8	0.3	18	1	AR168817	ACCESSION:AR168817	C 377	14.4	0.3	16	1	AX030132	ACCESSION:AX030132
C 305	14.8	0.3	18	1	BD145040	ACCESSION:BD145040	C 378	14.4	0.3	16	1	AX030145	ACCESSION:AX030145
C 306	14.8	0.3	18	1	BD166040	ACCESSION:BD166040	C 379	14.4	0.3	16	1	AX316453	ACCESSION:AX316453
C 307	14.8	0.3	18	1	BD234905	ACCESSION:BD234905	C 380	14.4	0.3	16	1	AX316466	ACCESSION:AX316466
C 308	14.8	0.3	18	1	BD234909	ACCESSION:BD234909	C 381	14.4	0.3	16	1	AX419943	ACCESSION:AX419943
C 309	14.8	0.3	18	1	BD234912	ACCESSION:BD234912	C 382	14.4	0.3	16	1	BD065908	ACCESSION:BD065908
C 310	14.8	0.3	18	1	BD234961	ACCESSION:BD234961	C 383	14.4	0.3	16	1	BD065915	ACCESSION:BD065915
C 311	14.8	0.3	18	1	CQ080382	ACCESSION:CQ080382	C 384	14.4	0.3	16	1	BD066595	ACCESSION:BD066595
C 312	14.8	0.3	18	1	E32455	ACCESSION:E32455	C 385	14.4	0.3	16	1	BD066607	ACCESSION:BD066607
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C 179	16	0.4	16	1	AX030151	ACCESSION:AX030151	C 252	15.4	0.4	19	1	AR167910	ACCESSION:AR167910

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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 09:41:44 ; Search time 32 Seconds
(without alignments)
3.676 Million cell updates/sec

Title: US-10-633-163-47

Perfect score: 4267

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Searched: 790 seqs, 13783 residues

Total number of hits satisfying chosen parameters: 1580

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 832 summaries

Database : fetchrge47.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ORGANISM unidentified
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AUTHORS
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EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
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KEYWORDS
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ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 101 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1971 GGTATTGATGGCAC 1984
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Db 14 GGTATTGATGGCAC 1

RESULT 485
A40566/c
LOCUS 14 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 103 from Patent WO9425578.
ACCESSION A40566
VERSION A40566.1 GI:2296601
KEYWORDS
SOURCE unidentified

ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 103 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
source Location/Qualifiers
1..14
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1997 CAGTGGTGATCAGA 2010
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Db 14 CAGTGGTGATCAGA 1

RESULT 486
A40569/c
LOCUS 14 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 106 from Patent WO9425578.
ACCESSION A40569
VERSION A40569.1 GI:2296604
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 106 10-NOV-1994;
BIOGNOSTIK GES (DE)
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2046 AAGACCCCATCTCT 2059
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Db 14 AAGACCCCATCTCT 1

RESULT 487
A40585/c
LOCUS 14 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 122 from Patent WO9425578.
ACCESSION A40585
VERSION A40585.1 GI:2296620
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 122 10-NOV-1994;
BIOGNOSTIK GES (DE)
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291
Db 14 GGAGTTCAGACACT 1

RESULT 488
A40599/c
LOCUS      14 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 136 from Patent WO9425578.
ACCESSION A40599
VERSION A40599.1 GI:2296634
SOURCE .
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9425578-A 136 10-NOV-1994;
BIOGHOSTIK GES (DE)
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source
Location/Qualifiers
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 489
A88371/c
LOCUS      14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 519 from Patent WO9833904.
ACCESSION A88371
VERSION A88371.1 GI:6736941
SOURCE .
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 519 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GCACTACTGTGTGC 1233
Db 14 GCACTACTGTGTGC 1

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1919 TAATAATTACATCA 1932
Db 14 TAATAATTACATCA 1

RESULT 492
A89047/c
LOCUS      14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1195 from Patent WO9833904.
ACCESSION A89047
VERSION A89047.1 GI:6737617
SOURCE .
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
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RESULT 490
A88399/c
LOCUS      14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 547 from Patent WO9833904.
ACCESSION A88399
VERSION A88399.1 GI:6736969
SOURCE .
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 547 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2159 GGATAATTGCTGCC 2172
Db 14 GGATAATTGCTGCC 1

RESULT 491
A88439/c
LOCUS      14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 587 from Patent WO9833904.
ACCESSION A88439
VERSION A88439.1 GI:6737009
SOURCE .
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 587 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1919 TAATAATTACATCA 1932
Db 14 TAATAATTACATCA 1

RESULT 492
A89047/c
LOCUS      14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1195 from Patent WO9833904.
ACCESSION A89047
VERSION A89047.1 GI:6737617
SOURCE .
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
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JOURNAL Patent: WO 9833904-A 1195 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACCTACTGTGTG 1232
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14 TGCACCTACTGTGTG 1

Db 14 TGCACCTACTGTGTG 1

RESULT 493
A89053/c
LOCUS 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1201 from Patent WO9833904.
ACCESSION A89053
VERSION A89053.1 GI:6737623
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1201 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357
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14 CAGATCCTGAGCAA 1

Db 14 CAGATCCTGAGCAA 1

RESULT 494
A89060/c
LOCUS 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1208 from Patent WO9833904.
ACCESSION A89060
VERSION A89060.1 GI:6737630
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1208 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES
source
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520
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14 AGTACTACGCCAAG 1

Db 14 AGTACTACGCCAAG 1

RESULT 495
A89062/c
LOCUS 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1210 from Patent WO9833904.
ACCESSION A89062
VERSION A89062.1 GI:6737632
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1210 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574
|||||
14 AAAATGCCATCCCG 1

Db 14 AAAATGCCATCCCG 1

RESULT 496
A89063/c
LOCUS 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1211 from Patent WO9833904.
ACCESSION A89063
VERSION A89063.1 GI:6737633
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1211 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTTCTACAG 1588
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14 CCCACTTTCTACAG 1

Db 14 CCCACTTTCTACAG 1

RESULT 497
A89079/c
LOCUS 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1227 from Patent WO9833904.
ACCESSION A89079
VERSION A89079.1 GI:6737649
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

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unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1227 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1807 AATGGCTCTCCTTC 1820
Db 14 AATGGCTCTCCTTC 1

RESULT 498
A89089/c
LOCUS A89089
DEFINITION Sequence 1237 from Patent WO9833904.
ACCESSION A89089
VERSION A89089.1 GI:6737659
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1237 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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                /db_xref="taxon:32644"

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCAC 1984
Db 14 GGTATTGATGGCAC 1

RESULT 499
A89091/c
LOCUS A89091
DEFINITION Sequence 1239 from Patent WO9833904.
ACCESSION A89091
VERSION A89091.1 GI:6737661
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1239 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 502
A90338/c
LOCUS A90338
DEFINITION Sequence 519 from Patent EP0856579.
ACCESSION A90338
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unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1227 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGGTGATCAGA 2010
Db 14 CAGTGGTGATCAGA 1

RESULT 500
A89109/c
LOCUS A89109
DEFINITION Sequence 1257 from Patent WO9833904.
ACCESSION A89109
VERSION A89109.1 GI:6737679
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1257 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCACACACT 2291
Db 14 GGAGTTCACACACT 1

RESULT 501
A89123/c
LOCUS A89123
DEFINITION Sequence 1271 from Patent WO9833904.
ACCESSION A89123
VERSION A89123.1 GI:6737693
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1271 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 502
A90338/c
LOCUS A90338
DEFINITION Sequence 519 from Patent EP0856579.
ACCESSION A90338
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VERSION A90338.1 GI:6738852
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 519 05-AUG-1998;
BIOGHOSTIK GES (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GCACTACTGTGTC 1233
Db 14 GCACTACTGTGTC 1

RESULT 503
A90366/c
LOCUS A90366 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 547 from Patent EP0856579.
ACCESSION A90366
VERSION A90366.1 GI:6738880
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 547 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2159 GGATAATTGCTGCC 2172
Db 14 GGATAATTGCTGCC 1

RESULT 504
A90406/c
LOCUS A90406 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 587 from Patent EP0856579.
ACCESSION A90406
VERSION A90406.1 GI:6738920
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 587 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
source
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/organism="unidentified"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAATTCATCA 2587
Db 14 TTAATAATTCATCA 1

RESULT 506
AR174031/c
LOCUS AR174031 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 21 from patent US 6306624.
ACCESSION AR174031
VERSION AR174031.1 GI:17914351
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 21 23-OCT-2001;
BIOGHOSTIK GES (DE)
FEATURES
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/organism="unassigned DNA"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAATTCATCA 2814
Db 14 TGAATAATTCATCA 1

RESULT 507
BD176798
LOCUS BD176798 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
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ACCESSION      BD176798
VERSION        WO 02074951-A/45
KEYWORDS       synthetic construct
SOURCE         other sequences; artificial sequences.
ORGANISM       1 (bases 1 to 14)
REFERENCE      Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS        Method of constructing cDNA tag for identifying expressed gene and
TITLE          method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 45 26-SEP-2002;
               KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT        KUNITAKA HIROSE,JUN SAKAI
               OS Artificial Sequence
               PN WO 02074951-A/45
               PD 26-SEP-2002
               PF 13-MAR-2002 WO 2002JP002338
               PR 15-MAR-2001 JP 01P 073959
               PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
               C12N15/09,C12Q1/68
               CC Synthetic DNA
               FH Key Location/Qualifiers
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Query Match    0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2576 AAAAAAAAAAAT 2589
Db 1 AAAAAAAAAAAT 14
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RESULT 508
LOCUS          BD176799
DEFINITION    14 bp DNA linear PAT 18-MAR-2003
               Method of constructing cDNA tag for identifying expressed gene and
               method of analyzing gene expression.
ACCESSION     BD176799
VERSION       WO 02074951-A/46
KEYWORDS      synthetic construct
SOURCE        other sequences; artificial sequences.
ORGANISM      1 (bases 1 to 14)
REFERENCE      Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS        Method of constructing cDNA tag for identifying expressed gene and
TITLE          method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 46 26-SEP-2002;
               KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT        KUNITAKA HIROSE,JUN SAKAI
               OS Artificial Sequence
               PN WO 02074951-A/46
               PD 26-SEP-2002
               PF 13-MAR-2002 WO 2002JP002338
               PR 15-MAR-2001 JP 01P 073959
               PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
               C12N15/09,C12Q1/68
               CC Synthetic DNA
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Query Match    0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2803 AAAAAAAAAACA 2816
Db 1 AAAAAAAAAACA 14
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RESULT 509
LOCUS          BD176801/c
DEFINITION    14 bp DNA linear PAT 18-MAR-2003
               Method of constructing cDNA tag for identifying expressed gene and
               method of analyzing gene expression.
ACCESSION     BD176801
VERSION       WO 02074951-A/48
KEYWORDS      synthetic construct
SOURCE        other sequences; artificial sequences.
ORGANISM      1 (bases 1 to 14)
REFERENCE      Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS        Method of constructing cDNA tag for identifying expressed gene and
TITLE          method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 48 26-SEP-2002;
               KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT        KUNITAKA HIROSE,JUN SAKAI
               OS Artificial Sequence
               PN WO 02074951-A/48
               PD 26-SEP-2002
               PF 13-MAR-2002 WO 2002JP002338
               PR 15-MAR-2001 JP 01P 073959
               PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
               C12N15/09,C12Q1/68
               CC Synthetic DNA
               FH Key Location/Qualifiers
               FT source 1..14
               FT /organism='Artificial Sequence'.
FEATURES       source
               1..14
               /organism='synthetic construct'
               /mol_type='genomic DNA'
               /db_xref='taxon:32630'
Query Match    0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2575 TAAAAAAAAA 2588
Db 14 TAAAAAAAAA 1
|||||

RESULT 510
LOCUS          BD234897/c
DEFINITION    14 bp DNA linear PAT 17-JUL-2003
               A method for stimulating the immune system.
ACCESSION     BD234897
VERSION       BD234897.1 GI:33044667
KEYWORDS      JP 2002517434-A/1.
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE          A method for stimulating the immune system
JOURNAL        Patent: JP 2002517434-A 1 18-JUN-2002;
               BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT        OS Homo sapiens (human)
               PN JP 2002517434-A/1
               PD 18-JUN-2002
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PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
/organism='Homo sapiens (human)'.

FEATURES
source
1..14
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACTACTGTGTG 1232
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Db 14 TGCACTACTGTGTG 1

RESULT 511
BD234898/c
LOCUS BD234898 14 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234898
VERSION BD234898.1 GI:33044668
KEYWORDS JP 2002517434-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 2 18-JUN-2002;
BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/2
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
/organism='Homo sapiens (human)'.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GCACACTGTGTGC 1233
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Db 14 GCACACTGTGTGC 1

RESULT 512
BD234901/c
LOCUS BD234901 14 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234901
VERSION BD234901.1 GI:33044671
KEYWORDS JP 2002517434-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 5 18-JUN-2002;
BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/5
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
/organism='Homo sapiens (human)'.

FEATURES
source
1..14
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520
|||||
Db 14 AGTACTACGCCAAG 1

RESULT 513
BD234907/c
LOCUS BD234907 14 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234907
VERSION BD234907.1 GI:33044677
KEYWORDS JP 2002517434-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 11 18-JUN-2002;
BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/11
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
/organism='Homo sapiens (human)'.

FEATURES
source
1..14
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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FEATURES
source
  Location/Qualifiers
    1..14
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1575 CCACATTTCTACAG 1588
Db 14 CCCACTTTCTACAG 1

RESULT 514
BD234955/c
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234955
VERSION BD234955.1 GI:33044725
KEYWORDS JP 2002517434-A/59.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 59 18-JUN-2002;
COMMENT BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/59
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.

FEATURES
source
  Location/Qualifiers
    1..14
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1478 CGCCTCGAGCGCG 1491
Db 14 CGCCTCGAGCGCG 1

RESULT 516
BD234986/c
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234986
VERSION BD234986.1 GI:33044756
KEYWORDS JP 2002517434-A/90.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
JOURNAL Patent: JP 2002517434-A 90 18-JUN-2002;
COMMENT BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/90
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.

FEATURES
source
  Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 CGCGGGAAGCGG 2122
Db 14 CGCGGGAAGCGG 1

RESULT 515
BD234960/c
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234960
VERSION BD234960.1 GI:33044730
KEYWORDS JP 2002517434-A/64.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
JOURNAL Patent: JP 2002517434-A 64 18-JUN-2002;
COMMENT BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/64
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.

FEATURES
source
  Location/Qualifiers
    1..14
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1328 CGAGGCCATCCGCG 1341
Db 14 CGAGGCCATCCGCG 1341
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Db 14 CGAGCCATCCGCG 1
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RESULT 517
AR232800/c
LOCUS AR232800 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 57 from patent US 6455689.
ACCESSION AR232800
VERSION AR232800.1 GI:27275138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 57 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1219 TGCACACTGTGTG 1232
|||||
Db 14 TGCACACTGTGTG 1
RESULT 518
AR232806/c
LOCUS AR232806 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 63 from patent US 6455689.
ACCESSION AR232806
VERSION AR232806.1 GI:27275144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 63 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1344 CAGATCCTGAGCAA 1357
|||||
Db 14 CAGATCCTGAGCAA 1
RESULT 519
AR232814/c
LOCUS AR232814 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 71 from patent US 6455689.
ACCESSION AR232814
VERSION AR232814.1 GI:27275152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 71 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1507 AGTACTACGCCAAG 1520
|||||
Db 14 AGTACTACGCCAAG 1
RESULT 520
AR232817/c
LOCUS AR232817 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 74 from patent US 6455689.
ACCESSION AR232817
VERSION AR232817.1 GI:27275155
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 74 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1561 AAAATGCCATCCCG 1574
|||||
Db 14 AAAATGCCATCCCG 1
RESULT 521
AR232818/c
LOCUS AR232818 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 75 from patent US 6455689.
ACCESSION AR232818
VERSION AR232818.1 GI:27275156
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 75 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.3%; Score 14; DB 1; Length 14;

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCACATTTCTACAG 1588
Db 14 CCACATTTCTACAG 1

RESULT 522
AR232834/c
LOCUS AR232834 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 91 from patent US 6455689.
ACCESSION AR232834
VERSION AR232834.1 GI:27275172
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 91 24-SEP-2002;
FEATURES
source
Location/Qualifiers
1..14
/mol_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1807 AATGGCTCTCCTTC 1820
Db 14 AATGGCTCTCCTTC 1

RESULT 523
AR232844/c
LOCUS AR232844 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 101 from patent US 6455689.
ACCESSION AR232844
VERSION AR232844.1 GI:27275182
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 101 24-SEP-2002;
FEATURES
source
Location/Qualifiers
1..14
/mol_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGCAC 1984
Db 14 GGTATTGATGCAC 1

RESULT 524
AR232846/c
LOCUS AR232846 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 103 from patent US 6455689.
ACCESSION AR232846
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VERSION AR232846.1 GI:27275184
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 103 24-SEP-2002;
FEATURES
source
Location/Qualifiers
1..14
/mol_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGGTGATCAGA 2010
Db 14 CAGTGGTGATCAGA 1

RESULT 525
AR232849/c
LOCUS AR232849 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 106 from patent US 6455689.
ACCESSION AR232849
VERSION AR232849.1 GI:27275187
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 106 24-SEP-2002;
FEATURES
source
Location/Qualifiers
1..14
/mol_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AAGACCCCATCTCT 2059
Db 14 AAGACCCCATCTCT 1

RESULT 526
AR232865/c
LOCUS AR232865 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 122 from patent US 6455689.
ACCESSION AR232865
VERSION AR232865.1 GI:27275203
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 122 24-SEP-2002;
FEATURES
source
Location/Qualifiers
1..14
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291
|||||
Db 14 GGAGTTCAGACACT 1

RESULT 527
AR232879/c
LOCUS
DEFINITION Sequence 136 from patent US 6455689.
ACCESSION AR232879
VERSION AR232879.1 GI:27275217
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor- β .
(TGF- β .beta.)
JOURNAL Patent: US 6455689-A 136 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
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Db 14 ACTACTGTGTGCTG 1

RESULT 528
AR242022
LOCUS
DEFINITION Sequence 310 from patent US 6472154.
ACCESSION AR242022
VERSION AR242022.1 GI:27287834
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 310 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAAA 944
|||||
Db 1 AAAAAAAAAACAAA 14

RESULT 529
AX008968/c
LOCUS

DEFINITION Sequence 1 from Patent WO9963975.
ACCESSION AX008968
VERSION AX008968.1 GI:9996342
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 1 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACACTGTGTG 1232
|||||
Db 14 TGCACACTGTGTG 1

RESULT 530
AX008969/c
LOCUS
DEFINITION Sequence 2 from Patent WO9963975.
ACCESSION AX008969
VERSION AX008969.1 GI:9996343
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 2 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GCACTACTGTGTGC 1233
|||||
Db 14 GCACTACTGTGTGC 1

RESULT 531
AX008972/c
LOCUS
DEFINITION Sequence 5 from Patent WO9963975.
ACCESSION AX008972
VERSION AX008972.1 GI:9996346
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

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AUTHORS      Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE        A method for stimulating the immune system
JOURNAL      Patent: WO 963975-A 5 16-DEC-1999;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
              HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1507 AGTACTACGCCAAG 1520
Db      14 AGTACTACGCCAAG 1

RESULT 532
AX008978/c
LOCUS      AX008978      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 11 from Patent WO9963975.
ACCESSION  AX008978
VERSION     AX008978.1 GI:9996352
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 963975-A 11 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1575 CCCACTTCTCAG 1588
Db      14 CCCACTTCTCAG 1

RESULT 533
AX009026/c
LOCUS      AX009026      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 59 from Patent WO9963975.
ACCESSION  AX009026
VERSION     AX009026.1 GI:9996400
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 963975-A 59 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"

AUTHORS      Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE        A method for stimulating the immune system
JOURNAL      Patent: WO 963975-A 5 16-DEC-1999;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
              HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1575 CCCACTTCTCAG 1588
Db      14 CCCACTTCTCAG 1

RESULT 533
AX009026/c
LOCUS      AX009026      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 59 from Patent WO9963975.
ACCESSION  AX009026
VERSION     AX009026.1 GI:9996400
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 963975-A 59 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1478 CGCCTGCGAGCGCG 1491
Db      14 CGCCTGCGAGCGCG 1

RESULT 535
AX009057/c
LOCUS      AX009057      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 90 from Patent WO9963975.
ACCESSION  AX009057
VERSION     AX009057.1 GI:9996431
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 963975-A 90 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1478 CGCCTGCGAGCGCG 1491
Db      14 CGCCTGCGAGCGCG 1

RESULT 534
AX009031/c
LOCUS      AX009031      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 64 from Patent WO9963975.
ACCESSION  AX009031
VERSION     AX009031.1 GI:9996405
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 963975-A 64 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CGGCGGAGAGCGG 2122
Db      14 CGGCGGAGAGCGG 1

RESULT 534
AX009031/c
LOCUS      AX009031      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 64 from Patent WO9963975.
ACCESSION  AX009031
VERSION     AX009031.1 GI:9996405
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 963975-A 64 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1328 CGAGGCCATCCGCG 1341
Db      14 CGAGGCCATCCGCG 1
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RESULT 536
AX030095/c
LOCUS AX030095 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 57 from Patent EP1008649.
ACCESSION AX030095
VERSION AX030095.1 GI:10190312
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 57 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source
Location/Qualifiers
1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1219 TGCACCTACTGTGTG 1232
Db 14 TGCACCTACTGTGTG 1
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1219 TGCACCTACTGTGTG 1232
Db 14 TGCACCTACTGTGTG 1
RESULT 537
AX030101/c
LOCUS AX030101 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 63 from Patent EP1008649.
ACCESSION AX030101
VERSION AX030101.1 GI:10190318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 63 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source
Location/Qualifiers
1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1344 CAGATCCTGAGCAA 1357
Db 14 CAGATCCTGAGCAA 1
RESULT 538
AX030109/c
LOCUS AX030109 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 71 from Patent EP1008649.
ACCESSION AX030109
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VERSION AX030109.1 GI:10190326
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 71 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source
Location/Qualifiers
1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1507 AGTACTACGCCAAG 1520
Db 14 AGTACTACGCCAAG 1
RESULT 539
AX030112/c
LOCUS AX030112 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 74 from Patent EP1008649.
ACCESSION AX030112
VERSION AX030112.1 GI:10190329
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 74 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source
Location/Qualifiers
1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1561 AAAATGCCATCCCG 1574
Db 14 AAAATGCCATCCCG 1
RESULT 540
AX030113/c
LOCUS AX030113 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 75 from Patent EP1008649.
ACCESSION AX030113
VERSION AX030113.1 GI:10190330
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
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AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 75 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1575 CCCACTTCTACAG 1588
Db 14 CCCACTTCTACAG 1
RESULT 541
AX030129/c
LOCUS AX030129 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 91 from Patent EP1008649.
ACCESSION AX030129
VERSION AX030129.1 GI:10190346
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 91 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1807 AATGGCTCTCCTTC 1820
Db 14 AATGGCTCTCCTTC 1
RESULT 542
AX030139/c
LOCUS AX030139 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 101 from Patent EP1008649.
ACCESSION AX030139
VERSION AX030139.1 GI:10190356
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 101 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers

source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1971 GGTATTGATGGCAC 1984
Db 14 GGTATTGATGGCAC 1
RESULT 543
AX030141/c
LOCUS AX030141 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 103 from Patent EP1008649.
ACCESSION AX030141
VERSION AX030141.1 GI:10190358
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 103 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 CAGTGGTGATCAGA 2010
Db 14 CAGTGGTGATCAGA 1
RESULT 544
AX030144/c
LOCUS AX030144 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 106 from Patent EP1008649.
ACCESSION AX030144
VERSION AX030144.1 GI:10190361
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 106 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 CAGTGGTGATCAGA 2010
Db 14 CAGTGGTGATCAGA 1
RESULT 544
AX030144/c
LOCUS AX030144 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 106 from Patent EP1008649.
ACCESSION AX030144
VERSION AX030144.1 GI:10190361
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 106 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AAGACCCCATCT 2059
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Db 14 AAGACCCCATCT 1

RESULT 545
AX030160/c
LOCUS
DEFINITION Sequence 122 from Patent EP1008649.
ACCESSION AX030160
VERSION AX030160.1 GI:10190377
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 122 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source Location/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291
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Db 14 GGAGTTCAGACACT 1

RESULT 546
AX030174/c
LOCUS
DEFINITION Sequence 136 from Patent EP1008649.
ACCESSION AX030174
VERSION AX030174.1 GI:10190391
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 136 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
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Db 14 ACTACTGTGTGCTG 1

RESULT 547
AX316416/c
LOCUS
DEFINITION Sequence 57 from Patent EP1160319.
ACCESSION AX316416
VERSION AX316416.1 GI:117899589
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 57 05-DEC-2001;
BIOGNOSTIK GES/LLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACACTGTGTG 1232
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Db 14 TGCACACTGTGTG 1

RESULT 548
AX316422/c
LOCUS
DEFINITION Sequence 63 from Patent EP1160319.
ACCESSION AX316422
VERSION AX316422.1 GI:117899595
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 63 05-DEC-2001;
BIOGNOSTIK GES/LLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
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/note="Description of unknown: unknown"

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357
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Db 14 CAGATCCTGAGCAA 1

RESULT 549
AX316430/c
LOCUS
DEFINITION Sequence 71 from Patent EP1160319.
ACCESSION AX316430
VERSION AX316430.1 GI:117899603
KEYWORDS

SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 71 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="unidentified"
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/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520
Db 14 AGTACTACGCCAAG 1
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RESULT 550
AX316433/c
LOCUS AX316433 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 74 from Patent EP1160319.
ACCESSION AX316433
VERSION AX316433.1 GI:17899606
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 74 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="unidentified"
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/note="Description of unknown: unknown"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574
Db 14 AAAATGCCATCCCG 1
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RESULT 551
AX316434/c
LOCUS AX316434 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 75 from Patent EP1160319.
ACCESSION AX316434
VERSION AX316434.1 GI:17899607
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive

JOURNAL effects of transforming growth factor-beta (tgf-beta)
Patent: EP 1160319-A 75 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="unidentified"
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/note="Description of unknown: unknown"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTTCTACAG 1588
Db 14 CCCACTTTCTACAG 1
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RESULT 552
AX316450/c
LOCUS AX316450 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 91 from Patent EP1160319.
ACCESSION AX316450
VERSION AX316450.1 GI:17899623
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 91 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES Location/Qualifiers
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/note="Description of unknown: unknown"

Query Match 0.3%; Score 14; DB 1; Length 14;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1807 AATGGCTCTCCTTC 1820
Db 14 AATGGCTCTCCTTC 1
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RESULT 553
AX316460/c
LOCUS AX316460 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 101 from Patent EP1160319.
ACCESSION AX316460
VERSION AX316460.1 GI:17899633
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 101 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

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LOCUS BD065884 14 bp DNA linear PAT 27-AUG-2002
 DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD065884
 VERSION BD065884.1 GI:22611487
 KEYWORDS JP 2001511000-A/519.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Schlingensiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 519 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Unknown
 PN JP 2001511000-A/519
 PD 07-AUG-2001
 PF 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
 PC C12N15/11,C07H21/04,A61K31/70
 CC An antisense oligonucleotide preparation method FH Key
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 14 GCATACTGTGTC 1
 RESULT 559
 BD065912/c
 LOCUS
 DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD065912
 VERSION BD065912.1 GI:22611515
 KEYWORDS JP 2001511000-A/547.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Schlingensiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 547 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Unknown
 PN JP 2001511000-A/547
 PD 07-AUG-2001
 PF 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
 PC C12N15/11,C07H21/04,A61K31/70
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 RESULT 559
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 DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD065912
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 KEYWORDS JP 2001511000-A/547.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Schlingensiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 547 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Unknown
 PN JP 2001511000-A/547
 PD 07-AUG-2001
 PF 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
 PC C12N15/11,C07H21/04,A61K31/70
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LOCUS BD065952 14 bp DNA linear PAT 27-AUG-2002
 DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD065952
 VERSION BD065952.1 GI:22611555
 KEYWORDS JP 2001511000-A/587.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Schlingensiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 587 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Unknown
 PN JP 2001511000-A/587
 PD 07-AUG-2001
 PF 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
 PC C12N15/11,C07H21/04,A61K31/70
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 QY 1919 TAATAATTACATCA 1932
 Db 14 TAATAATTACATCA 1
 RESULT 561
 BD066560/c
 LOCUS
 DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD066560
 VERSION BD066560.1 GI:22612163
 KEYWORDS JP 2001511000-A/1195.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Schlingensiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 1195 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Unknown
 PN JP 2001511000-A/1195
 PD 07-AUG-2001
 PF 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
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 /db_xref="taxon:32644"

SOURCE unidentified
ORGANISM unclassified
RESULT 567
BD066602/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1211 07-AUG-2001;
BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1211
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
LOCATION/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1575 CCCACTTTCTACAG 1588
DB 14 CCCACTTTCTACAG 1
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|
RESULT 566
BD066592/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1227 07-AUG-2001;
BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1227
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1807 AATGGCTCTCCTTC 1820
DB 14 AATGGCTCTCCTTC 1
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|

RESULT 567
BD066602/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1237 07-AUG-2001;
BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1237
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
LOCATION/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1971 GGTATTGATGGCAC 1984
DB 14 GGTATTGATGGCAC 1
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RESULT 568
BD066604/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1239 07-AUG-2001;
BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1239
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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1. .14 /organism="unidentified"
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGGTGATCAGA 2010
Db 14 CAGTGGTGATCAGA 1

RESULT 569
BD066622/c
LOCUS      14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066622
VERSION     BD066622.1 GI:22612225
KEYWORDS   JP 2001511000-A/1257.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 1257 07-AUG-2001;
           BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
           PN JP 2001511000-A/1257
           PD 07-AUG-2001
           PF 30-JAN-1998 JP 1998532533
           PR 31-JAN-1997 EP 97101531.8
           PI KARL HERMANN SCHLINGENSTIEPEN,WOLFGANG BRYSCH
           PC C12N15/11,C07H21/04,A61K31/70
           CC An antisense oligonucleotide preparation method FH Key
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FEATURES
source
Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 571
BD073880/c
LOCUS      14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION  BD073880
VERSION     BD073880.1 GI:22619483
KEYWORDS   JP 2001512698-A/5.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Suishelm,K., Hosier,S. and Kubbies,M.
TITLE      Isolation of novel aging factor gene P23
JOURNAL    Patent: JP 2001512698-A 5 28-AUG-2001;
           UNIVERSITY OF WASHINGTON
COMMENT    OS Unidentified
           PN JP 2001512698-A/5
           PD 28-AUG-2001
           PF 05-AUG-1998 JP 2000506375
           PR 08-AUG-1997 US 08/908873
           PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
           CC C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N15/09, PC
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           CC C12P21/08,C12N15/00
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FEATURES
source
Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587
Db 14 TTAATAAAAAAAAAA 1

RESULT 572
BD073882/c
LOCUS      14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION  BD073882
VERSION     BD073882.1 GI:22619485
KEYWORDS   JP 2001512698-A/7.
SOURCE     unidentified

PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
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FT Location/Qualifiers
FT 1. .14
FT /organism='Unknown'.

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QY 2574 TTAATAAAAAAAAAA 2587
Db 14 TTAATAAAAAAAAAA 1

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LOCUS      14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066636
VERSION     BD066636.1 GI:22612239
KEYWORDS   JP 2001511000-A/1271.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 1271 07-AUG-2001;
           BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
           PN JP 2001511000-A/1271
           PD 07-AUG-2001
           PF 30-JAN-1998 JP 1998532533
           PR 31-JAN-1997 EP 97101531.8
           PI KARL HERMANN SCHLINGENSTIEPEN,WOLFGANG BRYSCH
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ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 7 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/7
PD 28-AUG-2001
PF 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
C12P21/02.
PC C12P21/08,C12N15/00
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CC Topology: Linear;
CC Isolation of novel aging factor gene P23
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Db 14 TGAATAAATACAT 1
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DEFINITION Sequence 586 from Patent WO9833904.
ACCESSION A88438
VERSION A88438.1 GI:6737008
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 586 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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Db 14 TCTAATAATTACAT 1
RESULT 574
A90405/c
LOCUS A90405 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 586 from Patent EP0856579.
ACCESSION A90405
VERSION A90405.1 GI:6738919

KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 586 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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Db 14 TCTAATAATTACAT 1
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DEFINITION Sequence 299 from patent US 5869253.
ACCESSION AR033533
VERSION AR033533.1 GI:5949138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 299 09-FEB-1999;
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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Db 15 TGCCCAGAGGCCT 2
RESULT 576
AR033534/c
LOCUS AR033534 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 300 from patent US 5869253.
ACCESSION AR033534
VERSION AR033534.1 GI:5949139
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 300 09-FEB-1999;
FEATURES
source
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/mol_type="unassigned DNA"
Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 359 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15		REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 359 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15	
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REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 365 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15		REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 365 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15	
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REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 360 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15		REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 360 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15	
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REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 364 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15		REFERENCE 1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G. TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes JOURNAL Patent: US 5837542-A 364 17-NOV-1998; FEATURES Location/Qualifiers source 1. .15	
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REFERENCE 1 (bases 1 to 15) Guzaev,A., AzhayeV,A. and Lonnberg,H. TITLE Chemical phosphorylation of oligonucleotides and reactants used therefor JOURNAL Patent: US 5959090-A 1 28-SEP-1999; FEATURES Location/Qualifiers source 1. .15		REFERENCE 1 (bases 1 to 15) Guzaev,A., AzhayeV,A. and Lonnberg,H. TITLE Chemical phosphorylation of oligonucleotides and reactants used therefor JOURNAL Patent: US 5959090-A 1 28-SEP-1999; FEATURES Location/Qualifiers source 1. .15	
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RESULT 582
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LOCUS AR113355 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 299 from patent US 6132966.
ACCESSION AR113355
VERSION AR113355.1 GI:14093677
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 299 17-OCT-2000;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3210 TGCCCGAGAGGCCT 3223
Db 15 TGCCCGAGAGGCCT 2
RESULT 583
AR113356/c
LOCUS AR113356 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 300 from patent US 6132966.
ACCESSION AR113356
VERSION AR113356.1 GI:14093678
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 300 17-OCT-2000;
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QY 3210 TGCCCGAGAGGCCT 3223
Db 15 TGCCCGAGAGGCCT 2
RESULT 584
AR113913/c
LOCUS AR113913 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 359 from patent US 6132967.
ACCESSION AR113913
VERSION AR113913.1 GI:14094235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 359 17-OCT-2000;
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LOCUS AR113914 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 360 from patent US 6132967.
ACCESSION AR113914
VERSION AR113914.1 GI:14094236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 360 17-OCT-2000;
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Db 14 AAAAAAAAAAAT 1
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LOCUS AR113918 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 364 from patent US 6132967.
ACCESSION AR113918
VERSION AR113918.1 GI:14094240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 364 17-OCT-2000;
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QY 2576 AAAAAAAAAAAT 2589
Db 14 AAAAAAAAAAAT 1
RESULT 586
AR113918/c
LOCUS AR113918 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 364 from patent US 6132967.
ACCESSION AR113918
VERSION AR113918.1 GI:14094240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 364 17-OCT-2000;
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2801 TGAAGAAAAA 2814
Db 15 TGAAGAAAAA 2

RESULT 587
AR113919/c
LOCUS AR113919 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 365 from patent US 6132967.
ACCESSION AR113919
VERSION AR113919.1 GI:14094241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 365 17-OCT-2000;
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QY 2801 TGAAGAAAAA 2814
Db 14 TGAAGAAAAA 1

RESULT 588
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LOCUS BD207266 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207266.1 GI:33017036
VERSION JP 2002512791-A/856.
KEYWORDS unidentified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 856 08-MAY-2002;
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/856
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K48/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
FH Key Location/Qualifiers
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FT /organism='Hepatitis virus (hepatitis C virus)'
FT Location/Qualifiers

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Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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QY 3210 TGCCCAAGAGGCT 3223
Db 14 TGCCCAAGAGGCT 1

RESULT 590
IS7762/c
LOCUS IS7762 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 299 from patent US 5610054.
ACCESSION IS7762
VERSION IS7762.1 GI:2482826
KEYWORDS
SOURCE Unknown.

QY 3210 TGCCCAAGAGGCT 3223
Db 14 TGCCCAAGAGGCT 1

RESULT 590
IS7762/c
LOCUS IS7762 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 299 from patent US 5610054.
ACCESSION IS7762
VERSION IS7762.1 GI:2482826
KEYWORDS
SOURCE Unknown.
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ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 299 11-MAR-1997;
FEATURES
Location/Qualifiers
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Query Match
0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCAGAGGCGCT 3223
Db 15 TGCCAGAGGCGCT 2

RESULT 591
AX633193/c
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DEFINITION
Sequence 300 from patent US 5610054.
ACCESSION
157763
VERSION
157763.1 GI:2482827
KEYWORDS
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SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 300 11-MAR-1997;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 TGCCAGAGGCGCT 1

RESULT 592
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DEFINITION
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ACCESSION
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VERSION
AX633193.1 GI:28468807
KEYWORDS
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SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 299 11-MAR-1997;
FEATURES
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Query Match
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCAGAGGCGCT 3223
Db 15 TGCCAGAGGCGCT 2

RESULT 591
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ACCESSION
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VERSION
157763.1 GI:2482827
KEYWORDS
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SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 300 11-MAR-1997;
FEATURES
Location/Qualifiers
source
1..15
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Query Match
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCAGAGGCGCT 3223
Db 14 TGCCAGAGGCGCT 1

RESULT 592
AX633193/c
LOCUS
AX633193
DEFINITION
Sequence 332 from Patent EP1260586.
ACCESSION
AX633193
VERSION
AX633193.1 GI:28468807
KEYWORDS
.
SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source
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/db_xref="taxon:32644"

ORGANISM
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Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 299 11-MAR-1997;
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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QY 3210 TGCCAGAGGCGCT 3223
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RESULT 591
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LOCUS
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DEFINITION
Sequence 300 from patent US 5610054.
ACCESSION
157763
VERSION
157763.1 GI:2482827
KEYWORDS
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SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 300 11-MAR-1997;
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QY 3210 TGCCAGAGGCGCT 3223
Db 14 TGCCAGAGGCGCT 1

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LOCUS
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DEFINITION
Sequence 332 from Patent EP1260586.
ACCESSION
AX633193
VERSION
AX633193.1 GI:28468807
KEYWORDS
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SOURCE
unidentified
ORGANISM
unclassified.

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1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
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TITLE
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genes
JOURNAL
Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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Unclassified.
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AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 299 11-MAR-1997;
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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QY 3210 TGCCAGAGGCGCT 3223
Db 15 TGCCAGAGGCGCT 2

RESULT 591
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LOCUS
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DEFINITION
Sequence 300 from patent US 5610054.
ACCESSION
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VERSION
157763.1 GI:2482827
KEYWORDS
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SOURCE
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ORGANISM
Unclassified.
REFERENCE
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JOURNAL
Patent: US 5610054-A 300 11-MAR-1997;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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QY 3210 TGCCAGAGGCGCT 3223
Db 14 TGCCAGAGGCGCT 1

RESULT 592
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LOCUS
AX633193
DEFINITION
Sequence 332 from Patent EP1260586.
ACCESSION
AX633193
VERSION
AX633193.1 GI:28468807
KEYWORDS
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SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
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AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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Location/Qualifiers
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/db_xref="taxon:32644"

ORGANISM
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Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 299 11-MAR-1997;
FEATURES
Location/Qualifiers
source
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0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCAGAGGCGCT 3223
Db 15 TGCCAGAGGCGCT 2

RESULT 591
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LOCUS
AX633193
DEFINITION
Sequence 300 from patent US 5610054.
ACCESSION
157763
VERSION
157763.1 GI:2482827
KEYWORDS
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SOURCE
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ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Draper,K.G.
TITLE
Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL
Patent: US 5610054-A 300 11-MAR-1997;
FEATURES
Location/Qualifiers
source
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Query Match
0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCAGAGGCGCT 3223
Db 14 TGCCAGAGGCGCT 1

RESULT 592
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LOCUS
AX633193
DEFINITION
Sequence 332 from Patent EP1260586.
ACCESSION
AX633193
VERSION
AX633193.1 GI:28468807
KEYWORDS
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SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
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AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
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Db 15 TGAATAAAAAAAAAA 2

RESULT 595
AX633205/c
LOCUS
DEFINITION
Sequence 344 from Patent EP1260586.
ACCESSION
AX633205
VERSION
AX633205.1 GI:28468819
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggan,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
Patent: EP 1260586-A 344 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
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QY 2801 TGAATAAAAAAAAAA 2814
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Db 14 TGAATAAAAAAAAAA 1

RESULT 596
AX769806
LOCUS
DEFINITION
Sequence 17 from Patent WO03020980.
ACCESSION
AX769806
VERSION
AX769806.1 GI:32437503
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.

REFERENCE
1
AUTHORS
Kaytes,P.S. and Teng,C.H.
TITLE
Single nucleotide polymorphisms diagnostic for schizophrenia
JOURNAL
Patent: WO 03020980-A 17 13-MAR-2003;
PHARMACIA & UPJOHN COMPANY (US)

FEATURES
source
1..15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3718 CCCTGCTGTATT 3731
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Db 1 CCCTGCTGTATT 14

RESULT 597

BD065951/c
LOCUS
DEFINITION
An antisense oligonucleotide preparation method.
ACCESSION
BD065951
VERSION
BD065951.1 GI:22611554
KEYWORDS
JP 2001511000-A/586.
SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
1 (bases 1 to 15)
AUTHORS
Schlingensiepen,K.H. and Brysch,W.
TITLE
An antisense oligonucleotide preparation method
JOURNAL
Patent: JP 2001511000-A 586 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/586
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
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FT /organism='Unknown'.
Location/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 15;
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QY 1917 TCTAATAATACAT 1930
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Db 14 TCTAATAATACAT 1

RESULT 598
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LOCUS
DEFINITION
Sequence 30 from patent US 5571937.
ACCESSION
I28577
VERSION
I28577.1 GI:1819353
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.

REFERENCE
1 (bases 1 to 16)
AUTHORS
Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE
Complementary DNA and toxins
JOURNAL
Patent: US 5571937-A 30 05-NOV-1996;
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"

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Db 15 TTTTTCCTTACTTT 2

RESULT 599
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LOCUS
DEFINITION
Sequence 30 from patent US 5652350.
ACCESSION
I58739

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VERSION 158739.1 GI:2477977
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Watanabe,K.A., Ren,W.-Y. and Well,R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 30 29-JUL-1997;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 15 TTTTTCCTTACTTT 2
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AX676082/c
LOCUS AX676082 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 35 from Patent WO02059381.
ACCESSION AX676082
VERSION AX676082.1 GI:29333766
KEYWORDS .
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Slaugenhaupt,S. and Gusella,J.F.
TITLE Gene for identifying individuals with familial dysautonomia
JOURNAL Patent: WO 02059381-A 35 01-AUG-2002;
The General Hospital Corporation (US)
FEATURES
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2801 TGAATAAAAAAAAAA 2814
Db 14 TGAATAAAAAAAAAA 1
RESULT 601
AX738493
LOCUS AX738493 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4083 from Patent WO03025177.
ACCESSION AX738493
VERSION AX738493.1 GI:30517781
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 4083 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 ATCTTTTCTTTT 15
RESULT 602
AX757892
LOCUS AX757892 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1213 from Patent WO03040369.
ACCESSION AX757892
VERSION AX757892.1 GI:32252508
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 1213 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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QY 2742 ATCTTTTCTTTT 2755
Db 2 ATCTTTTCTTTT 15
RESULT 603
BD142808/c
LOCUS BD142808 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142808
VERSION BD142808.1 GI:23237753
KEYWORDS WO 0224903-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T., Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 2 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI TAKAHASHI
COMMENT
    OS Artificial Sequence
    PN WO 0224903-A/2
    PD 28-MAR-2002
    PF 21-SEP-2001 WO 2001JP008246
    PR 25-SEP-2000 JP 00P 291318
    PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI TAKESHI NAGASU,
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PI GOZO TSUJIMOTO,EIKI TAKAHASHI
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
C12Q1/68,
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
CC CC Location/Qualifiers
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FT Location/Qualifiers

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588

Db 17 TAAAAA 4

RESULT 604
BD143834/C
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD143834
VERSION BD143834.1 GI:27849592
KEYWORDS JP 2002095500-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 2 02-APR-2002;
GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT OS Artificial Sequence
PN JP 2002095500-A/2
PD 02-APR-2002
PF 25-SEP-2000 JP 200291316
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI KOZO TSUJIMOTO
PC C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
C07K14/47,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
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PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
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FT Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2575 TAAAAA 2588
Db 17 TAAAAA 4

RESULT 605
BD167835/C
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination of allergosis.
ACCESSION BD167835
VERSION BD167835.1 GI:27873647
KEYWORDS WO 0233122-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 2 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO,EIKI TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0233122-A/2
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO,EIKI TAKAHASHI
PC C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
A61K39/395,
PC A01K67/027//C07K16/18,C12N5/10
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FT Location/Qualifiers

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QY 2575 TAAAAA 2588

Db 17 TAAAAA 4

RESULT 606
BD167907/C
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167907
VERSION BD167907.1 GI:27873719
KEYWORDS WO 0226962-A/6.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease

CC CC sequence primer
CC CC Location/Qualifiers
FH Key 1..17
FT source /organism='Artificial Sequence'.
FT Location/Qualifiers

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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

JOURNAL Patent: WO 0226962-A 6 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/6
PD 04-APR-2002
PP 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence: an artificially synthesized

CC primer
CC sequence
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.
FEATURES
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1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588
Db 17 TAAAAA 4

RESULT 607
BD171177/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171177
VERSION BD171177.1 GI:27876989
KEYWORDS WO 0250269-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 (bases 1 to 17)
Matsumoto, Y., Imai, Y., Oshida, T., Sugita, Y., Nagasu, T. and
Tsujiimoto, G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 2 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
GOZO TSUJIMOTO
OS Artificial Sequence
PN WO 0250269-A/2
PD 27-JUN-2002
PP 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI
TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,
PC A61P37/08,
PC C12Q1/68, G01N33/50
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CC primer sequence
FH Key Location/Qualifiers
FT source 1..17
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source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588
Db 17 TAAAAA 4

RESULT 609
BD171177/c
LOCUS 17 bp DNA linear PAT 29-SEP-1997

JOURNAL Patent: WO 0226962-A 6 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/6
PD 04-APR-2002
PP 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence: an artificially synthesized

CC primer
CC sequence
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.
FEATURES
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1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588
Db 17 TAAAAA 4

RESULT 607
BD168111/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168111
VERSION BD168111.1 GI:27873923
KEYWORDS WO 0233069-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Sugita, Y., Hashida, R., Ogawa, K., Obayashi, M., Nagasu, T. and
Saito, H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 18 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, MASAYA ODAYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0233069-A/18
PD 25-APR-2002
PP 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
A61K39/395,
CC C07K14/47, C07K16/18//C12P21/02, C12P21/08
CC Description of Artificial Sequence: an artificially synthesized
anchor

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DEFINITION DNA encoding DNA primer for typing DR antigen of human leukocyte
antigen.
ACCESSION E02988
VERSION E02988.1 GI:2171210
KEYWORDS JP 1991164180-A/5.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kashiwagi,N., Obata,B. and Abe,A.
TITLE NEW DNA BASE SEQUENCE AND USE THEREOF
JOURNAL Patent: JP 1991164180-A 5 16-JUL-1991;
COMMENT KASHIWAGI NOBORU, KITASATO INST:THE
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1991164180-A/5
PD 16-JUL-1991
PR 07-AUG-1990 JP 1990208901
PR 10-AUG-1989 JP 89P 207153
PI KASHIWAGI NOBORU, OBATA BUNYA, ABE AKIO
PC C12N15/12.C12N15/11.C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=PPR5;
FH Key Location/Qualifiers
FT misc_feature 1..17
FT /note='DNA primer for typing DR antigen of leukocyte antigen'
FT
FT
FT Location/Qualifiers
FEATURES
source 1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GCAGAGCTGCTGAA 44
Db 4 GCAGAGCTGCTGAA 17

RESULT 610
E34258/c
LOCUS
DEFINITION Pollinosis-associated gene.
ACCESSION E34258
VERSION E34258.1 GI:18624263
KEYWORDS JP 2000106879-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 2 18-APR-2000;
COMMENT GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/2
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA

DNA encoding DNA primer for typing DR antigen of human leukocyte
antigen.
ACCESSION E02988
VERSION E02988.1 GI:2171210
KEYWORDS JP 1991164180-A/5.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kashiwagi,N., Obata,B. and Abe,A.
TITLE NEW DNA BASE SEQUENCE AND USE THEREOF
JOURNAL Patent: JP 1991164180-A 5 16-JUL-1991;
COMMENT KASHIWAGI NOBORU, KITASATO INST:THE
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1991164180-A/5
PD 16-JUL-1991
PR 07-AUG-1990 JP 1990208901
PR 10-AUG-1989 JP 89P 207153
PI KASHIWAGI NOBORU, OBATA BUNYA, ABE AKIO
PC C12N15/12.C12N15/11.C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=PPR5;
FH Key Location/Qualifiers
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FT /note='DNA primer for typing DR antigen of leukocyte antigen'
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FT Location/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GCAGAGCTGCTGAA 44
Db 4 GCAGAGCTGCTGAA 17

RESULT 610
E34258/c
LOCUS
DEFINITION Pollinosis-associated gene.
ACCESSION E34258
VERSION E34258.1 GI:18624263
KEYWORDS JP 2000106879-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 2 18-APR-2000;
COMMENT GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/2
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA

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PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.
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source 1..17
Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAAA 2588
Db 17 TAAAAAATAAAAAA 4

RESULT 611
AR266625/c
LOCUS
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION AR266625
VERSION AR266625.1 GI:29695689
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 63 17-DEC-2002;
FEATURES
source 1..17
Location/Qualifiers
/organism='unknown'
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAAA 2588
Db 17 TAAAAAATAAAAAA 4

RESULT 612
AX215415/c
LOCUS
DEFINITION Sequence 857 from Patent WO0159103.
ACCESSION AX215415
VERSION AX215415.1 GI:15525458
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 857 16-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
Mcswiggen, James (US); Chowrira, Bharat M. (US)
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source 1..17
Location/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 17;

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCGCTCCGGGCG 578
Db 17 GCGCTCCGGGCG 4

RESULT 613
AX216957/c
LOCUS AX216957 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2399 from Patent WO0159103.
ACCESSION AX216957
VERSION AX216957.1 GI:15527018
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B. M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 2399 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
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/note="Nucleic Acid"

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCGCTCCGGGCG 578
Db 16 GCGCTCCGGGCG 3

RESULT 614
AX216958/c
LOCUS AX216958 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2400 from Patent WO0159103.
ACCESSION AX216958
VERSION AX216958.1 GI:15527019
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B. M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 2400 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
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/note="Nucleic Acid"

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCGCTCCGGGCG 578
Db 15 GCGCTCCGGGCG 2

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCTCGCTG 1903
Db 16 CACTGCCCTCGCTG 3

RESULT 617
AX532504/c
LOCUS AX532504 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 2013 from Patent EP1239051.
ACCESSION AX532504
VERSION AX532504.1 GI:25256779
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 2011 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1..17
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/db_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCTCGCTG 1903
Db 17 CACTGCCCTCGCTG 4

RESULT 616
AX532503/c
LOCUS AX532503 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 2012 from Patent EP1239051.
ACCESSION AX532503
VERSION AX532503.1 GI:25256777
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 2012 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCTCGCTG 1903
Db 17 CACTGCCCTCGCTG 4

RESULT 616
AX532503/c
LOCUS AX532503 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 2012 from Patent EP1239051.
ACCESSION AX532503
VERSION AX532503.1 GI:25256777
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 2012 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCTCGCTG 1903
Db 16 CACTGCCCTCGCTG 3

RESULT 617
AX532504/c
LOCUS AX532504 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 2013 from Patent EP1239051.
ACCESSION AX532504
VERSION AX532504.1 GI:25256779
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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[illegible]

PI KAORU OGAWA,KEIKO MATSUI
PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers.

FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAA 2588
Db 17 TAAAAAATAAAAA 4

RESULT 626
BD091750/c
LOCUS
DEFINITION
465, a novel gene related to pollen allergy.
PAT 27-AUG-2002
BD091750 17 bp DNA linear
ACCESSION
BD091750.1 GI:22637361
VERSION
WO 0073439-A/2.
KEYWORDS
synthetic construct
SOURCE
ORGANISM
other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 17)
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
AUTHORS
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.

TITLE
JOURNAL
465, a novel gene related to pollen allergy
Patent: WO 0073439-A 2 07-DEC-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI

OS Artificial Sequence
PN WO 0073439-A/2
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191
PI 27-MAY-1999 JP 99P 148784

PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC Description
of Artificial Sequence:Artificially Synthesized CC Primer
Sequence

FH Key Location/Qualifiers.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAA 2588
Db 17 TAAAAAATAAAAA 4

RESULT 627
BD091773/c
LOCUS
DEFINITION
787, a novel gene related to pollen allergy.
PAT 27-AUG-2002
BD091773 17 bp DNA linear
ACCESSION
BD091773

BD091773.1 GI:22637384
WO 0073440-A/2.
synthetic construct
SOURCE
ORGANISM
other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 17)
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
AUTHORS
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.

TITLE
JOURNAL
787, a novel gene related to pollen allergy
Patent: WO 0073440-A 2 07-DEC-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI

OS Artificial Sequence
PN WO 0073440-A/2
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PI 27-MAY-1999 JP 99P 148785

PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C12Q1/68,C12N5/08,C07K14/415 CC Description of
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FH Key Location/Qualifiers.

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Query Match 0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAA 2588
Db 17 TAAAAAATAAAAA 4

RESULT 628
BD097334/c

LOCUS
DEFINITION
Method for examination for allergosis.
PAT 27-AUG-2002
BD097334 17 bp DNA linear
ACCESSION
BD097334

VERSION
BD097334.1 GI:22642908
KEYWORDS
WO 0165259-A/5.
synthetic construct
SOURCE
ORGANISM
other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 17)
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
AUTHORS
Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE
JOURNAL
Method for examination for allergosis
Patent: WO 0165259-A 5 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
OBAYASHI,KEIKO MATSUI, HIROHISA SAITO

OS Artificial Sequence
PN WO 0165259-A/5
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PI 02-MAR-2000 JP 00P 61832

PI TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
HIROHISA SAITO
PC G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
PC A61P37/08
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
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                /db_xref="taxon:32630"
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QY 2575 TAAAAAATAAAAAA 2588
Db 17 TAAAAAATAAAAAA 4

RESULT 629
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LOCUS AR266625 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION AR266625
VERSION AR266625.1 GI:29695689
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 63 17-DEC-2002;
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QY 3263 ATTTTTCCTTTT 3279
Db 1 ATTTTTCCTTTT 17

RESULT 630
AR8312
LOCUS AR8312 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 460 from Patent WO9833904.
ACCESSION AR8312
VERSION AR8312.1 GI:6736882
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 460 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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QY 2570 GTGTTTAAAAA 2586
Db 1 GTCTTTAAAAA 17

RESULT 631
AR90279
LOCUS AR90279 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 460 from Patent EP0856579.
ACCESSION AR90279
VERSION AR90279.1 GI:6738793
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 460 05-AUG-1998;
BIOGOSTIK GES (DE)
FEATURES
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Query Match
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QY 2570 GTGTTTAAAAA 2586
Db 1 GTCTTTAAAAA 17

RESULT 632
AR040485
LOCUS AR040485 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1333 from patent US 5807743.
ACCESSION AR040485
VERSION AR040485.1 GI:5959848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 1333 15-SEP-1998;
FEATURES
    source
        Location/Qualifiers
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                /mol_type="unassigned DNA"
Query Match
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Db 1 ACCTGGGTCCATTCCTC 17

RESULT 633
AR053084
LOCUS AR053084 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 54 from patent US 5834181.
ACCESSION AR053084
VERSION AR053084.1 GI:5977946
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
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JOURNAL Patent: US 5834181-A 54 10-NOV-1998;
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
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Db 1 GATTGTTTTTTGTTTC 17

RESULT 634
AR065045
LOCUS AR065045 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 54 from patent US 5849483.
ACCESSION AR065045
VERSION AR065045.1 GI:5995261
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic
alterations in nucleic acids
JOURNAL Patent: US 5849483-A 54 15-DEC-1998;
FEATURES
  source      1. .17
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
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Db 1 GATTGTTTTTTGTTTC 17

RESULT 635
AR164696
LOCUS AR164696 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 7 from patent US 6274332.
ACCESSION AR164696
VERSION AR164696.1 GI:16237815
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human minK which cause
arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6274332-A 7 14-AUG-2001;
FEATURES
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCTCTGAGCAAGCT 1360
    ||||| | |||||
Db 1 CAGATCTCTGAGGATGCT 17

RESULT 636
BD142809/c
LOCUS BD142809 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142809
VERSION BD142809.1 GI:23237754
KEYWORDS WO 0224903-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 3 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/3
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 231318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
C12Q1/68,
PC A01K67/027,A61K31/713,A61K45/00,A61P17/00,A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized
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CC sequence
FH Key Location/Qualifiers
FT source 1. .17
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FEATURES
  source      1. .17
              Location/Qualifiers
Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAACAACCAACC 946
    ||||| | |||||
Db 17 GAAAAAACAACCAAC 1

RESULT 637
BD143835/c
LOCUS BD143835 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD143835
VERSION BD143835.1 GI:27849593
KEYWORDS JP 2002095500-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 3 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT OS Artificial Sequence
PN JP 2002095500-A/3
PD 02-APR-2002
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PF 25-SEP-2000 JP 2000291316
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI KOZO TSUJINOTO
PC
C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
C07K14/47,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
,C12N15/09,C12P21/02,
PC C12Q1/02,G01N33/15,G01N33/50/C12P21/08,C12N5/00,C12N5/00, PC
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CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
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FT source 1..17
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
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Qy 930 GAAAAAAACAAACC 946
Db 17 GAAAAAAACAAACC 1

RESULT 638
BD167908/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 7 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
C12Q1/68,
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
PC G01N33/15,
PC G01N33/50/C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
CC Key Location/Qualifiers
FH Key 1..17
FT source /organism='Artificial Sequence'.

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Location/Qualifiers
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/db_xref="taxon:32630"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAAACAAACC 946
Db 17 GAAAAAAACAAACC 1

RESULT 640
BD168112/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112.1 GI:27873924
KEYWORDS WO 0233069-A/19.
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PF 25-SEP-2000 JP 2000291316
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI KOZO TSUJINOTO
PC
C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
C07K14/47,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
,C12N15/09,C12P21/02,
PC C12Q1/02,G01N33/15,G01N33/50/C12P21/08,C12N5/00,C12N5/00, PC
C12N15/00
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
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FEATURES
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Location/Qualifiers
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAAACAAACC 946
Db 17 GAAAAAAACAAACC 1

RESULT 638
BD167836/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination of allergosis.
ACCESSION BD167836
VERSION BD167836.1 GI:27873648
KEYWORDS WO 0233122-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 3 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
SAITO,EIKI TAKAHASHI
OS Artificial Sequence
PN WO 0233122-A/3
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI HIROHISA SAITO,EIKI TAKAHASHI
PC C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
A61K39/395,
PC A01K67/027/C07K16/18,C12N5/10
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CC anchor
CC primer sequence
FH Key Location/Qualifiers
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FEATURES
source
1..17
Location/Qualifiers
/organism="synthetic construct"
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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 19 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
COMMENT PN WO 0233069-A/19
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC A61K39/395,
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
CC Description of Artificial Sequence: an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
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FT Location/Qualifiers
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAAACAAACC 946
DB 17 GAAAAAAACAAACC 1

RESULT 641
BD171178/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD171178.1 GI:27876990
VERSION BD171178.1
KEYWORDS WO 0250269-A/3.
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 17)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 3 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA, YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU, GOZO TSUJIMOTO
COMMENT OS Artificial Sequence
PN WO 0250269-A/3
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,

PC A61P37/08,
PC C12Q1/68, G01N33/50
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CC primer sequence Location/Qualifiers
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FT source 1..17
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAAACAAACC 946
DB 17 GAAAAAAACAAACC 1

RESULT 642
BD177281/c
LOCUS
DEFINITION Sulfotransferase for nonreducing beta-galactose and nucleic acid encoding the same.
ACCESSION BD177281.1 GI:30014542
VERSION BD177281.1
KEYWORDS JP 2002300879-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 17)
AUTHORS Motoie,K.
TITLE Sulfotransferase for nonreducing beta-galactose and nucleic acid encoding the same
JOURNAL Patent: JP 2002300879-A 2 15-OCT-2002;
J G S INC

COMMENT OS Artificial Sequence
PN JP 2002300879-A/2
PD 15-OCT-2002
PF 03-APR-2001 JP 2001105201
PI KOICHI MOTOIE
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/10, C12Q1/68, C12N15/00,
PC C12N5/00
CC Oligonucleotide forward primer used in PCR for amplifying CC GP3ST cDNA
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2526 GACCATGATGTTTGCA 2542
DB 17 GAACATGATGTTTGCA 1

RESULT 643
BD201512
LOCUS
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.

ACCESSION BD201512
 VERSION BD201512.1 GI:33011282
 KEYWORDS JP 2002509721-A/4538
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 AUTHORS Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
 TITLE Method and reagent for treating diseases or conditions concerning
 molecule participating in vasculogenic response
 JOURNAL RIBOZYME PHARMACEUTICALS INC
 PATENT: JP 2002509721-A 4538 02-APR-2002;
 COMMENT OS Homo sapiens (human)
 PN JP 2002509721-A/4538
 PD 02-APR-2002
 PF 24-MAR-1999 JP 2000541291
 PR 27-MAR-1998 US 60/079678
 PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
 PI JAMES A MCSWIGGEN
 PC

C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
 A61P29/00,
 PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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 CC participating in vasculogenic response
 FH Key Location/Qualifiers
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 /db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 4.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3600 TTTTTCATGATCAT 3616
 Db 1 TTTTTCATGATCAT 17

RESULT 644
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 LOCUS KVLQTI-QT extension syndrome.
 DEFINITION KVLQTI-QT extension syndrome.
 ACCESSION BD222807
 VERSION BD222807.1 GI:33032577
 KEYWORDS JP 2002521045-A/5.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 AUTHORS Keating, M.T., Sanguinetti, M.C., Karan, M.E., Landes, G.M.,
 Connors, T.D., Burn, T.C. and Splawski, I.
 TITLE KVLQTI-QT extension syndrome
 JOURNAL UNIVERSITY OF UTAH RESEARCH FOUNDATION, GENZYME CORP
 PATENT: JP 2002521045-A 5 16-JUL-2002;
 COMMENT OS Homo sapiens (human)
 PN JP 2002521045-A/5
 PD 16-JUL-2002
 PF 12-MAY-1999 JP 2000562052
 PR 29-JUL-1998 US 60/094477, 17-AUG-1998 US 09/135010 PI
 MARK T KEATING, MICHAEL C SANGUINETTI, MARK E KARAN, GREGORY M PI
 LANDES,
 PI TIMOTHY D CONNORS, TIMOTHY C BURN IGOR SPLAWSKI PC
 C12N15/09,A01K67/027,C07K14/46,C07K14/47,C07K16/18,C12N1/15, PC
 C12N1/19,

PC C12N1/21,C12N5/10,C12P21/08,C12Q1/02,C12Q1/68,G01N33/15,G01N33/PC
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 PC C12N15/00,
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 /db_xref="taxon:9606"

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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360
 Db 1 CAGATCCTGAGGATGCT 17

RESULT 645
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 LOCUS A method for stimulating the immune system.
 DEFINITION A method for stimulating the immune system.
 ACCESSION BD235082
 VERSION BD235082.1 GI:33044852
 KEYWORDS JP 2002517434-A/186.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 AUTHORS Schlingensiepen, K.H., Schlingensiepen, R. and Brysch, W.
 TITLE A method for stimulating the immune system
 JOURNAL Patent: JP 2002517434-A 186 18-JUN-2002;
 BIOLOGIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Homo sapiens (human)
 PN JP 2002517434-A/186
 PD 18-JUN-2002
 PF 10-JUN-1999 JP 2000553044
 PR 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI
 KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
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 PC 00,A61P35/00,
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1320 AAGCGATCGAGCCAT 1336
 Db 17 AAGCGATCGAGCCAT 1

RESULT 646
 BD254578
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DEFINITION      Regulation of repressor genes using nucleic acid molecules.
ACCESSION       BD254578
VERSION         BD254578.1 GI:33064348
KEYWORDS        JP 2002541795-A/2371.
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 17)
AUTHORS        Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE          Regulation of repressor genes using nucleic acid molecules
JOURNAL        Patent: JP 2002541795-A 2371 10-DEC-2002;
               RIBOZYME PHARMACEUTICALS INC
COMMENT        OS Eukaryote
               PN JP 2002541795-A/2371
               PD 10-DEC-2002
               PF 11-APR-2000 JP 2000611654
               PR 12-APR-1999 US 60/129390
               PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
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               C12P21/02,
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               C12R1:91),
               PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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Query Match    0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3631 TGTTCCTTTAGCTGGC 3647
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      1 TGTTCCTTTACTGGC 17

Db

RESULT 647
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LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION     BD254579
VERSION       BD254579.1 GI:33064349
KEYWORDS      JP 2002541795-A/2372.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 17)
AUTHORS       Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 2372 10-DEC-2002;
               RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
               PN JP 2002541795-A/2372
               PD 10-DEC-2002
               PF 11-APR-2000 JP 2000611654
               PR 12-APR-1999 US 60/129390
               PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
               C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
               C12P21/02,
               PC
               C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
               C12R1:91),
               PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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               CC Regulation of repressor genes using nucleic acid molecules FH
               Key Location/Qualifiers
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Query Match    0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3632 GTTTCCTTTAGCTGGC 3648
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      1 GTTTCCTTTACTGGC 17

Db

RESULT 648
BD254580
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION     BD254580
VERSION       BD254580.1 GI:33064350
KEYWORDS      JP 2002541795-A/2373.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 17)
AUTHORS       Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 2373 10-DEC-2002;
               RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
               PN JP 2002541795-A/2373
               PD 10-DEC-2002
               PF 11-APR-2000 JP 2000611654
               PR 12-APR-1999 US 60/129390
               PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
               C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
               C12P21/02,
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               C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
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               PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3633 TTTTCCTTTAGCTGGCA 3649
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      1 TTTTCCTTTACTGGCCA 17

Db

RESULT 649
BD254790
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION     BD254790

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BD254790.1 GI:33064560
SOURCE JP 2002541795-A/2583.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2583 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2583
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2593 AGAAAAAATCGGTAC 2609
Db 17 AGAAAAAATCTGAAC 1

RESULT 651
BD256406/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256406
VERSION BD256406.1 GI:33066176
KEYWORDS JP 2002541795-A/4199.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4199 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/4199
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
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C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
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QY 21 TTTGCTCGGAGCAGAGC 37
Db 17 TTTGCTTGAGTAGAGC 1

RESULT 652
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LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256854
VERSION BD256854.1 GI:33066624
KEYWORDS JP 2002541795-A/4647.

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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 6131 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/6131
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
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BD258340/C
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DEFINITION
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VERSION
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Eukaryote
PN JP 2002541795-A/6133
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
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PC (C12N5/00,C12R1:91)
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QY 2812 AAACATCAAAACAAAC 2828
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DB 17 AAACAACAACAAAGC 1
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BD258340/C
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OS Eukaryote
PN JP 2002541795-A/6133
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
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Best Local Similarity 88.2%; Pred.No.4.1e+02;
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QY 2808 AAAAAACATCAAAACA 2824
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DB 17 AAACAACAACAAACA 1
RESULT 657
BD258484
LOCUS
DEFINITION
ACCESSION
VERSION
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AUTHORS
TITLE
JOURNAL
COMMENT
OS Eukaryote
PN JP 2002541795-A/6277
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1633 AAAATGCTTCGAATCTG 1649
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DB 1 AAAATCCTTCTAATCTG 17
RESULT 658
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 6277 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/6277
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91)
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No.4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1 AAAATCCTTCTAATCTG 17
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BD258512/C
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DEFINITION
ACCESSION
VERSION
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ORGANISM
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 6305.
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/6305
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
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C12R1:91)
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE Regulation of repressor genes using nucleic acid molecules
 JOURNAL Patent: JP 2002541795-A 6305 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 COMMENT OS Eukaryote
 PN JP 2002541795-A/6305
 PD 10-DEC-2002
 PF 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/129390
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 LOCUS 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Regulation of repressor genes using nucleic acid molecules.
 ACCESSION BD258513
 VERSION BD258513.1 GI:33068283
 KEYWORDS JP 2002541795-A/6306.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE Regulation of repressor genes using nucleic acid molecules
 JOURNAL Patent: JP 2002541795-A 6306 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 COMMENT OS Eukaryote
 PN JP 2002541795-A/6306
 PD 10-DEC-2002
 PF 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/129390
 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
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 DB 17 TGTATAATAATAAAAA 1
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 LOCUS 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Regulation of repressor genes using nucleic acid molecules.
 ACCESSION BD258574
 VERSION BD258574.1 GI:33068344
 KEYWORDS JP 2002541795-A/6367.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE Regulation of repressor genes using nucleic acid molecules
 JOURNAL Patent: JP 2002541795-A 6367 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 COMMENT OS Eukaryote
 PN JP 2002541795-A/6367
 PD 10-DEC-2002
 PF 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/129390
 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
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 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
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 DB 1 GCACATTTTAAAT 17
 RESULT 661
 BD258575
 LOCUS 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Regulation of repressor genes using nucleic acid molecules.
 ACCESSION BD258575
 VERSION BD258575.1 GI:33068345
 KEYWORDS JP 2002541795-A/6368.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE Regulation of repressor genes using nucleic acid molecules

JOURNAL Patent: JP 2002541795-A 6368 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/6368
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12N5/10, PC
C12P21/02,
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C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1.91),(C12P21/02, PC
C12R1.91),
PC (C12P21/02,C12R1.91),(C12P21/02,C12R1.91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1.91)
CC Regulation of repressor genes using nucleic acid molecules FH
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
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Db 1 CACATTTTCTTTAATT 17
RESULT 662
CQ615503
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 243 from Patent WO0192524.
ACCESSION CQ615503
VERSION CQ615503.1 GI:41665721
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 243 06-DEC-2001;
Aeomica, Inc. (US)
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Db 1 ATCTCGCGCCCTCC 17
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CQ616325/c
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 1065 from Patent WO0192524.
ACCESSION CQ616325
VERSION CQ616325.1 GI:41666543

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 1065 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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RESULT 664
CQ616326/c
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 1066 from Patent WO0192524.
ACCESSION CQ616326
VERSION CQ616326.1 GI:41666544
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 1066 06-DEC-2001;
Aeomica, Inc. (US)
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Db 17 CCTACGTCCTTAGAC 1
RESULT 665
CQ617482
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2222 from Patent WO0192524.
ACCESSION CQ617482
VERSION CQ617482.1 GI:41667700
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle

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JOURNAL Patent: WO 0192524-A 2222 06-DEC-2001;
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RESULT 666
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DEFINITION Sequence 8557 from Patent WO0192524.
ACCESSION CQ623817
VERSION CQ623817.1 GI:41674035
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8557 06-DEC-2001;
Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
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Db 1 CGATGAGGACCGAGTG 17

RESULT 667
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DEFINITION Sequence 9226 from Patent WO0192524.
ACCESSION CQ624486
VERSION CQ624486.1 GI:41674704
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 9226 06-DEC-2001;
Aeomica, Inc. (US)
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ACCESSION CQ625768
VERSION CQ625768.1 GI:41675986
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10508 06-DEC-2001;
Aeomica, Inc. (US)
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RESULT 669
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DEFINITION Sequence 10509 from Patent WO0192524.
ACCESSION CQ625769
VERSION CQ625769.1 GI:41675987
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10509 06-DEC-2001;
Aeomica, Inc. (US)
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CQ868213
 LOCUS CQ868213 17 bp DNA linear PAT 13-SEP-2004
 DEFINITION Sequence 7 from Patent EP1454915.
 ACCESSION CQ868213
 VERSION CQ868213.1 GI:51998263
 KEYWORDS
 SOURCE
 ORGANISM
 Canis familiaris (dog)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1
 Murayama,M. and Ito,S.
 Polynucleotides, polypeptides and method for screening for
 useful dog candidates
 Patent: EP 1454915-A 7 08-SEP-2004;
 President of Gifu University (JP)
 JOURNAL
 FEATURES
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 Db 1 CCGCGGCTGCCAGGC 17
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 LOCUS E34259 17 bp DNA linear PAT 31-JAN-2002
 DEFINITION Pollinosis-associated gene.
 ACCESSION E34259
 VERSION E34259.1 GI:18624264
 KEYWORDS JP 2000106879-A/3.
 SOURCE
 ORGANISM
 synthetic construct
 synthetic construct
 other sequences; artificial sequences.
 1 (bases 1 to 17)
 Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
 Gunji,S., Obayashi,I., Imai,Y., No.N. and Ogawa,K.
 Pollinosis-associated gene
 Patent: JP 2000106879-A 3 18-APR-2000;
 GENOX RESEARCH INC
 OS Artificial Sequence
 PN JP 2000106879-A/3
 PD 18-APR-2000
 PE 06-OCT-1998 JP 1998284610
 PR
 PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
 PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
 PI NING NO,
 PI KAORU OGAWA
 PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
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 Db 17 GAAAAAACAACACC 1
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 RESULT 672
 I32590
 LOCUS I32590 17 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 54 from patent US 5589330.
 ACCESSION I32590
 VERSION I32590.1 GI:1823381
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unassigned.
 1 (bases 1 to 17)
 Shuber,A.P.
 High-throughput screening method for sequence or genetic
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 complementary oligonucleotides
 Patent: US 5589330-A 54 31-DEC-1996;
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 Db 1 GATTGTATTTGTTTC 17
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 1 GATTGTATTTGTTTC 17
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 AR186202/c
 LOCUS AR186202 17 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 1690 from patent US 6346398.
 ACCESSION AR186202
 VERSION AR186202.1 GI:20232167
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unassigned.
 1 (bases 1 to 17)
 Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
 Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 Patent: US 6346398-A 1690 12-FEB-2002;
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 QY 4228 AGGTTTTCAGACACATT 4244
 Db 17 AGGTTTTCAGACACATT 1
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 17 AGGTTTTCAGACACATT 1
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 AR186698/c
 LOCUS AR186698 17 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 2186 from patent US 6346398.
 ACCESSION AR186698
 VERSION AR186698.1 GI:20232663
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2186 12-FEB-2002;
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/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 17 GTCAAAAAAAAAAAGCA 1
RESULT 675
AR186827
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2315 from patent US 6346398.
ACCESSION AR186827
VERSION AR186827.1 GI:20232792
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2315 12-FEB-2002;
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 862 ACTGAACCTCATTCTT 878
Db 1 ACTTAACCAATTCTT 17
RESULT 676
AR187056/c
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2544 from patent US 6346398.
ACCESSION AR187056
VERSION AR187056.1 GI:20233021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2544 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2579 AAAAAAAAAAATTGGAGA 2595
Db 17 AAAAAAAAAAAGTAGAGA 1
RESULT 677
AR187057/c
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2545 from patent US 6346398.
ACCESSION AR187057
VERSION AR187057.1 GI:20233022
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2545 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 17 AAAAAAAAAAAGTAGAG 1
RESULT 678
AR187058/c
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2546 from patent US 6346398.
ACCESSION AR187058
VERSION AR187058.1 GI:20233023
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2546 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2577 AAAAAAAAAAATTGGA 2593
Db 17 AAAAAAAAAAAGTAGA 1
RESULT 679
AR187059/c
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2547 from patent US 6346398.
ACCESSION AR187059
VERSION AR187059.1 GI:20233024
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

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REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 2547 12-FEB-2002;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATTGG 2592
|||||
Db 17 AAAAAAAAAAAAGTAG 1

RESULT 680
AR187063/c
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2551 from patent US 6346398.
ACCESSION AR187063
VERSION AR187063.1 GI:20233028
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 2551 12-FEB-2002;
source Location/Qualifiers
1. .17
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 GAGAAAAAAACAA 944
|||||
Db 17 GAAAAAA 1

RESULT 681
AR187064/c
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 2552 12-FEB-2002;
source Location/Qualifiers
1. .17
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGAGAAAAAAACAA 943
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Db 17 GAAAAAA 1

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 2547 12-FEB-2002;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 GAGAAAAAAACAA 944
|||||
Db 17 GAAAAAA 1

RESULT 682
AR187068/c
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2556 from patent US 6346398.
ACCESSION AR187068
VERSION AR187068.1 GI:20233033
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 2556 12-FEB-2002;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2798 ATGTGAAAAAAA 2814
|||||
Db 17 ATTTGAAAAAAA 1

RESULT 683
AR187239
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2727 from patent US 6346398.
ACCESSION AR187239
VERSION AR187239.1 GI:20233204
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 2727 12-FEB-2002;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3702 TTTTATATACATCTTC 3718
|||||
Db 1 TTTTGATACCATCTTC 17

RESULT 684
AR188517
LOCUS 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4005 from patent US 6346398.
ACCESSION AR188517
VERSION AR188517.1 GI:20234482
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
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AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4005 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1811 GCTCTCTCTTCGACGTGA 1827
Db 1 GATCTCTTCACAGTGA 17
RESULT 685
LOCUS AR188526 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4014 from patent US 6346398.
ACCESSION AR188526
VERSION AR188526.1 GI:20234491
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4014 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1849 TTCACCACAAAGACAGC 1865
Db 17 TGCACCACAAAGACAGC 1
RESULT 686
LOCUS AR188812 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4300 from patent US 6346398.
ACCESSION AR188812
VERSION AR188812.1 GI:20234777
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4300 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4030 TATGAGACTCTCTTTGCC 4046
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Db 1 TCTGGACTCTCTCTGCC 17
RESULT 687
LOCUS AR190075 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5563 from patent US 6346398.
ACCESSION AR190075
VERSION AR190075.1 GI:20236040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5563 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 246 TGGAGCTAGGAGAGC 262
Db 1 TGGCAGCTAGGAGAGC 17
RESULT 688
LOCUS AR190475 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5963 from patent US 6346398.
ACCESSION AR190475
VERSION AR190475.1 GI:20236440
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5963 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4035 ACTCTCTTTGGCGTTCA 4051
Db 1 ACTCTCTTTCCATTCA 17
RESULT 689
LOCUS AR192138 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7626 from patent US 6346398.
ACCESSION AR192138
VERSION AR192138.1 GI:20238103
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
| | | | | | | | | | | | | | | | | |

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7626 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 GAGCTGCTGAACCTGCC 50
|||||
17 GAGCTGCTGACACTGTC 1

Db

RESULT 690
AR196413/c
LOCUS AR196413 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 878 from patent US 6350934.
ACCESSION AR196413
VERSION AR196413.1 GI:20245850
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edgington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens., Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 878 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 931 AAAAAAAAAACCACT 947
|||||
17 AAAAAATAAAACAAAGCT 1

Db

RESULT 691
AR218660
LOCUS AR218660 17 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 7 from patent US 6420124.
ACCESSION AR218660
VERSION AR218660.1 GI:23319555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQT1--a long qt syndrome gene
JOURNAL Patent: US 6420124-A 7 16-JUL-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1344 CAGATCCTGAGCAAGCT 1360
|||||
1 CAGATCCTGAGGATGCT 17

Db

RESULT 692
AR223075
LOCUS AR223075 17 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6432644.
ACCESSION AR223075
VERSION AR223075.1 GI:23330928
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human mink which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6432644-A 7 13-AUG-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1344 CAGATCCTGAGCAAGCT 1360
|||||
1 CAGATCCTGAGGATGCT 17

Db

RESULT 693
AR229837
LOCUS AR229837 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6451534.
ACCESSION AR229837
VERSION AR229837.1 GI:27269715
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6451534-A 7 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1344 CAGATCCTGAGCAAGCT 1360
|||||
1 CAGATCCTGAGGATGCT 17

Db

RESULT 694
AR241830/c
LOCUS AR241830 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 118 from patent US 6472154.
ACCESSION AR241830
VERSION AR241830.1 GI:27287642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes

JOURNAL Patent: US 6472154-A 118 29-OCT-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGAGRAAAAAAAAAACAA 943
Db 17 GGAAAAAAAAAAAAAAAAA 1

RESULT 695
AR262093 AR262093 17 bp DNA linear PAT 29-JAN-2003
LOCUS Sequence 7 from patent US 6323026.
ACCESSION AR262093
VERSION AR262093.1 GI:28073454
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human mink which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6323026-A 7 27-NOV-2001;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360
Db 1 CAGATCCTGAGGTGCT 17

RESULT 696
AR286385/c AR286385 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 757 from patent US 6528640.
ACCESSION AR286385
VERSION AR286385.1 GI:29723981
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 757 04-MAR-2003;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCAGAAG 3220
Db 17 GGCAGATGCCAGAAG 1

RESULT 697
AR322833/c AR322833 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 235 from patent US 6566127.
ACCESSION AR322833
VERSION AR322833.1 GI:33708641
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 235 20-MAY-2003;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4228 AGTTTTTGAAGACATT 4244
Db 17 AGTTTTTAAACACATT 1

RESULT 698
AR323329/c AR323329 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 731 from patent US 6566127.
ACCESSION AR323329
VERSION AR323329.1 GI:33709137
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 731 20-MAY-2003;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTCAAAAAAAAAAACA 2816
Db 17 GTCAAAAAAAAAAAGCA 1

RESULT 699
AR323458 AR323458 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 860 from patent US 6566127.
ACCESSION AR323458
VERSION AR323458.1 GI:33709266
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 860 20-MAY-2003;

RESULT 702

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source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 GAGAAAAAAACAA 944
Db 17 GAAAAAAACAA 1

RESULT 705
AR323674/c
LOCUS AR323674 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1076 from patent US 6566127.
ACCESSION AR323674
VERSION AR323674.1 GI:33709482
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGAGAAAAAAACAA 943
Db 17 GGAAAAAAACAA 1

RESULT 706
AR323678/c
LOCUS AR323678 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1080 from patent US 6566127.
ACCESSION AR323678
VERSION AR323678.1 GI:33709486
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1080 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2798 ATGTGAAAAAAACAA 2814
Db 17 ATTTGAAAAAAACAA 1

RESULT 707
AR323849
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LOCUS AR323849 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1251 from patent US 6566127.
ACCESSION AR323849
VERSION AR323849.1 GI:33709657
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1251 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3702 TTTTATATATCTTC 3718
Db 1 TTTGTATACCATCTTC 17

RESULT 708
AR324370
LOCUS AR324370 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1772 from patent US 6566127.
ACCESSION AR324370
VERSION AR324370.1 GI:33710178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1772 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GCTCTCTTCCAGCTGA 1827
Db 1 GATCTCTTCCAGCTGA 17

RESULT 709
AR324379/c
LOCUS AR324379 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1781 from patent US 6566127.
ACCESSION AR324379
VERSION AR324379.1 GI:33710187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1781 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match
  0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1849 TTCACCACAAAGACAGG 1865
Db 17 TGCACCACAAAGACAGC 1

RESULT 710
LOCUS AR324665 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2067 from patent US 6566127.
ACCESSION AR324665
VERSION AR324665.1 GI:33710473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2067 20-MAY-2003;
FEATURES
  Location/Qualifiers
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        /organism="unknown"
        /mol_type="unassigned RNA"

Query Match
  0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTTGCCGTTC 4051
Db 1 ACTCTCTTTTCATTCA 17

RESULT 713
LOCUS AR326016 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3418 from patent US 6566127.
ACCESSION AR326016
VERSION AR326016.1 GI:33711824
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3418 20-MAY-2003;
FEATURES
  Location/Qualifiers
    source
      1..17
        /organism="unknown"
        /mol_type="unassigned RNA"

Query Match
  0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAAACTGCC 50
Db 17 GAGCTGCTGACACTGTC 1

RESULT 714
LOCUS AR327833 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5235 from patent US 6566127.
ACCESSION AR327833
VERSION AR327833.1 GI:33713641
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5235 20-MAY-2003;
FEATURES
  Location/Qualifiers
    source
      1..17
        /organism="unknown"

/organism="unknown"
/mol_type="unassigned RNA"

Query Match
  0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 246 TGGAGCTAGGAGAAGC 262
Db 1 TGGCAGCTAGAGAAGC 17

RESULT 712
LOCUS AR325398 17 bp RNA linear PAT 17-AUG-2003
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/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 CACTGAACCTCCATTCT 877
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Db 1 CACTTAACCAATTCT 17

RESULT 715
AR328033/c
LOCUS AR328033 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5435 from patent US 6566127.
ACCESSION AR328033
VERSION AR328033.1 GI:33713841
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5435 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGGAGAA 2596
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Db 17 AAAAAAAAGTAGAGAA 1

RESULT 716
AR328180/c
LOCUS AR328180 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5582 from patent US 6566127.
ACCESSION AR328180
VERSION AR328180.1 GI:33713988
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5582 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2750 TTTTAAAGGAAAAAA 2766
    || ||| ||||| |||||
Db 17 TTATTTTAGGAAAAAA 1

RESULT 717
AR328181/c
LOCUS AR328181 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5583 from patent US 6566127.

/mol_type="unassigned RNA"

ACCESSION AR328181
VERSION AR328181.1 GI:33713989
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5583 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2749 TTTTAAAGGAAAAAA 2765
    ||| ||| ||||| |||||
Db 17 TTATTTTAGGAAAAAA 1

RESULT 718
AR329412
LOCUS AR329412 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6814 from patent US 6566127.
ACCESSION AR329412
VERSION AR329412.1 GI:33715220
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6814 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTTCG 4045
    || ||||| ||||| |||||
Db 1 TTCTGGACTCTCTCTGC 17

RESULT 719
AR344531
LOCUS AR344531 17 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 7 from patent US 6582913.
ACCESSION AR344531
VERSION AR344531.1 GI:33740600
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
TITLE Diagnostic method for KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6582913-A 7 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAGCT 1360
|||||
Db 1 CAGATCCTGAGGATGCT 17

RESULT 720
AR398375/c
LOCUS AR398375 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 756 from patent US 6617438.
ACCESSION AR398375
VERSION AR398375.1 GI:40136135
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Svedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 756 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCCGAAGG 3220
|||||
Db 17 GGCAGATGCCGAGAAGG 1

RESULT 721
AR402307/c
LOCUS AR402307 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 647 from patent US 6623962.
ACCESSION AR402307
VERSION AR402307.1 GI:40149757
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 647 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3058 GATGCTTAAGGATTT 3074
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Db 17 GATGGCTAAAGGAGATT 1

RESULT 722
AR456566
LOCUS AR456566 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 243 from patent US 6686188.
ACCESSION AR456566

AR456566.1 GI:42691623
Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 243 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 496 ATCTCTCGCGCCTGCTC 512
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Db 1 ATCTCTCGCGCCTCTCTC 17

RESULT 723
AR457388/c
LOCUS AR457388 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1065 from patent US 6686188.
ACCESSION AR457388
VERSION AR457388.1 GI:42692445
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 1065 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2713 CTACTTCCTAAGAGACA 2729
|||||
Db 17 CTACGTCCTTAGAGACA 1

RESULT 724
AR457389/c
LOCUS AR457389 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1066 from patent US 6686188.
ACCESSION AR457389
VERSION AR457389.1 GI:42692446
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 1066 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17


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/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2712 CCTACTTCCTTAAGAGAC 2728
Db 17 CCTACGTCCTTAGAGAC 1

RESULT 725
AR458545
LOCUS      AR458545
DEFINITION Sequence 2222 from patent US 6686188.
ACCESSION  AR458545
VERSION     AR458545.1 GI:42693602
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 2222 03-FEB-2004;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 675 GTGTGAAGCAGGGCC 691
Db 1 GTGTGGATGGCAGGGTC 17

RESULT 726
AR464880
LOCUS      AR464880
DEFINITION Sequence 8557 from patent US 6686188.
ACCESSION  AR464880
VERSION     AR464880.1 GI:42699937
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 8557 03-FEB-2004;
FEATURES    Location/Qualifiers
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            1..17
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2519 CGATGACGACCATGATG 2535
Db 1 CGATGAGGACCGAGGATG 17

RESULT 727
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AR465549
LOCUS      AR465549
DEFINITION Sequence 9226 from patent US 6686188.
ACCESSION  AR465549
VERSION     AR465549.1 GI:42700606
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 9226 03-FEB-2004;
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1462 CAAGCCGAGGGCAGCC 1478
Db 1 CCAGCCAGAGGGCAGCC 17

RESULT 728
AR466831/c
LOCUS      AR466831
DEFINITION Sequence 10508 from patent US 6686188.
ACCESSION  AR466831
VERSION     AR466831.1 GI:42701888
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 10508 03-FEB-2004;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2928 CTCCTCGTCCTTCCTC 2944
Db 17 CTCCTCGTCCTTCGGCTC 1

RESULT 729
AR466832/c
LOCUS      AR466832
DEFINITION Sequence 10509 from patent US 6686188.
ACCESSION  AR466832
VERSION     AR466832.1 GI:42701889
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
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predominantly in heart and muscle
Patent: US 6686188-A 10509 03-FEB-2004;
Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2927 CCTCCCGTCCTTCCT 2943
Db 17 CCTCCCGTCCTTCGCT 1

RESULT 730
AX009153/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AX009153
Sequence 186 from Patent WO9963975.
AX009153
AX009153.1 GI:9996527
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R.
A method for stimulating the immune system
Patent: WO 9963975-A 186 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1320 AAGAGGATCGAGGCCAT 1336
Db 17 AAGCGCATCGAGGCCAT 1

RESULT 731
AX214795
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AX214795
Sequence 237 from Patent WO0159103.
AX214795
AX214795.1 GI:15524838
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 237 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.3%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2582 AAAAAAATTGGAGAAA 2598
Db 1 AAAAAAATAGAGAAA 17

RESULT 732
AX215493
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AX215493
Sequence 935 from Patent WO0159103.
AX215493
AX215493.1 GI:15525536
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 935 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCGCCGCC 989
Db 1 CCCCCCTCCACCGCCGCC 17

RESULT 733
AX215509
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AX215509
Sequence 951 from Patent WO0159103.
AX215509
AX215509.1 GI:15525552
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Blatt, L., McSwiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 951 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1234 TGAGACCTTTTGTCTC 1250
Db 1 TGAGACCTTTTGTCTC 17

RESULT 734
AX215783
LOCUS AX215783 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1225 from Patent WO0159103.
ACCESSION AX215783
VERSION AX215783.1 GI:15525826
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1225 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 934 AAAAAACAAACCTTTC 950
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Db 1 AAAAAACAAAGCTTTC 17
RESULT 735
AX216730
LOCUS AX216730 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2172 from Patent WO0159103.
ACCESSION AX216730
VERSION AX216730.1 GI:15526791
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2172 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2580 AAAAAAAATTGGAGAA 2596
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Db 1 AAAAAAATAGAGAA 17
RESULT 736
AX217212/c
LOCUS AX217212 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2654 from Patent WO0159103.
ACCESSION AX217212
VERSION AX217212.1 GI:15527273

KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2654 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1182 TAAATAACAACATCAAC 1198
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Db 17 TAAATACCAACATCAAC 1
RESULT 737
AX217483/c
LOCUS AX217483 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2925 from Patent WO0159103.
ACCESSION AX217483
VERSION AX217483.1 GI:15527544
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2925 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 72 GAAAGAGAGAGCGCT 88
|||||
Db 17 GTAAGAGAGAGCGCT 1
RESULT 738
AX217485
LOCUS AX217485 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2927 from Patent WO0159103.
ACCESSION AX217485
VERSION AX217485.1 GI:15527546
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression
Patent: WO 0159103-A 2927 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2384 CATTCTCTTACATTG 2400
Db 1 CCTTCTCTTACATTG 17

RESULT 739
AX217486 AX217486 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 2928 from Patent WO0159103.
ACCESSION AX217486
VERSION AX217486.1 GI:15527547
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2928 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2386 TTCTCTTACATTGGA 2402
Db 1 TTCTCTTACATTGAA 17

RESULT 740
AX217558/c AX217558 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 3000 from Patent WO0159103.
ACCESSION AX217558
VERSION AX217558.1 GI:15527619
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 3000 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"

/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2798 ATGTGAAAAA 2814
Db 17 ATGTGATAAAAAA 1

RESULT 741
AX217577 AX217577 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 3019 from Patent WO0159103.
ACCESSION AX217577
VERSION AX217577.1 GI:15527638
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 3019 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
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1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4251 AGGCTGATTA 4267
Db 1 AGGATGATAAAAAA 17

RESULT 742
AX226925/c AX226925 17 bp RNA linear PAT 10-SEP-2001
LOCUS
DEFINITION Sequence 297 from Patent WO0157206.
ACCESSION AX226925
VERSION AX226925.1 GI:15556066
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme
JOURNAL Patent: WO 0157206-A 297 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAATTTGGA 2593


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FEATURES
  source
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2428 CCAATATGATTCGAAG 2444
Db 17 CCAATATGATTCGAAG 1

RESULT 748
AX265075/c
LOCUS AX265075 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 2466 from Patent WO0173002.
ACCESSION AX265075
VERSION AX265075.1 GI:16513874
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Kniec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
PATENT: WO 0173002-A 2466 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
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    Location/Qualifiers
    1..17
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 859 CACACTGAATCCATT 875
Db 17 CACACTGAATCCATTCT 1

RESULT 749
AX265076
LOCUS AX265076 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 2467 from Patent WO0173002.
ACCESSION AX265076
VERSION AX265076.1 GI:16513875
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Kniec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
PATENT: WO 0173002-A 2467 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
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    Location/Qualifiers
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      /mol_type="unassigned DNA"
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Query Match
  Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 859 CACACTGAATCCATT 875
Db 17 CACACTGAATCCATTCT 1

RESULT 750
AX273239
LOCUS AX273239 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 808 from Patent WO0162911.
ACCESSION AX273239
VERSION AX273239.1 GI:16545976
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
  Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 808 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
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      /mol_type="unassigned RNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2716 CTTCTTAAGACACAA 2732
Db 1 CTTCTTAAGACAGAA 17

RESULT 751
AX326509/c
LOCUS AX326509 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2647 from Patent WO0192512.
ACCESSION AX326509
VERSION AX326509.1 GI:18097273
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
  1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
PATENT: WO 0192512-A 2647 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
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      /mol_type="unassigned DNA"
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Query Match
  Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
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QY 501 CGCGCCCTGCTCCGCC 517
Db 17 CGCCTCTACTCCGCC 1

RESULT 752
AX326510

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LOCUS AX326510 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2648 from Patent WO0192512.
ACCESSION AX326510
VERSION AX326510.1 GI:18097274
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
PATENT: WO 0192512-A 2648 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
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/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 501 CGCGCGCTGCTCGGCG 517
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Db 1 CGCCTCTACTCGGCG 17
RESULT 753
AX361606/c
LOCUS AX361606 17 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 24 from Patent WO0208461.
ACCESSION AX361606
VERSION AX361606.1 GI:18694225
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
TITLE A method and an algorithm for mrna expression analysis
JOURNAL Patent: WO 0208461-A 24 31-JAN-2002;
Global Genomics AB (SE)
FEATURES
source Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Double-stranded product DNA"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 928 GAGAAAAAACAACA 944
||||| ||||| ||||| |||||
Db 17 GAAAAAANAANAANA 1
RESULT 754
AX422617/c
LOCUS AX422617 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 953 from Patent WO0188124.
ACCESSION AX422617
VERSION AX422617.1 GI:121525999
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 953 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3774 CCTCCCCAACCCCGT 3790
||||| ||||| ||||| |||||
Db 17 CCTTCCCCAGCCCCAGT 1
RESULT 755
AX423623/c
LOCUS AX423623 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1959 from Patent WO0188124.
ACCESSION AX423623
VERSION AX423623.1 GI:21527005
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1959 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3773 TCCTCCCCAACCCCG 3789
||||| ||||| ||||| |||||
Db 17 TCCTTCCCCAGCCCCAG 1
RESULT 756
AX423624/c
LOCUS AX423624 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1960 from Patent WO0188124.
ACCESSION AX423624
VERSION AX423624.1 GI:21527006
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1960 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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source Location/Qualifiers
1. .17
/organism="Homo sapiens"

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/mol_type="unassigned RNA"  
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3772 TTCTTCCCCCAACCCCA 3788
      |||||
Db 17 TTCTTCCCCAGCCCCA 1

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RESULT	757
AX530538	
LOCUS	AX530538 17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 47 from Patent EP1239051.
ACCESSION	AX530538
VERSION	AX530538.1 GI:25252453
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS      Shannon,M.
TITLE         Human posh-like protein 1
JOURNAL       Patent: EP 1239051-A 47 11-SEP-2002;
              Aesomica, Inc. (US)
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source        i. 17
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

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Query Match	0.3%	Score 13.8;	DB 1;	Length 17;
Best Local Similarity	88.2%;	Pred. No. 4.1e+00;		
Matches 15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	425	GGCAGCAGCGCGGCTG	441	
Db	1	GGCAGCAGCGCGGCTTG	17	

RESULT 758
AX530550/c
LOCUS AX530550
DEFINITION Sequence 59 from Patent EP1239051.
ACCESSION AX530550
VERSION AX530550.1 GI:25252477
SOURCE.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1. Shannon, M.
AUTHORS
Human posh-like protein 1
TITLE
Patent: EP 1239051-A 59 11-SEP-2002;
JOURNAL
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers
1. .17
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2933  CGTCCCTTCTCCAAGC 2949
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Db       17  CTTCCCTTCTCCAAGC 1

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RESULT 759	AX530607/c	AX530607	Sequence 116 from Patent EP1239051.	17 bp	DNA	linear	PAT 22-NOV-2002
LOCUS	AX530607						
DEFINITION	AX530607						
ACCESSION	AX530607						
VERSION	AX530607.1	GI:25253021					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						

REFERENCE
1 Shannon, M.
AUTHORS
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 116 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      826 GAGTTCAGATCAGCCAC 842
Db      17 GAGTTCAGCTCAGCCCC 1

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RESULT	760
AX530609/c	
LOCUS	AX530609
DEFINITION	Sequence 118 from Patent EP1239051.
ACCESSION	AX530609
VERSION	AX530609.1 GI:25253025
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	linear
	17 bp DNA
	PAT 22-NOV-2002

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REFERENCE
1 Shannon, M.
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 118 11-SEP-2002;
Leomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match	0.3%;	Score 13.8;	DB 1;	Length 17;
Best Local Similarity	88.2%;	Pred. No. 4.1e+02;		
Matches 15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	824	CGGAGTTCAGATCAGCC	840	
Db	17	CTGAGTTCAGCTCAGCC	1	

RESULT 761
AX532047
LOCUS
AX532047
DEFINITION
Sequence 1556 from Patent EP1239051.
ACCESSION
AX532047
VERSION
AX532047.1 GI:25255857
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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REFERENCE 1
AUTHORS Shannon,M.
TITLE Human poeh-like protein 1
JOURNAL Patent: Ep 1239051-A 1556 11-SEP-2002;
          Aeomica, Inc. (US)
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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
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QY 1920 AATAATTACATCATCCC 1936
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DB 1 AACAAATACGTCATCCC 17
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RESULT 762
AX544872/c
LOCUS AX544872 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 385 from Patent EP1243660.
ACCESSION AX544872
VERSION AX544872.1 GI:25810083
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang,J., Gu,Y. and Nguyen,C.T.
TITLE Human ude-galnac:polypeptide n-acetyl-galatosaminyltransferase 10
JOURNAL Patent: Ep 1243660-A 385 25-SEP-2002;
          Aeomica, Inc. (US)
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      /db_xref="taxon:9606"

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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3857 AGCCTTTTCGCTCAG 3873
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DB 17 AGCCTTTTCCTCTTCAG 1
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RESULT 763
AX579530
LOCUS AX579530 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1368 from Patent WO0211674.
ACCESSION AX579530
VERSION AX579530.1 GI:27648732
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
          and Grube,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
          channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1368 14-FEB-2002;
          RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
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FEATURES
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Qy 2929 TCCCGGTCCTTCCTCC 2945
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RESULT 766
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LOCUS
DEFINITION Sequence 397 from Patent EP1273660.
ACCESSION AX648557
VERSION AX648557.1 GI:29151375
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 397 08-JAN-2003;
Acomica, Inc. (US)
FEATURES
source
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1154 TCTTTTATATATATT 1170
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Db 17 TCTTTGATTTATATT 1

RESULT 767
AX671693/c
LOCUS
DEFINITION Sequence 138 from Patent WO03004526.
ACCESSION AX671693
VERSION AX671693.1 GI:29330041
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 138 16-JAN-2003;
Molecular Engines Laboratories (FR)
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 17 TCTTTGATTTATATT 1

RESULT 767
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ACCESSION AX671693
VERSION AX671693.1 GI:29330041
KEYWORDS
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 138 16-JAN-2003;
Molecular Engines Laboratories (FR)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3361 TGAAGTGGCTGTGATC 3377
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Db 17 TGGAGTGGCGTTGATC 1

RESULT 768
AX672167
LOCUS
DEFINITION Sequence 612 from Patent WO03004526.
ACCESSION AX672167
VERSION AX672167.1 GI:29331181
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ACCESSION AX672167
VERSION AX672167.1 GI:29330515
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 612 16-JAN-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1305 GATCAGTTTATCGCAA 1321
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Db 1 GATCAGTGATCGAAA 17

RESULT 769
AX672731/c
LOCUS
DEFINITION Sequence 1176 from Patent WO03004526.
ACCESSION AX672731
VERSION AX672731.1 GI:29331079
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1176 16-JAN-2003;
Molecular Engines Laboratories (FR)
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1241 CTTTGTGCTCTGCATC 1257
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Db 17 CTTTGTCTCTGGATC 1

RESULT 770
AX672833/c
LOCUS
DEFINITION Sequence 1278 from Patent WO03004526.
ACCESSION AX672833
VERSION AX672833.1 GI:29331181
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE	1	Teleman,A., Anson,R. and Tuijnder,M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines Patent: WO 03004526-A 1278 16-JAN-2003; Molecular Engines Laboratories (FR) Location/Qualifiers	1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match Best Local Similarity Matches	0.3%; 88.2%; 15; Conservative	Score 13.8; Pred. No. 4.1e+02; 0; Mismatches	DB 1; Length 17; Indels	0; Gaps	0;
JOURNAL									
FEATURES									
source									
LOCUS	AX674271/c	AX674271	17 bp	DNA	linear	PAT 27-MAR-2003			
DEFINITION		Sequence 2716 from Patent WO03004526.							
ACCESSION	AX674271								
VERSION	AX674271.1	GI:29332619							
KEYWORDS									
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							
REFERENCE									
AUTHORS		Teleman,A., Anson,R. and Tuijnder,M.							
TITLE		Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines							
JOURNAL		Patent: WO 03004526-A 2716 16-JAN-2003; Molecular Engines Laboratories (FR) Location/Qualifiers							
FEATURES									
source									
LOCUS	AX674271/c	AX674271	17 bp	DNA	linear	PAT 27-MAR-2003			
DEFINITION		Sequence 2716 from Patent WO03004526.							
ACCESSION	AX674271								
VERSION	AX674271.1	GI:29332619							
KEYWORDS									
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							
REFERENCE									
AUTHORS		Teleman,A., Anson,R. and Tuijnder,M.							
TITLE		Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines							
JOURNAL		Patent: WO 03004526-A 2716 16-JAN-2003; Molecular Engines Laboratories (FR) Location/Qualifiers							
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source									
LOCUS	AX674271/c	AX674271	17 bp	DNA	linear	PAT 27-MAR-2003			
DEFINITION		Sequence 2716 from Patent WO03004526.							
ACCESSION	AX674271								
VERSION	AX674271.1	GI:29332619							
KEYWORDS									
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ORGANISM		Homo sapiens							
REFERENCE									
AUTHORS		Teleman,A., Anson,R. and Tuijnder,M.							
TITLE		Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines							
JOURNAL		Patent: WO 03004526-A 2716 16-JAN-2003; Molecular Engines Laboratories (FR) Location/Qualifiers							
FEATURES									
source									
LOCUS	AX674271/c	AX674271	17 bp	DNA	linear	PAT 27-MAR-2003			
DEFINITION		Sequence 2716 from Patent WO03004526.							
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VERSION	AX674271.1	GI:29332619							
KEYWORDS									
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							
REFERENCE									
AUTHORS		Teleman,A., Anson,R. and Tuijnder,M.							
TITLE		Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines							
JOURNAL		Patent: WO 03004526-A 2716 16-JAN-2003; Molecular Engines Laboratories (FR) Location/Qualifiers							
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source									
LOCUS	AX674271/c	AX674271	17 bp	DNA	linear	PAT 27-MAR-2003			
DEFINITION		Sequence 2716 from Patent WO03004526.							
ACCESSION	AX674271								
VERSION	AX674271.1	GI:29332619							
KEYWORDS									
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							
REFERENCE									
AUTHORS		Teleman,A., Anson,R. and Tuijnder,M.</							

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Qy 2572 GTTTAAAAA 2588
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17 GTCTCAAAAAA 1

RESULT 775
AX692531/c
LOCUS AX692531 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5263 from Patent EP1281758.
ACCESSION AX692531
VERSION AX692531.1 GI:29415489
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 5263 05-FEB-2003;
Asomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2571 TGTTTAAAAA 2587
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17 TGTCAAAAA 1

RESULT 776
AX722447
LOCUS AX722447 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 134 from Patent WO03025176.
ACCESSION AX722447
VERSION AX722447.1 GI:30422948
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 134 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2373 GRACCACTGACCATCT 2389
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1 GATCCAGTGACCATCT 17

RESULT 777
AX723926/c
LOCUS AX723926 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 539 from Patent WO03025176.
ACCESSION AX723926
VERSION AX723926.1 GI:30506995
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DEFINITION Sequence 1613 from Patent WO03025176.
ACCESSION AX723926
VERSION AX723926.1 GI:30503269
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1613 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 374 GCAAGAAAAAGGAGGATC 390
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17 GAAGAAATGGAGGATC 1

Db 17 GAAGAAATGGAGGATC 1

RESULT 778
AX725994
LOCUS AX725994 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3681 from Patent WO03025176.
ACCESSION AX725994
VERSION AX725994.1 GI:30505337
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 3681 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
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Qy 2004 GATCAGAAACTATAAA 2020
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1 GATCATAAAAATATAAA 17

Db 1 GATCATAAAAATATAAA 17

RESULT 779
AX727652
LOCUS AX727652 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5339 from Patent WO03025176.
ACCESSION AX727652
VERSION AX727652.1 GI:30506995
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Best Local Similarity	88.2%;	Pred. No. 4.1e+02;
Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	3230	AAAGAAACTTGAATC 3246
Db	17	AAAGAAACTTGGATC 1
RESULT 782		
AX730368	linear PAT 08-MAY-2003	
LOCUS	AX730368	17 bp DNA
DEFINITION	Sequence 2002 from Patent WO03025175.	
ACCESSION	AX730368	
VERSION	AX730368.1	GI:30509711
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Teleman,A., Anson,R. and Tuijnder,M.	
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as	
JOURNAL	Patent: WO 03025175-A 2002 27-MAR-2003;	
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Best Local Similarity	88.2%;	Pred. No. 4.1e+02;
Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	34	GAGCTGCTGAAACTGCC 50
Db	1	GATCTGCTGAAACTGCC 17
RESULT 783		
AX730497	linear PAT 08-MAY-2003	
LOCUS	AX730497	17 bp DNA
DEFINITION	Sequence 2131 from Patent WO03025175.	
ACCESSION	AX730497	
VERSION	AX730497.1	GI:30509840
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Teleman,A., Anson,R. and Tuijnder,M.	
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as	
JOURNAL	Patent: WO 03025175-A 2131 27-MAR-2003;	
	Molecular Engines Laboratories (FR)	
FEATURES	Location/Qualifiers	
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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3611 GATCATTTCAGATTGTAT 3627
Db 1 GATCATTCAAATTGAAT 17

RESULT 784
AX730996/c
LOCUS AX730996 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2630 from Patent WO03025175.
ACCESSION AX730996
VERSION AX730996.1 GI:30510339
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 2630 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3230 AAAGAAACTTGGATC 3246
Db 17 AAAGAAACTTGTGATC 1

RESULT 785
AX731845/c
LOCUS AX731845 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3479 from Patent WO03025175.
ACCESSION AX731845
VERSION AX731845.1 GI:30511188
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3479 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTNTTTTAAATGATC 3614
Db 17 TATTTTTTTTATGATC 1

RESULT 786
AX732633/c
LOCUS AX732633 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4267 from Patent WO03025175.
ACCESSION AX732633
VERSION AX732633.1 GI:30511976
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4267 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3262 GATTTTTTTTCCTTTT 3278
Db 1 GATCTTTTTCCTTTT 17

RESULT 788
AX733744
LOCUS AX733744 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5378 from Patent WO03025175.
ACCESSION AX733744
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VERSION
KEYWORDS
SOURCE      AX733744.1 GI:30513087
ORGANISM    Homo sapiens (human)

REFERENCE
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025175-A 5378 27-MAR-2003;
            Molecular Engines Laboratories (FR)

JOURNAL
FEATURES    source
            1. .17
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      34  GAGCTGCTGAAACTGCC 50
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Db

RESULT 789
AX734489/c
LOCUS      AX734489          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 79 from Patent WO03025177.
ACCESSION  AX734489
VERSION     AX734489.1 GI:30513766
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025177-A 79 27-MAR-2003;
            Molecular Engines Laboratories (FR)

JOURNAL
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3598 TTTTCTTTTAAATGATC 3614
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          17 TTTATTTTTCATGATC 1

Db

RESULT 790
AX734527/c
LOCUS      AX734527          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 117 from Patent WO03025177.
ACCESSION  AX734527
VERSION     AX734527.1 GI:30513804
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025177-A 1460 27-MAR-2003;
            Molecular Engines Laboratories (FR)

JOURNAL
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3598 TTTTCTTTTAAATGATC 3614
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          17 TTTATTTTTCATGATC 1

Db

RESULT 792
AX735870/c
LOCUS      AX735870          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 1460 from Patent WO03025177.
ACCESSION  AX735870
VERSION     AX735870.1 GI:30515147
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025177-A 1460 27-MAR-2003;
            Molecular Engines Laboratories (FR)

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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2206 TTGGATGGAATGGATC 2222
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          17 TTGTGATCAATGGATC 1

Db

RESULT 792
AX735870/c
LOCUS      AX735870          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 1460 from Patent WO03025177.
ACCESSION  AX735870
VERSION     AX735870.1 GI:30515147
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025177-A 1460 27-MAR-2003;
            Molecular Engines Laboratories (FR)

JOURNAL
FEATURES    source
            1. .17
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2206 TTGGATGGAATGGATC 2222
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          17 TTGTGATCAATGGATC 1

Db
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RESULT 797
AX738113/c
LOCUS AX738113 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3703 from Patent WO03025177.
ACCESSION AX738113
VERSION AX738113.1 GI:30517401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Anson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 3703 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3598 TTTTGTGTTGAATGATC 3614
Db 17 TTTTGTGTTGAATGATC 1
RESULT 798
AX738194
LOCUS AX738194 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3784 from Patent WO03025177.
ACCESSION AX738194
VERSION AX738194.1 GI:30517482
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Anson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 3784 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2202 GATCTTGGATGGAATG 2218
Db 1 GATCTTGGATGGAATG 17
RESULT 799
AX738406/c
LOCUS AX738406 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3996 from Patent WO03025177.
ACCESSION AX738406
VERSION AX738406.1 GI:30517694
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Anson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 3996 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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1. .17
/organism="Homo sapiens"
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2354 CTGTGTGCCAGGATC 2370
Db 17 CTATGTGCCAGGATC 1
RESULT 800
AX739252
LOCUS AX739252 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4842 from Patent WO03025177.
ACCESSION AX739252
VERSION AX739252.1 GI:30518549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Anson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 4842 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/organism="Homo sapiens"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 821 GATCGAGTTCAGATCA 837
Db 1 GATCGAGTTCAGAAC 17
RESULT 801
AX739583/c
LOCUS AX739583 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5173 from Patent WO03025177.
ACCESSION AX739583
VERSION AX739583.1 GI:30518880
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Anson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour

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reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
Patent: WO 03025177-A 5173 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTTCTTTTCTGATC 1

RESULT 802
AX739654 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION Sequence 5244 from Patent WO03025177.
ACCESSION AX739654
VERSION AX739654.1 GI:30518951
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Zhang, J.
AUTHORS A human G protein coupled receptor
TITLE Patent: WO 03031621-A 1395 17-APR-2003;
JOURNAL Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1151 GTTCTCTTTTATATAT 1167
Db 17 GTTCTTTTATATCTAT 1

RESULT 805
AX757514 17 bp DNA linear PAT 25-JUN-2003
LOCUS
DEFINITION Sequence 835 from Patent WO03040369.
ACCESSION AX757514
VERSION AX757514.1 GI:32252130
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman, A., Anson, R. and Tuijinder, M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 835 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTTCTTTTCTGATC 1

RESULT 803
AX739654 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION Sequence 5244 from Patent WO03025177.
ACCESSION AX739654
VERSION AX739654.1 GI:30518951
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman, A., Anson, R. and Tuijinder, M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5244 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Db 17 TTTATTTTATTGATC 1

RESULT 806
AX758804/c

LOCUS AX758804 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2125 from Patent WO03040369.
ACCESSION AX758804
VERSION AX758804.1 GI:32253420
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 2125 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3361 TGAAGTGGCTGTTGATC 3377
Db 17 TGGAGTGGCGTTGATC 1

RESULT 807
AX761941

LOCUS AX761941 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5262 from Patent WO03040369.
ACCESSION AX761941
VERSION AX761941.1 GI:32256557
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 5262 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/mol_type="unassigned DNA"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2414 GATCCACAGCTTCCA 2430
Db 1 GATCCACAGCTTCCA 17

RESULT 808
AX762729/c

LOCUS AX762729 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 6050 from Patent WO03040369.

ACCESSION AX762729
VERSION AX762729.1 GI:32257345
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 6050 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3598 TTTTNTTTTATGATC 3614
Db 17 TTTTNTTTTCTTGATC 1

RESULT 809
AX762737/c

LOCUS AX762737 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 6058 from Patent WO03040369.
ACCESSION AX762737
VERSION AX762737.1 GI:32257353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 6058 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1..17
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 374 GCAAGAAAAGGAGGATC 390
Db 17 GTNAGAAAAGGTGGATC 1

RESULT 810
AX781715

LOCUS AX781715 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 46 from Patent WO03050284.
ACCESSION AX781715
VERSION AX781715.1 GI:32949549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 46 17-JUL-2003;
Molecular Engines Laboratories (FR)
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REFERENCE AUTHORS TITLE JOURNAL FEATURES source	1	Guo,J. Human prostate cancer candidate protein 1 Patent: WO 03050284-A 46 19-JUN-2003; Amersham Biosciences (SV) Corp. (US) Location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	0.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	QY	628 CACGGCGCACACGGCG 644 1 CCGCGCGCACACGGCAC 17	
	Db		
	RESULT 811		
	AX781744		
	LOCUS	AX781744 17 bp DNA linear PAT 17-JUL-2003	
	DEFINITION	Sequence 75 from Patent WO03050284.	
	ACCESSION	AX781744	
	VERSION	AX781744.1 GI:32949578	
	KEYWORDS		
REFERENCE AUTHORS TITLE JOURNAL FEATURES source	1	Guo,J. Human prostate cancer candidate protein 1 Patent: WO 03050284-A 75 19-JUN-2003; Amersham Biosciences (SV) Corp. (US) Location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	0.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	QY	631 GCGCGCACACGGCGACA 647 1 GCGAGCAGACGGCGACA 17	
	Db		
	RESULT 812		
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	LOCUS	AX781745 17 bp DNA linear PAT 17-JUL-2003	
	DEFINITION	Sequence 76 from Patent WO03050284.	
	ACCESSION	AX781745	
	VERSION	AX781745.1 GI:32949579	
	KEYWORDS		
REFERENCE AUTHORS TITLE JOURNAL FEATURES source	1	Guo,J. Human prostate cancer candidate protein 1 Patent: WO 03050284-A 76 19-JUN-2003; Amersham Biosciences (SV) Corp. (US) Location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	0.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	QY	632 CGCGCACACGGCGACAC 648 1 CGAGCAGACGGCGACAC 17	
	Db		
	RESULT 813		
	AX814938/c		
	LOCUS	AX814938 17 bp DNA linear PAT 05-DEC-2003	
	DEFINITION	Sequence 24 from Patent WO03064691.	
	ACCESSION	AX814938	
	VERSION	AX814938.1 GI:39104076	
	KEYWORDS		
REFERENCE AUTHORS TITLE JOURNAL FEATURES source	1	Guo,J. Human prostate cancer candidate protein 1 Patent: WO 03050284-A 75 19-JUN-2003; Amersham Biosciences (SV) Corp. (US) Location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	0.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	QY	928 GAGAAAAAACAACAAA 944 17 GAAAAAACAACAAA 1	
	Db		
	RESULT 814		
	BD011731/c		
	LOCUS	BD011731 17 bp DNA linear PAT 02-AUG-2002	
	DEFINITION	795. a novel gene related to pollen allergy.	
	ACCESSION	BD011731	
	VERSION	BD011731.1 GI:22091920	
	KEYWORDS	WO 0065050-A/3. synthetic construct synthetic construct other sequences; artificial sequences.	
REFERENCE AUTHORS TITLE JOURNAL COMMENT	1	Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A. 795. a novel gene related to pollen allergy Patent: WO 0065050-A 3 02-NOV-2000; GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI OS Artificial Sequence PN WO 0065050-A/3 PD 02-NOV-2000 PF 26-APR-2000 WO 2000JP002734 PR 27-APR-1999 JP 99P 120494 PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA, PI MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,YUKIHO IMAI, PI NEI YOSHIDA, PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC A61P37/00	

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Primer Sequence
FH Key Location/Qualifiers
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Db 17 GAAAAAACAACAC 1

RESULT 815
BD065825 17 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065825
VERSION BD065825.1 GI:22611428
KEYWORDS JP 2001511000-A/460.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 460 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/460
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSTIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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Qy 2570 GTGTTTAAAAA 2586
Db 1 GTCTTTAAAAAACA 17

RESULT 816
BD067807/c 17 bp RNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067807
VERSION BD067807.1 GI:22613410
KEYWORDS JP 2001511003-A/647.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Meswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
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to levels of epidermal growth factor receptors
Patent: JP 2001511003-A 647 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
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PN JP 2001511003-A/647
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PT
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
Topology: linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
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FH Key Location/Qualifiers
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source 1..17
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3058 GATGGCTTAAGGAGTTT 3074
Db 17 GATGGCTAAAGGAGATT 1

RESULT 817
BD089823 17 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION A method of arraying genome clone.
ACCESSION BD089823
VERSION BD089823.1 GI:22635433
KEYWORDS JP 2001321190-A/2067.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 2067 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
COMMENT OS Artificial Sequence
PN JP 2001321190-A/2067
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09.C12N15/09.C12M1/00.C12Q1/68.G01N33/53.G01N33/566, PC
C12N15/00
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1 CACACATGCACATGCAC 17

RESULT 818
BD091743/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD091743 17 bp DNA linear PAT 27-AUG-2002
441, a novel gene related to pollen allergy.
BD091743
BD091743.1 GI:22637354
WO 0073435-A/3.
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
441, a novel gene related to pollen allergy
Patent: WO 0073435-A 3 07-DEC-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
OS Artificial Sequence
PN WO 0073435-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI
PC Cl2N15/10,Cl2Q1/68,G01N33/15,G01N33/50
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RESULT 820
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD091774 17 bp DNA linear PAT 27-AUG-2002
787, a novel gene related to pollen allergy.
BD091774
BD091774.1 GI:22637385
WO 0073440-A/3.
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
787, a novel gene related to pollen allergy
Patent: WO 0073440-A 3 07-DEC-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
OS Artificial Sequence
PN WO 0073440-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
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QY 930 GAAAAAACAACCAACC 946
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DB 17 GAAAAAACAACCAACC 1

RESULT 821
BD097335/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD097335 17 bp DNA linear PAT 27-AUG-2002
465, a novel gene related to pollen allergy.
BD097335
BD097335.1 GI:22637362
WO 0073439-A/3.
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
465, a novel gene related to pollen allergy
Patent: WO 0073439-A 3 07-DEC-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
OS Artificial Sequence
PN WO 0073439-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191

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LOCUS BD097335 17 bp DNA linear PAT 27-AUG-2002
 DEFINITION Method for examination for allergosis.
 ACCESSION BD097335
 VERSION WO 0169259-A/6.
 KEYWORDS synthetic construct
 SOURCE other sequences; artificial sequences.
 ORGANISM 1 (bases 1 to 17)
 REFERENCE Nagasu T., Oshida T., Obayashi I., Matsui K. and Sait H.
 AUTHORS Method for examination for allergosis
 TITLE Patent: WO 016259-A 6 07-SEP-2001;
 JOURNAL GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
 NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
 FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
 OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
 COMMENT OS Artificial Sequence
 PN WO 016259-A/6
 PD 07-SEP-2001
 PF 23-FEB-2001 WO 2001JP001372
 PR 02-MAR-2000 JP 00P 61832
 PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
 HIROHISA SAITO
 PC GOIN33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,
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 Db 17 GAAAAAAAAAAAAAAC 1
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 BD104864
 LOCUS BD104864 17 bp DNA linear PAT 27-AUG-2002
 DEFINITION Kit and method for determining HLA type.
 ACCESSION BD104864
 VERSION BD104864.1 GI:22650438
 KEYWORDS WO 0192572-A/968.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Inoko H., Kagiya T., Ichihara T., Matsumura Y., Moriya S. and
 Nishida M.
 TITLE Kit and method for determining HLA type
 JOURNAL Patent: WO 0192572-A 968 06-DEC-2001;
 NISHINO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDETOSHI INOKO, TAEKO
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
 NISHIDA
 COMMENT OS Artificial Sequence
 PN WO 0192572-A/968
 PD 06-DEC-2001
 PF 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP 00P 164798
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
 MATSUMURA,
 PI SHOGO MORIYA, MICHIO NISHIDA
 CC C12Q1/68, C12N15/00, C12N15/09, G01N33/53
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 QY 547 CACCGAGTCTCCGAGTG 563
 Db 1 CACAGAGTCACCGAGTG 17
 RESULT 823
 AB068038
 LOCUS AB068038 17 bp DNA linear SYN 21-MAY-2003
 DEFINITION Synthetic construct DNA, forward primer for human STS sts-D1S2660
 at 1p36.
 ACCESSION AB068038
 VERSION AB068038.1 GI:15128842
 KEYWORDS synthetic construct
 SOURCE other sequences; artificial sequences.
 ORGANISM
 REFERENCE 1
 AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
 Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
 Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
 and Soeda, E.
 TITLE A BAC-based STS-content map spanning a 35-Mb region of human
 chromosome 1p35-p36
 JOURNAL Genomics 74 (1), 55-70 (2001)
 MEDLINE 21269192
 PUBMED 11374902
 REFERENCE 2 (bases 1 to 17)
 AUTHORS Horii, A.
 TITLE Direct Submission
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
 Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
 Tel: 81-22-717-8042, Fax: 81-22-717-8047)
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 B126H16, B126H15, B126E9, B113J1, B6J17, B6K19, Human BAC
 library RPCI-11"
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 QY 644 CACATCCACACGCAC 660
 Db 1 CACACATGCACATGCAC 17
 RESULT 824
 E32456
 LOCUS E32456 18 bp DNA linear PAT 18-JUN-2001
 DEFINITION Mammal-derived tissue specific physiologically active protein.
 ACCESSION E32456
 VERSION E32456.1 GI:13018692
 KEYWORDS JP 2000037190-A/16.

SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 16 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/16
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
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Location/Qualifiers
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Db 2 TTTTTCCTCTTTTAA 18
RESULT 825
AX048440
LOCUS AX048440 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 39 from Patent WO0071747.
ACCESSION AX048440
VERSION AX048440.1 GI:12225604
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 39 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
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Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2743 TCTTTTTCCTTTTAAAGG 2759
Db 1 TTTTTCCTTTTAAAG 17
RESULT 826
AX048441
LOCUS AX048441 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 39 from Patent WO0071747.
ACCESSION AX048441
VERSION AX048441.1 GI:12225604
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 39 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
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Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2743 TCTTTTTCCTTTTAAAGG 2759
Db 1 TTTTTCCTTTTAAAG 17
RESULT 827
AX048442
LOCUS AX048442 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 41 from Patent WO0071747.
ACCESSION AX048442
VERSION AX048442.1 GI:12225606
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 41 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
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Best Local Similarity 88.2%; Pred. No. 5.6e+02;
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QY 2743 TCTTTTTCCTTTTAAAGG 2759
Db 1 TTTTTCCTTTTAAAG 17
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AX048443
LOCUS AX048443 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 42 from Patent WO0071747.
ACCESSION AX048443
VERSION AX048443.1 GI:12225607
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

DEFINITION Sequence 40 from Patent WO0071747.
ACCESSION AX048441
VERSION AX048441.1 GI:12225605
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 40 30-NOV-2000;
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Sequenz:Erkennungssystem"
Query Match 0.3%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 TTTTTCCTTTTAAAG 17
RESULT 827
AX048442
LOCUS AX048442 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 41 from Patent WO0071747.
ACCESSION AX048442
VERSION AX048442.1 GI:12225606
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 41 30-NOV-2000;
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Query Match 0.3%; Score 13.8; DB 1; Length 20;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 TTTTTCCTTTTAAAG 17
RESULT 828
AX048443
LOCUS AX048443 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 42 from Patent WO0071747.
ACCESSION AX048443
VERSION AX048443.1 GI:12225607
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.


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REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
        production and use of the same
JOURNAL Patent: WO 0071747-A 42 30-NOV-2000;
        Aventis Research & Technologies GmbH & Co. KG (DE)
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Sequenz:Erkennungssystem"

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Db 1 TTTTCTTTTAAAG 17

RESULT 829
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LOCUS AR409916 33 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 29 from patent US 6635422.
ACCESSION AR409916
VERSION AR409916.1 GI:40161051
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein
        (mRNP) complexes
JOURNAL Patent: US 6635422-A 29 21-OCT-2003;
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DEFINITION Sequence 17 from patent US 6306624.
ACCESSION AR174027
VERSION AR174027.1 GI:17914347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 17 23-OCT-2001;
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REFERENCE 1
AUTHORS Matsunaga,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 5 28-AUG-2001;
        UNIVERSITY OF WASHINGTON
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RESULT 832
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LOCUS AR084519 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 8 from patent US 5981185.
ACCESSION AR084519
VERSION AR084519.1 GI:10011290
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 8 09-NOV-1999;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 09:48:14 ; Search time 24 Seconds
(without alignments)
3.698 Million cell updates/sec

Title: US-10-633-163-47

Perfect score: 4267

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

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Listing first 579 summaries

Database : fetchrng47.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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265	16.8	0.4	20	1	ADP86263	Rat TGF-beta 2 PCR	c 338	16	0.4	18	1	AAQ38707	First chimeric pri
266	16.8	0.4	20	1	ABZ86060	Human oligonucleot	c 339	16	0.4	18	1	AAZ96107	First chimeric pri
267	16.8	0.4	20	1	ABZ89592	Human oligonucleot	c 340	16	0.4	18	1	AAZ88678	Chimeric primer #1
268	16.8	0.4	20	1	ABD22290	Human stanniocalci	c 341	16	0.4	18	1	ADL95318	Anti-proliferative
269	16.8	0.4	20	1	ABD25822	AI085559-derived o	342	16	0.4	19	1	AAZ11781	Oligonucleotide pr
270	16.8	0.4	20	1	ADH67307	Human glucocortic	343	16	0.4	19	1	ADF31846	Human IGF-1R siNA
271	16.8	0.4	20	1	ADI80180	Human transforming	c 344	16	0.4	19	1	ADF31569	Human IGF-1R trans
272	16.8	0.4	20	1	ADI80070	Human transforming	345	16	0.4	19	1	ABD24924	AI095492-derived o
273	16.8	0.4	20	1	ADI80187	Human transforming	c 346	16	0.4	20	1	AAQ75580	Reverse transcript
274	16.8	0.4	20	1	ADI80040	Human transforming	347	16	0.4	20	1	AAQ63692	Rat P2X 7/P2Z PCR
275	16.8	0.4	20	1	ADI80185	Human transforming	c 348	16	0.4	20	1	AAQ82917	Human S-9 derived
276	16.8	0.4	20	1	ADI80006	Human transforming	c 349	16	0.4	20	1	AAQ82918	Human S-9 derived
277	16.8	0.4	20	1	ADI80034	Human transforming	c 350	16	0.4	20	1	AAQ82919	Human S-9 derived
278	16.8	0.4	20	1	ADI80022	Human transforming	c 351	16	0.4	20	1	AAQ82920	Human S-9 derived
279	16.8	0.4	20	1	ADI80043	Human transforming	352	16	0.4	20	1	ADA09834	Antisense nested P
280	16.8	0.4	20	1	ADI80173	Human transforming	353	16	0.4	20	1	ABZ91658	Human oligonucleot
281	16.8	0.4	20	1	ADI80045	Human transforming	c 354	16	0.4	20	1	ABZ98155	Human CD23 + AI261
282	16.8	0.4	20	1	ADK79195	Chimeric phosphoro	355	16	0.4	20	1	ABZ89703	Human oligonucleot
283	16.8	0.4	20	1	ADOS3074	Farnesoid X recept	356	16	0.4	20	1	ABZ88813	Human oligonucleot
284	16.8	0.4	21	1	AAQ73754	Rice starch branch	357	16	0.4	20	1	ABZ88694	Human oligonucleot
285	16.8	0.4	21	1	AAQ73754	Reverse transcript	358	16	0.4	20	1	ABD25043	AI128305-derived o
286	16.6	0.4	24	1	ADD29304	Molecular and biol	c 359	16	0.4	20	1	ABD31186	Human CD23-derived
287	16.4	0.4	18	1	AAQ78427	TGF-beta gene phos	360	16	0.4	20	1	ABD27888	AA258395-derived o
288	16.4	0.4	18	1	AAQ78484	TGF-beta gene phos	c 361	16	0.4	20	1	ADJ60020	Oligonucleotide as
289	16.4	0.4	18	1	AAZ65442	Immunosuppressant	c 362	16	0.4	20	1	ADL58072	Human ESM-1 antise
290	16.4	0.4	18	1	AAZ65510	Immunosuppressant	c 363	16	0.4	20	1	ADL58071	Human ESM-1 antise
291	16.4	0.4	18	1	AAZ65466	Immunosuppressant	c 364	16	0.4	20	1	ADO45510	Human oligonucleot
292	16.4	0.4	18	1	ABA97624	Probe c. Unidenti	c 365	16	0.4	24	1	AAZ59725	DNA target used fo
293	16.4	0.4	18	1	ABL95897	Probe c. for assay	c 366	16	0.4	24	1	ADH34300	Hairpin oligonucle
294	16.4	0.4	19	1	AAAB5942	Cdc 25 hs ribozyme	c 367	16	0.4	25	1	ADH28312	3' untranslated re
295	16.4	0.4	19	1	AAAB5941	Cdc 25 hs ribozyme	c 368	15.8	0.4	19	1	AAV48959	TGF-beta2 antisens
296	16.4	0.4	19	1	AAH61103	Cdc25 hs ribozyme	c 369	15.8	0.4	19	1	AAV48939	TGF-beta2 antisens
297	16.4	0.4	19	1	AAH61104	Cdc25 hs ribozyme	c 370	15.8	0.4	19	1	AAZ65447	Immunosuppressant
298	16.4	0.4	19	1	ADQ60911	Anti-BMX siRNA rel	c 371	15.8	0.4	19	1	AAZ86481	PCBA HH ribozyme b
299	16.4	0.4	19	1	ADQ90660	Oligonucleotide of	372	15.8	0.4	19	1	AAF99013	Immunostimulatory
300	16.4	0.4	20	1	AAZ32003	MSH2 gene specific	c 373	15.8	0.4	19	1	AAF99013	Immunostimulatory
301	16.4	0.4	20	1	AAZ93327	PCR primer used to	c 374	15.8	0.4	19	1	AAZ83562	DNA synthesis meth
302	16.4	0.4	20	1	ABN89197	Human Talin antise	c 375	15.8	0.4	19	1	AAH61643	PCNA HH ribozyme b
303	16.4	0.4	20	1	ADG90460	Human talin phosph	c 376	15.8	0.4	19	1	ABZ77654	Angiogenesis inhib
304	16.4	0.4	20	1	ADA45244	Human MSH2 gene PC	c 377	15.8	0.4	19	1	ABZ77654	Angiogenesis inhib
305	16.4	0.4	20	1	ABZ86070	Human oligonucleot	c 378	15.8	0.4	19	1	ABL38943	Immunostimulatory
306	16.4	0.4	20	1	ABZ89593	Human oligonucleot	c 379	15.8	0.4	19	1	ABL38943	Immunostimulatory
307	16.4	0.4	20	1	ABZ89178	Human oligonucleot	380	15.8	0.4	19	1	ACD99445	Immunostimulatory
308	16.4	0.4	20	1	ABZ97995	Human RANTES oligo	c 381	15.8	0.4	19	1	ACD99445	Immunostimulatory
309	16.4	0.4	20	1	ABD25408	AI122807-derived o	382	15.8	0.4	19	1	ADB36515	Immunostimulatory
310	16.4	0.4	20	1	ABD31026	Human RANTES-deriv	c 383	15.8	0.4	19	1	ADB36515	Immunostimulatory
311	16.4	0.4	20	1	ABD22300	Human stanniocalci	384	15.8	0.4	19	1	ADB42503	Human infertility
312	16.4	0.4	20	1	AI085559	AI085559-derived o	385	15.8	0.4	19	1	ADF50074	Human BCL2 siNA lo
313	16.4	0.4	20	1	ADI80176	Human transforming	386	15.8	0.4	19	1	ADF49399	Human BCL2 siNA up
314	16.4	0.4	20	1	ADI80026	Human transforming	c 387	15.8	0.4	19	1	ADP49660	Human BCL2 siNA up
315	16.4	0.4	20	1	ADJ59860	Oligonucleotide as	c 388	15.8	0.4	19	1	ADP49813	Human TGF-1R siNA
316	16.4	0.4	20	1	ADK81339	Chimeric phosphoro	c 389	15.8	0.4	19	1	ADF31627	Human TGF-1R trans
317	16.4	0.4	20	1	ADL58169	Chimeric phosphoro	390	15.8	0.4	19	1	ADF31350	TGF beta 2 3'-UTR
318	16.4	0.4	20	1	ADL58169	Human ESM-1 antise	c 391	15.6	0.4	22	1	ADQ14537	TGF beta 2 3'-UTR
319	16.4	0.4	20	1	ADI58390	Human ESM-1 antise	392	15.4	0.4	17	1	AAZ63947	Rabbit stromelysin
320	16.4	0.4	20	1	ADO45350	Human oligonucleot	393	15.4	0.4	17	1	AAZ63948	Rabbit stromelysin
321	16.4	0.4	20	1	ADP85665	Human Talin antise	394	15.4	0.4	17	1	AAV93710	Human B-rat subatr
322	16.4	0.4	20	1	ADP69475	Human mitONEET-spe	c 395	15.4	0.4	17	1	ABZ59897	Immunosuppressant
323	16.4	0.4	20	1	ADP69581	Human mitONEET-spe	396	15.4	0.4	17	1	ABZ59897	Human K-Ras DNazym
324	16.4	0.4	20	1	ADP69398	Human mitONEET-spe	c 397	15.4	0.4	17	1	ADL49626	Human tumour suppr
325	16	0.4	16	1	AAQ78464	TGF-beta gene phos	c 398	15.4	0.4	17	1	ADL49413	Human PKR subtrat

C 399	15.4	0.4	17	1	ADL49412	Human PKR substrat	c 472	14.8	0.3	18	1	AA18718	Human oligonucleo
C 400	15.4	0.4	18	1	AAQ78463	TGF-beta gene phos	473	14.8	0.3	18	1	AAF32524	Primer #2. Uniden
C 401	15.4	0.4	18	1	AAZ57445	Phosphothioate o	c 474	14.8	0.3	18	1	ABL30793	Human HLA genotypi
C 402	15.4	0.4	18	1	ABL57541	Nucleic acid probe	475	14.8	0.3	18	1	ACA62280	Oligo (dC) primer.
C 403	15.4	0.4	18	1	ABA97626	Probe f. Unidenti	c 476	14.8	0.3	18	1	ADB54824	Hybridisation olig
C 404	15.4	0.4	18	1	ABA97626	Probe h. Unidenti	c 477	14.8	0.3	18	1	ADC64808	484 clone cDNA lib
C 405	15.4	0.4	18	1	ABL95901	Probe h for assayi	c 478	14.8	0.3	18	1	ADL06307	Kid lingual tissue
C 406	15.4	0.4	18	1	ABL95901	Probe f for assayi	c 479	14.8	0.3	18	1	ADL06309	Kid lingual tissue
C 407	15.4	0.4	18	1	ABL95898	Probe d for assayi	c 480	14.8	0.3	18	1	ADF31330	Human MEGSIN gene
C 408	15.4	0.4	18	1	ABZ10862	Haematopoietic cel	481	14.8	0.3	18	1	AD28562	Displacement oligo
C 409	15.4	0.4	19	1	AAV40352	Maize oligonucleot	c 482	14.8	0.3	18	1	ADO26670	Synthetic leader s
C 410	15.4	0.4	19	1	AAA72748	PCR primer WB242 f	c 483	14.8	0.3	18	1	ADO26652	Synthetic leader s
C 411	15.4	0.4	19	1	AAA85943	Cdc 25 hs ribozyme	c 484	14.8	0.3	18	1	ADO26640	Synthetic leader s
C 412	15.4	0.4	19	1	AAA85940	Cdc 25 hs ribozyme	485	14.8	0.3	18	1	ADO26688	Synthetic leader s
C 413	15.4	0.4	19	1	AAZ70263	Human biallelic ma	486	14.8	0.3	18	1	ADO26708	Synthetic leader s
C 414	15.4	0.4	19	1	AAZ29275	Antisense nucleoti	487	14.8	0.3	18	1	ADO26642	Synthetic leader s
C 415	15.4	0.4	19	1	AAZ15884	Human MPR0T13 forw	488	14.8	0.3	18	1	ADO26642	Oligonucleotide of
C 416	15.4	0.4	19	1	AAZ89901	Oligonucleotide #2	c 489	14.6	0.3	15	1	ABN87920	Human GSR allele s
C 417	15.4	0.4	19	1	AAH61102	Cdc25 hs ribozyme	c 490	14.4	0.3	16	1	AAQ78445	TGF-beta2 antisens
C 418	15.4	0.4	19	1	AAH61105	Cdc25 hs ribozyme	c 491	14.4	0.3	16	1	AAV48961	TGF-beta2 antisens
C 419	15.4	0.4	19	1	ABL41198	Human p27 gene pol	c 492	14.4	0.3	16	1	AAV48954	RT-PCR primer of t
C 420	15.4	0.4	19	1	ABA97625	Probe d. Unidenti	c 493	14.4	0.3	16	1	AAV18362	RT-PCR primer of t
C 421	15.4	0.4	19	1	ACA62440	HCV core protein f	c 494	14.4	0.3	16	1	AAV18363	Mouse scavenger re
C 422	15.4	0.4	19	1	ADS90818	Oligonucleotide of	c 495	14.4	0.3	16	1	ADL46313	Human PKR substrat
C 423	15.4	0.4	19	1	ADS75429	TAK-1 gene PCR pri	496	14.4	0.3	17	1	ADL49413	Human PKR substrat
C 424	15.4	0.4	20	1	AAH87713	Human glutathione	497	14.4	0.3	17	1	ADL49412	HLA-DR beta sub-ty
C 425	15	0.4	15	1	AAV48999	TGF-beta2 antisens	498	14.4	0.3	17	1	AAQ26183	Neuroblastoma spec
C 426	15	0.4	15	1	AAV48950	TGF-beta2 antisens	c 499	14.4	0.3	17	1	AAQ52216	B-cell mRNA ribozy
C 427	15	0.4	15	1	AAV48951	TGF-beta2 antisens	c 500	14.4	0.3	17	1	AAQ51975	Rabbit stromelysin
C 428	15	0.4	15	1	AAV53238	IGF-I oligonucleot	501	14.4	0.3	17	1	AAV63946	Rabbit stromelysin
C 429	15	0.4	15	1	AAV53230	IGFBP2 oligonucleo	502	14.4	0.3	17	1	AAV63949	Human KDR VEGF rec
C 430	15	0.4	15	1	AAV53237	IGF-I oligonucleot	503	14.4	0.3	17	1	AAV71256	Mouse flt-1 VEGF r
C 431	15	0.4	15	1	AAV60455	Oligonucleotide cl	c 504	14.4	0.3	17	1	AAV75078	Human B-raf substr
C 432	15	0.4	15	1	ABK96652	Interleukin-3 (IL-	505	14.4	0.3	17	1	AAV93711	Human B-raf substr
C 433	15	0.4	17	1	AAV18370	RT-PCR primer of t	506	14.4	0.3	17	1	AAV93709	Human B-raf substr
C 434	15	0.4	17	1	ABT35106	Tumour suppression	507	14.4	0.3	17	1	AAV14708	Triple helix formi
C 435	15	0.4	17	1	ADL49409	Human PKR substrat	508	14.4	0.3	17	1	AAV14705	Triple helix third
C 436	15	0.4	17	1	ADP86176	CpG immunostimulat	509	14.4	0.3	17	1	AAZ57107	Human FCMD-causing
C 437	15	0.4	18	1	AAV15450	Human apolipoprote	510	14.4	0.3	17	1	AAV05267	Hammerhead ribozym
C 438	15	0.4	18	1	AAV54164	Nucleotide sequenc	c 511	14.4	0.3	17	1	AAV06339	Hammerhead ribozym
C 439	15	0.4	18	1	AAV18372	RT-PCR primer of t	c 512	14.4	0.3	17	1	AAV03387	Hammerhead ribozym
C 440	15	0.4	18	1	AAZ90646	Human adipose tiss	c 513	14.4	0.3	17	1	AAV06340	Hammerhead ribozym
C 441	15	0.4	18	1	ADL95317	Anti-proliferative	c 514	14.4	0.3	17	1	AAV03071	Human Chk1 ribozym
C 442	15	0.4	20	1	AAV32003	MSH2 gene specific	515	14.4	0.3	17	1	AAH95613	Human NCOG Hammerh
C 443	15	0.4	20	1	ADA45244	Human MSH2 gene PC	516	14.4	0.3	17	1	ABK00233	Murine Ikbkap exon
C 444	15	0.4	23	1	ADQ14575	TGF beta 2 3'-UTR	517	14.4	0.3	17	1	ABQ99687	Tumour suppression
C 445	14.8	0.3	18	1	AAQ070698	C-Rich oligonucleo	518	14.4	0.3	17	1	ABT39218	Human K-Ras DNazym
C 446	14.8	0.3	18	1	AAQ57781	M. avium-intracellu	519	14.4	0.3	17	1	ABZ59895	Murine oligonucleo
C 447	14.8	0.3	18	1	AAQ79242	Guanosine rich oli	520	14.4	0.3	17	1	ACC66553	Murine oligonucleo
C 448	14.8	0.3	18	1	AAQ79243	Guanosine rich oli	521	14.4	0.3	17	1	ACC64890	Murine oligonucleo
C 449	14.8	0.3	18	1	AAQ78447	TGF-beta gene phos	c 522	14.4	0.3	17	1	ACC67051	Tumour suppression
C 450	14.8	0.3	18	1	AAQ78430	TGF-beta gene phos	c 523	14.4	0.3	17	1	ADB42062	Tumour suppression
C 451	14.8	0.3	18	1	AAQ78479	TGF-beta gene phos	524	14.4	0.3	17	1	ADB440778	Tumour suppression
C 452	14.8	0.3	18	1	AAQ78436	TGF-beta gene phos	c 525	14.4	0.3	17	1	ADB42783	Tumour suppression
C 453	14.8	0.3	18	1	AAQ78466	TGF-beta gene phos	c 526	14.4	0.3	17	1	ADB40065	Tumour suppression
C 454	14.8	0.3	18	1	AAQ78423	TGF-beta gene phos	527	14.4	0.3	17	1	ADB40890	Tumour suppression
C 455	14.8	0.3	18	1	AAQ78483	PCR primer. Synth	c 528	14.4	0.3	17	1	ADB31052	Cholesterol homeos
C 456	14.8	0.3	18	1	AAQ75026	Viral integrase in	c 529	14.4	0.3	17	1	ADF62143	Human PCCP1 DNA fr
C 457	14.8	0.3	18	1	AAV51660	Nucleotide sequenc	530	14.4	0.3	17	1	ADF62144	Human PCCP1 DNA fr
C 458	14.8	0.3	18	1	AAV54166	Nucleotide sequenc	531	14.4	0.3	17	1	ADF62144	Human PCCP1 DNA fr
C 459	14.8	0.3	18	1	AAV54169	Nuclease resistant	c 532	14.4	0.3	17	1	ADI48299	Human tumour suppr
C 460	14.8	0.3	18	1	AAV21971	Oligonucleotide #3	c 533	14.4	0.3	17	1	ADI49153	Human tumour suppr
C 461	14.8	0.3	18	1	AAV79242	Immunosuppressant	c 534	14.4	0.3	17	1	ADI50684	Human tumour suppr
C 462	14.8	0.3	18	1	AAZ65449	Immunosuppressant	535	14.4	0.3	17	1	ADI49419	Human tumour suppr
C 463	14.8	0.3	18	1	AAZ65505	Immunosuppressant	c 536	14.4	0.3	17	1	ADI52640	Human tumour suppr
C 464	14.8	0.3	18	1	AAZ65456	Immunosuppressant	c 537	14.4	0.3	17	1	ADI51580	Human tumour suppr
C 465	14.8	0.3	18	1	AAZ65453	Human adipose tiss	c 538	14.4	0.3	17	1	ADI52683	Human tumour suppr
C 466	14.8	0.3	18	1	AAZ90648	Human adipose tiss	539	14.4	0.3	17	1	ACC51571	Human tumour suppr
C 467	14.8	0.3	18	1	AAZ90645	Polynucleotide # 3	540	14.4	0.3	17	1	ACC53558	Human tumour suppr
C 468	14.8	0.3	18	1	AAV59387	Nucleic acid probe	541	14.4	0.3	17	1	ADL49414	Human PKR substrat
C 469	14.8	0.3	18	1	ABL57543	Simple sequence re	c 542	14.4	0.3	17	1	AAV63282	Delta-9 desaturase
C 470	14.8	0.3	18	1	AAV13708	Piporesinol/larici	543	14.4	0.3	18	1	AAZ22554	Antisense oligonuc
C 471	14.8	0.3	18	1	AAV12565		544	14.4	0.3	18	1		

PS Example 1; Page 11; 32pp; English.

XX The present sequence represents a probe used for the detection of cDNA

CC encoding the mature form of transforming growth factor-beta-2 (TGF-beta-

CC 2). Dimeric, biologically active TGF-beta-like protein can be produced by

CC subjecting the denatured monomeric form to refolding conditions. The new

CC monomeric S-sulphonated TGF-beta-like protein is useful for the

CC production of the dimeric, biologically active TGF-beta-like protein,

CC which is useful for the treatment of wounds (surface or internal) and

CC cancer in a mammal, in bone and tissue repair, as a bone marrow

CC protective agent, a mediator of cardioprotection, for the production of

CC an anti-inflammatory or immunosuppressive preparation. Treatment is

CC useful for animals, especially humans, and wound treatment (e.g. ulcers,

CC bed sores etc.) is particularly useful for the elderly. (Updated on 20-

CC MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to correct PR

CC field.)

XX Sequence 39 BP; 14 A; 6 C; 6 G; 13 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 34.2; DB 1; Length 39;

Best Local Similarity 92.3%; Pred. No. 1.7;

Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2424 CTTTCAATATGATGTCAGTCTTGTAAATGACGCTAA 2462

DB 39 CTTTCAATATGATGTCAGTCTTGTAAATGACGCTAA 1

RESULT 3

AAH28309

ID AAH28309 standard; RNA; 33 BP.

XX AAH28309;

AC AAH28309;

XX 05-SEP-2001 (first entry)

XX 3' untranslated region sequence from TGF-beta gene.

DE mRNA protein complex; tumour development; cell aging; death;

XX ribonomic profile; RNA-binding protein; ss.

KW Unidentified.

OS WO200148480-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035583.

XX 28-DEC-1999; 99US-0173338P.

XX (KEEN/) KEENE J D.

XX Keene JD, Tenenbaum SA, Carson C;

PI WPI; 2001-425706/45.

XX Partitioning endogenous mRNA-protein complexes in vivo, by contacting

PT sample comprising the complex with ligand that binds to a component of

PT the complex and separating complex by binding ligand with a binding

PT molecule.

XX Example 6; Page 31; 49pp; English.

XX The specification describes a method for partitioning endogenous cellular

CC mRNA-protein (mRNP) complexes. The method comprises contacting a

CC biological sample comprising mRNP complex with ligand that specifically

CC binds a component of mRNP complex, separating mRNP complex by binding the

CC ligand with a molecule specific for ligand, which is attached to the

CC solid support and then collecting the mRNP complex by removing the

CC complex from the support. The method is useful for in vivo partitioning

CC of cellular mRNA protein complexes in a biological sample. The method is

CC useful for determining the ribonomic profile of a cell which has numerous

CC

CC uses including monitoring of tumour development, state of growth or state

CC of development, perturbations of a biological system such as disease,

CC drug or toxin treatment and the state of cell aging or death,

CC distinguishing ribonomic profiles among organisms, to discriminate

CC between transcriptional and post-transcriptional contributions to gene

CC expression and to track the movement of RNAs through RNP complexes, RNP

CC including the interactions of combinations of proteins with RNAs in RNP

CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'

CC untranslated region (UTR) of mRNA of various genes. The sequences contain

CC target sequences for RNA-binding proteins

XX Sequence 33 BP; 5 A; 3 C; 3 G; 0 T; 22 U; 0 Other;

SQ Query Match 0.8%; Score 33; DB 1; Length 33;

Best Local Similarity 33.3%; Pred. No. 1.7;

Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTAAATGTAATGTTCTTT 3296

DB 1 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33

RESULT 4

ADQ14534

ID ADQ14534 standard; RNA; 33 BP.

XX ADQ14534;

AC ADQ14534;

XX 23-SEP-2004 (first entry)

XX TGF beta 2 3'-UTR consensus sequence SEQ ID NO:29.

DE metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;

XX mRNA complex-associated protein; mRNP complex-associated protein;

KW mRNA target; protein target; physiological pathway;

KW TGF beta 2 3'-UTR consensus sequence; ss.

XX Synthetic.

OS WO2004057032-A1.

XX 08-JUL-2004.

XX 04-DEC-2003; 2003WO-US038475.

XX 04-DEC-2002; 2002US-00309788.

XX (RIBO-) RIBONOMICS INC.

XX Keene JD, Tenenbaum SA, Carson CC, Phelps WC;

PI WPI; 2004-525445/50.

XX Assessing the metabolic state of a cell comprises isolating at least one

PT mRNP complex comprising at least one RNA binding protein, and at least

PT one mRNA or at least one mRNP complex-associated protein.

XX Example 4; SEQ ID NO 29; 86pp; English.

XX The present invention describes a method for assessing the metabolic

CC state of a cell. The method comprises isolating at least one mRNP complex

CC having at least one RNA binding protein, and at least one mRNA or at

CC least one mRNP complex-associated protein, and determining the expression

CC level of the mRNA or mRNP complex-associated protein, where the level of

CC expression of the at least one mRNA or the at least one mRNP complex-

CC associated protein is indicative of the metabolic state of the cell. The

CC method can be used for assessing the metabolic state in a cell, and for

CC identifying and evaluating mRNA and protein targets associated with mRNP

CC complexes and implicated in the expression of proteins involved in common

CC physiological pathways. The present sequence represents a TGF beta 2 3'-

CC UTR consensus sequence, which is used in an example from the present

CC invention.

XX

DT 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 PCR probe.
DE
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nototropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; mouse; murine; probe; ss.
XX
OS Mus musculus.
XX
XX US2004006030-A1.
PN
XX
XX 08-JAN-2004.
PD
XX
XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM, Dobie KW;
PI WPI; 2004-081742/08.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, a useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 13; SEQ ID NO 14; 135pp; English.
PS
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, notropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a probe used in the exemplification of the invention.
XX
SQ Sequence 25 BP; 8 A; 4 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1789 AAACGAGCGGAGGGTGAATGGCT 1813
Db 1 AAACGAGCGGAGGGTGAATGGCT 25
RESULT 8
ADQ14574
ID ADQ14574 standard; RNA; 25 BP.
XX
XX ADQ14574;
AC
XX 23-SEP-2004 (first entry)
DT
XX
XX TGF beta 2 3'-UTR consensus sequence.

XX metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;
KW mRNA complex-associated protein; mRNP complex-associated protein;
KW mRNA target; protein target; physiological pathway;
KW TGF beta 2 3'-UTR consensus sequence; ss.
XX
OS Synthetic.
XX
XX WO2004057032-A1.
PN
XX
XX 08-JUL-2004.
PD
XX
XX 04-DEC-2003; 2003WO-US038475.
PF
XX
XX 04-DEC-2002; 2002US-00309788.
PR
XX
XX (RIBO-) RIBONOMICS INC.
PA
XX
XX Keene JD, Tenenbaum SA, Carson CC, Phelps WC;
PI WPI; 2004-525445/50.
DR
XX
XX Assessing the metabolic state of a cell comprises isolating at least one
PT mRNP complex comprising at least one RNA binding protein, and at least
PT one mRNA or at least one mRNP complex-associated protein.
XX
XX Example 4; Page 35; 86pp; English.
PS
XX
XX The present invention describes a method for assessing the metabolic
CC state of a cell. The method comprises isolating at least one mRNP complex
CC having at least one RNA binding protein, and at least one mRNA or at
CC least one mRNP complex-associated protein, and determining the expression
CC level of the mRNA or mRNP complex-associated protein, where the level of
CC expression of the at least one mRNA or the at least one mRNP complex-
CC associated protein is indicative of the metabolic state of the cell. The
CC method can be used for assessing the metabolic state in a cell, and for
CC identifying and evaluating mRNA and protein targets associated with mRNP
CC complexes and implicated in the expression of proteins involved in common
CC physiological pathways. The present sequence represents a TGF beta 2 3'-
CC UTR consensus sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 25 BP; 6 A; 3 C; 0 G; 0 T; 16 U; 0 Other;
Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 36.0%; Pred. No. 16;
Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY 3693 TTCAAATTTTATATATATATCTT 3717
Db 1 UUCAUUUUUUUUUAUACUUCUU 25
RESULT 9
ADQ14536
ID ADQ14536 standard; RNA; 25 BP.
XX
XX ADQ14536;
AC
XX 23-SEP-2004 (first entry)
DT
XX
XX TGF beta 2 3'-UTR consensus sequence SEQ ID NO:31.
DE
XX
XX metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;
KW mRNA complex-associated protein; mRNP complex-associated protein;
KW mRNA target; protein target; physiological pathway;
KW TGF beta 2 3'-UTR consensus sequence; ss.
XX
OS Synthetic.
XX
XX WO2004057032-A1.
PN
XX
XX 08-JUL-2004.

```

XX 04-DEC-2003; 2003WO-US038475.
XX
XX 04-DEC-2002; 2002US-00309788.
XX
XX (RIBO-) RIBONOMICS INC.
XX
XX Keene JD, Tenenbaum SA, Carson CC, Phelps WC;
XX WPI; 2004-525445/50.
XX
XX Assessing the metabolic state of a cell comprises isolating at least one
XX mRNA complex comprising at least one RNA binding protein, and at least
XX one mRNA or at least one mRNA complex-associated protein.
XX
XX Example 4; SEQ ID NO 31; 86pp; English.
XX
XX The present invention describes a method for assessing the metabolic
XX state of a cell. The method comprises isolating at least one mRNA complex
XX having at least one RNA binding protein, and at least one mRNA or at
XX least one mRNA complex-associated protein, and determining the expression
XX level of the mRNA or mRNA complex-associated protein, where the level of
XX expression of the at least one mRNA or the at least one mRNA complex-
XX associated protein is indicative of the metabolic state of the cell. The
XX method can be used for assessing the metabolic state in a cell, and for
XX identifying and evaluating mRNA and protein targets associated with mRNA
XX complexes and implicated in the expression of proteins involved in common
XX physiological pathways. The present sequence represents a TGF beta 2 3'-
XX UTR consensus sequence, which is used in an example from the present
XX invention.
XX
XX Query Match 0.6%; Score 25; DB 1; Length 25;
XX Best Local Similarity 36.0%; Pred. No. 16;
XX Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3693 TTCAATTTTATATATATCTT 3717
Db 1 UUCAUUUUUUUAUAUACUUCU 25

RESULT 10
AD180005/c
ID AD180005 standard; DNA; 26 BP.
XX
XX AC AD180005;
XX
XX 22-APR-2004 (first entry)
XX
XX Human transforming growth factor-beta 2 reverse PCR primer.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytotatic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; human; primer; ss.
XX
XX Homo sapiens.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX

New compounds, particularly antisense oligonucleotides targeted to a
nucleic acid encoding TGF-beta 2, useful for treating cancer, a
neurodegenerative disorder, or a disease involving hyperactivation of
immune response.
Example 13; SEQ ID NO 6; 135pp; English.
The invention relates to a novel antisense compound of 8-80 nucleobases
in length targeted to, and which specifically hybridizes with, a nucleic
acid molecule encoding transforming growth factor (TGF)-beta 2, and
inhibits the expression of TGF-beta 2. The invention further relates to:
a compound 8-80 nucleobases in length that specifically hybridizes with
a molecule encoding TGF-beta 2; a composition comprising the compound and a
carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
tissues by contacting the cells or tissues with the compound so that
expression of TGF-beta 2 is inhibited; treating an animal having a
disease or condition associated with TGF-beta 2 by administering to the
animal a therapeutic or prophylactic amount of the compound so that
expression of TGF-beta 2 is inhibited; and screening an antisense
compound. The antisense compound has cytostatic, nontropic,
neuroprotective, and immunosuppressive activities. The compound,
composition and methods are useful for treating a disease or condition
associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
cancer, a neurodegenerative disorder, or a disease or condition involving
hyperactivation of an immune response. This polynucleotide sequence
represents a primer used in the exemplification of the invention.
Sequence 26 BP; 10 A; 6 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2142 TCGTTTAGAAATGTCAGGATAATT 2166
Db 25 TCGTTTAGAAATGTCAGGATAATT 1

RESULT 11
ADJ76723
ID ADJ76723 standard; DNA; 23 BP.
XX
XX AC ADJ76723;
XX
XX 20-MAY-2004 (first entry)
XX
XX TGFbeta forward PCR primer SEQ ID NO:1975.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX gene therapy; marker; PCR; primer; ss.
XX
XX Mus musculus.
XX
XX Synthetic.
XX
XX EP1394274-A2.
XX
XX 03-MAR-2004.
XX
XX 04-AUG-2003; 2003EP-00254857.
XX
XX 06-AUG-2002; 2002JP-00229312.
XX
XX 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX

```

PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
XX
XX Example 11; SEQ ID NO 1975; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 23 BP; 9 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 217 TTACCTTAAGCGAGAAAGTGCAA 239
Db 1 TTACCTTAAGCGAGAAAGTGCAA 23

RESULT 12
AAQ41629/c
ID AAQ41629 standard; cDNA; 26 BP.

XX AAQ41629;
XX
XX 25-MAR-2003 (revised)
DT 26-AUG-1993 (first entry)
XX
XX TGF-beta2 antisense strand (nucleotides 167-142) PCR primer.
XX
XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation;
KW polymerase chain reaction; ss.
XX
XX Synthetic.
OS
XX EP542679-A1.
PN
XX 19-MAY-1993.
PD
XX 03-NOV-1992; 92EP-00810845.
PF
XX 11-NOV-1991; 91EP-00810870.
PR
XX (CIBA) CIBA GEIGY AG.

PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX WPI; 1993-161126/20.
DR
XX
XX New hybrid transforming growth factor-beta molecules - comprise portions
PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,
PT antiinflammatory and immunosuppressive agents etc.
XX
XX Example 1; Page 40; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts of the
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600
CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-
CC beta polypeptides were constructed from the appropriate, PCR-amplified
CC segments of the wild-type isoforms. For the construction of hybrid DNA
CC molecules encoding TGF-beta hybrids all having the hinge points between
CC amino acids 56 and 57, the primers AAQ41626-Q41631 (corresp. to the hinge
CC regions) were used with the appropriate primers (see AAQ41608-Q41613)
CC which flank the regions coding for each of the three full-length mature
CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to
CC correct PN field.)

Sequence 26 BP; 8 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 40;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2265 TGCCCATATCTATGAGTTTCAGACAC 2290
Db 26 TGCCCGTATTTATGAGTTTCAGACAC 1

RESULT 13
AAQ41628
ID AAQ41628 standard; cDNA; 26 BP.

XX AAQ41628;
XX
XX 25-MAR-2003 (revised)
DT 26-AUG-1993 (first entry)
XX
XX TGF-beta2 sense strand (nucleotides 142-167) PCR primer.
XX
XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation;
KW polymerase chain reaction; ss.
XX
XX Synthetic.
OS
XX EP542679-A1.
PN
XX 19-MAY-1993.
PD
XX 03-NOV-1992; 92EP-00810845.
PF
XX 11-NOV-1991; 91EP-00810870.
PR
XX (CIBA) CIBA GEIGY AG.

PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX WPI; 1993-161126/20.
DR
XX
XX New hybrid transforming growth factor-beta molecules - comprise portions
PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,
PT antiinflammatory and immunosuppressive agents etc.
XX
XX Example 1; Page 40; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts of the
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600
CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-

CC beta polypeptides were constructed from the appropriate, PCR-amplified
 CC segments of the wild-type isoforms. For the construction of hybrid DNA
 CC molecules encoding TGF-beta hybrids all having the hinge points between
 CC amino acids 56 and 57, the primers AA041626-Q41631 (corresp. to the hinge
 CC regions) were used with the appropriate primers (see AAQ41608-Q41613)
 CC which flank the regions coding for each of the three full-length mature
 CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 26 BP; 6 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 22.8; DB 1; Length 26;
 Best Local Similarity 92.3%; Pred. No. 40;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2265 TGCCCATATCTATGAGGTTTCAGACAC 2290
 Db 1 TGCCCGTATTTATGGAGTTTCAGACAC 26
 RESULT 14
 AAA76086
 ID AAA76086 standard; DNA; 27 BP.
 XX
 AC AAA76086;
 XX
 DT 08-DEC-2000 (first entry)
 XX
 DE Transforming Growth Factor-beta2 TGF-beta2 PCR primer #1.
 XX
 KW PCR primer; prostate cancer cell line; androgen independent; CL-1; CL-2;
 KW LNCaP cell line; beta-actin; prostate-specific antigen;
 KW Prostate specific membrane antigen; Basic fibroblast growth factor;
 KW Vascular endothelial cell growth factor; Interleukin-6;
 KW Transforming Growth Factor-beta1; transforming growth factor-beta2;
 KW Transforming Growth Factor-beta-R; Epidermal growth factor receptor; PSA;
 KW AR; PSAM; IL-8; VEGF; bFGF; IL-6; TGF-beta1; TGF-beta2; TGF-beta-R;
 KW EGF-R; BCL-2; E-cadherin; p53; PTEN; Caveolin; c-myc; HER-2/neu; p27;
 KW Androgen receptor; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200044879-A1.
 PN
 XX
 PD 03-AUG-2000.
 XX
 XX 28-JAN-2000; 2000WO-US002223.
 PF
 XX
 PR 28-JAN-1999; 99US-0117562P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX
 PI Belldegrun AS, Teo C;
 XX
 DR WPI; 2000-499329/44.
 XX
 XX Androgen independent, aggressively tumorigenic prostate cancer cell lines
 PT designated CL-1 and CL-2, useful as tools for studying the cellular and
 PT molecular mechanisms of prostate cancer progression.
 XX
 XX Example 2; Page 30; 90pp; English.
 PS
 XX
 XX The present invention relates to androgen independent, aggressively
 CC tumorigenic prostate cancer cell lines, CL-1 and CL-2, which are
 CC sublines of the LNCaP cell line. The present sequence is a PCR primer
 CC used to amplify a coding sequence expressed by the cell lines. The coding
 CC sequences which were amplified in the present invention by the primers in
 CC AAA76068 to AAA76107 were: beta-actin, prostate-specific antigen (PSA),
 CC Androgen receptor (AR), Prostate specific membrane antigen (PSAM),
 CC Interleukin-8 (IL-8), Vascular endothelial cell growth factor (VEGF),
 CC Basic fibroblast growth factor (bFGF), Interleukin-6 (IL-6), Transforming
 CC Growth Factor-beta1 (TGF-beta1), Transforming Growth Factor-beta2 (TGF-
 CC beta2), Transforming Growth Factor-beta-R (TGF-beta-R), Epidermal growth

CC factor receptor (EGF-R), BCL-2, E-cadherin, p53, PTEN, Caveolin, c-myc,
 CC HER-2/neu and p27. RT-PCR was used to monitor changes in coding sequence
 CC expression, as the LNCaP parental lines progressed to the CL1 and CL2
 CC sublines. The CL-1 and CL-2 sublines can be used as tools for studying
 CC the cellular and molecular mechanisms of prostate cancer progression.
 CC such as the expression patterns of various transcripts and proteins that
 CC are associated with the progression of the non-metastatic, androgen-
 CC dependent state to the metastatic androgen-independent state
 XX
 SQ Sequence 27 BP; 6 A; 10 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 22.8; DB 1; Length 27;
 Best Local Similarity 92.3%; Pred. No. 45;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1278 CTGTCTACTCTGACGACACCTCGACAT 1303
 Db 2 CTGTCTACTCTGACGACACTCGATAT 27
 RESULT 15
 AAF82681/c
 ID AAF82681 standard; DNA; 27 BP.
 XX
 AC AAF82681;
 XX
 DT 18-JUN-2001 (first entry)
 XX
 DE Human TGF-beta2 PCR primer #2.
 XX
 KW Human; androgen response element; ARE; cytostatic; gene therapy;
 KW prostate-specific chimeric enhancer; transcriptional regulation;
 KW Targeted gene expression; prostate cancer; prostate disorder;
 KW prostate-specific antigen; PSA; transforming growth factor beta2;
 KW TGF-beta2; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200127256-A2.
 PN
 XX
 PD 19-APR-2001.
 XX
 XX 13-OCT-2000; 2000WO-US028444.
 PF
 XX
 PR 14-OCT-1999; 99US-0159691P.
 PR
 PR 15-OCT-1999; 99US-0159730P.
 XX
 XX (REGC) UNIV CALIFORNIA SYSTEM.
 PA
 XX
 XX Wu L, Carey MF, Belldegrun AS;
 XX
 XX WPI; 2001-273768/28.
 DR
 XX
 XX New polynucleotide, useful for treating prostatic cancer, comprises
 PT prostate specific chimeric enhancer and proximal promoter sequence
 PT operably linked to nucleic acid encoding heterologous polypeptide.
 XX
 XX Example 5; Page 73; 131pp; English.
 PS
 XX
 XX The present sequence was used in reverse transcriptase polymerase chain
 CC reaction (RT-PCR) analysis of human prostate cancer cells. The invention
 CC relates to an isolated polynucleotide comprising a prostate-specific
 CC chimeric enhancer (PSE) sequence and a proximal promoter sequence
 CC operably linked to a nucleic acid segment that encodes a heterologous
 CC polypeptide. The PSE contains an ARE and specifically activates
 CC transcription of the nucleic acid segment in a mammalian prostate cell.
 CC The construct is useful for the treatment of a prostate disorder or a
 CC metastasised prostate cancer, such as hyperplasia or hyperproliferation
 CC of prostate cells. It is also useful for directing the tissue-specific
 CC expression of a heterologous polypeptide in a human prostate cell. The
 CC construct may be administered by injection, infection, transfection, receptor
 CC liposome-mediated transfection, polybrene-mediated transfection, receptor
 CC -mediated uptake or Ca-PO4-mediated transfection

```
XX SQ Sequence 27 BP; 5 A; 7 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 0.5%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAAATCGACATGCGTC 1546
||||| ||||| ||||| ||||| ||||| |||||
Db 27 GGAGGTTTACAAAATAGACATGCGCC 1

RESULT 16
ID ADJ76725/c
ID ADJ76725 standard; DNA; 22 BP.
XX ADJ76725;
XX 20-MAY-2004 (first entry)
DE TGFEB2 probe SEQ ID NO:1977.
XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker; probe; ss.
XX Mus musculus.
OS Synthetic.
XX EP1394274-A2.
XX 03-MAR-2004.
XX 04-AUG-2003; 2003EP-00254857.
XX 06-AUG-2002; 2002JP-00229312.
PR 20-MAR-2003; 2003JP-00077212.
XX (GENO-) GENOX RES INC.
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX WPI; 2004-193155/19.
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX Example 11; SEQ ID NO 1977; 241pp; English.
XX The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
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```
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX Sequence 22 BP; 7 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGTGTTCACACAGGGTTAAGG 338
||||| ||||| ||||| ||||| ||||| |||||
Db 22 TGTGTTCACACAGGGTTAAGG 1

RESULT 17
ADQ14537
ID ADQ14537 standard; RNA; 22 BP.
XX ADQ14537;
XX 23-SEP-2004 (first entry)
DE TGF beta 2 3'-UTR consensus sequence SEQ ID NO:32.
XX metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;
KW mRNA complex-associated protein; mRNP complex-associated protein;
KW mRNA target; protein target; physiological pathway;
KW TGF beta 2 3'-UTR consensus sequence; ss.
XX Synthetic.
XX WO2004057032-A1.
PN 08-JUL-2004.
XX 04-DEC-2003; 2003WO-US038475.
PF 04-DEC-2002; 2002US-00309788.
XX (RIBO-) RIBONOMICS INC.
PA Keene JD, Tenenbaum SA, Carson CC, Phelps WC;
PI WPI; 2004-525445/50.
XX Assessing the metabolic state of a cell comprises isolating at least one
PT mRNP complex comprising at least one RNA binding protein, and at least
PT one mRNA or at least one mRNP complex-associated protein.
XX Example 4; SEQ ID NO 32; 86pp; English.
XX The present invention describes a method for assessing the metabolic
CC state of a cell. The method comprises isolating at least one mRNP complex
CC having at least one RNA binding protein, and at least one mRNA or at
CC least one mRNP complex-associated protein, and determining the expression
CC level of the mRNA or mRNP complex-associated protein, where the level of
CC expression of the at least one mRNA or the at least one mRNP complex-
CC associated protein is indicative of the metabolic state of the cell. The
CC method can be used for assessing the metabolic state in a cell, and for
CC identifying and evaluating mRNA and protein targets associated with mRNP
CC complexes and implicated in the expression of proteins involved in common
CC physiological pathways. The present sequence represents a TGF beta 2 3'-
CC UTR consensus sequence, which is used in an example from the present
XX invention.
XX Sequence 22 BP; 2 A; 1 C; 2 G; 0 T; 17 U; 0 Other;
Query Match 0.5%; Score 22; DB 1; Length 22;
```

```
Best Local Similarity 22.7%; Pred. No. 34;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAAATGGTTTTTTT 4099
Db 1 UUUUUUUUAUUGGUUUUUU 22

RESULT 18
AAH28312
ID AAH28312 standard; RNA; 25 BP.
XX
AC AAH28312;
XX
DT 05-SEP-2001 (first entry)
DE
DE 3' untranslated region sequence from TGF-beta gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEENE/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 25 BP; 2 A; 1 C; 2 G; 1 T; 17 U; 2 Other;

Query Match 0.5%; Score 22; DB 1; Length 25;
Best Local Similarity 22.7%; Pred. No. 49;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAAATGGTTTTTTT 4099
Db 1 UUUUUUUUAUUGGUUUUUU 22
```

```
RESULT 19
ADJ76622
ID ADJ76622 standard; DNA; 25 BP.
XX
AC ADJ76622;
XX
DT 20-MAY-2004 (first entry)
DE
DE TGPB2 reverse PCR primer SEQ ID NO:1874.
XX
KW bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker; PCR; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EP1394274-A2.
XX
PD 03-MAR-2004.
XX
PF 04-AUG-2003; 2003EP-00254857.
XX
PR 06-AUG-2002; 2002JP-00293112.
PR 20-MAR-2003; 2003JP-00077212.
XX
PA (GENO-) GENOX RES INC.
XX
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX
DR WPI; 2004-193155/19.
XX
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
PS Example 11; SEQ ID NO 1874; 241pp; English.
XX
CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 25 BP; 8 A; 9 C; 5 G; 3 T; 0 U; 0 Other;
```

Query Match		0.5%;	Score 21.8;	DB 1;	Length 25;		
Best Local Similarity		92.0%;	Pred. NO. 52;				
Matches	23;	Conservative	0;	Mismatches	2;		
				Indels	0;		
				Gaps	0;		
QY	1759	CCGAGCGCTACATCGATGACCAAGT	1783				
DB	1	CCGAGCGCTACATCGACACCAAGT	25				
RESULT 20							
ID	AAF82680	standard; DNA; 24 BP.					
XX	AC						
XX	AAF82680;						
XX	18-JUN-2001	(first entry)					
XX	Human TGF-beta2	PCR primer #1.					
XX	Human;	androgen response element; ARE; cytostatic; gene therapy;					
XX	prostate-specific chimeric enhancer;	transcriptional regulation;					
XX	targeted gene expression;	prostate cancer; prostate disorder;					
XX	prostate-specific antigen; PSA;	transforming growth factor beta2;					
XX	TGF-beta2;	PCR primer; ss.					
XX	Homo sapiens.						
XX	WO200127256-A2.						
XX	19-APR-2001.						
XX	13-OCT-2000;	2000WO-US028444.					
XX	14-OCT-1999;	99US-0159691P.					
XX	15-OCT-1999;	99US-0159730P.					
XX	(REGC)	UNIV CALIFORNIA SYSTEM.					
XX	Wu L, Carey MF, Belldegrun AS;						
XX	WPI; 2001-273768/28.						
XX	New polynucleotide, useful for treating	prostatic cancer, comprises					
XX	prostate specific chimeric enhancer and proximal promoter sequence						
XX	operably linked to nucleic acid encoding heterologous polypeptide.						
XX	Example 5; Page 73; 131pp;	English.					
XX	The present sequence was used in reverse transcriptase polymerase chain						
XX	reaction (RT-PCR) analysis of human prostate cancer cells. The invention						
XX	relates to an isolated polynucleotide comprising a prostate-specific						
XX	chimeric enhancer (PSE) sequence and a proximal promoter sequence						
XX	operably linked to a nucleic acid segment that encodes a heterologous						
XX	polypeptide. The PSE contains an ARE and specifically activates						
XX	transcription of the nucleic acid segment in a mammalian prostate cell.						
XX	The construct is useful for the treatment of a prostate disorder or a						
XX	metastatised prostate cancer, such as hyperplasia or hyperproliferation						
XX	of prostate cells. It is also useful for directing the tissue-specific						
XX	expression of a heterologous polypeptide in a human prostate cell. The						
XX	construct may be administered by injection, infection, transformation,						
XX	liposome-mediated transfection, polybrene-mediated transfection, receptor						
XX	-mediated uptake or Ca-PO4-mediated transformation						
XX	Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;						
Query Match							
Best Local Similarity		0.5%;	Score 21.4;	DB 1;	Length 24;		
Matches		22;	Conservative	0;	Mismatches		
				Indels	1;		
				Gaps	0;		
QY	1278	CTGTCTACCTGCAGCACCTCTCGA	1300				
DB	2	CTGTCTACCTGCAGCACCTCTCGA	24				
RESULT 21							
ID	ADQ14575	standard; RNA; 23 BP.					
XX	ADQ14575;						
XX	23-SEP-2004	(first entry)					
XX	TGF beta 2 3'-UTR	consensus sequence.					
XX	metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;						
XX	mRNA complex-associated protein; mRNP complex-associated protein;						
XX	mRNA target; protein target; physiological pathway;						
XX	TGF beta 2 3'-UTR	consensus sequence; ss.					
XX	Synthetic.						
XX	WO2004057032-A1.						
XX	08-JUL-2004.						
XX	04-DEC-2003;	2003WO-US038475.					
XX	04-DEC-2002;	2002US-00309788.					
XX	(RIBO-) RIBONOMICS INC.						
XX	Keene JD, Tenenbaum SA, Carson CC, Phelps WC;						
XX	WPI; 2004-525445/50.						
XX	Assessing the metabolic state of a cell comprises isolating at least one						
XX	mRNP complex comprising at least one RNA binding protein, and at least						
XX	one mRNA or at least one mRNP complex-associated protein.						
XX	Example 4; Page 35; 86pp; English.						
XX	The present invention describes a method for assessing the metabolic						
XX	state of a cell. The method comprises isolating at least one mRNP complex						
XX	having at least one RNA binding protein, and at least one mRNA or at						
XX	least one mRNP complex-associated protein, and determining the expression						
XX	level of the mRNA or mRNP complex-associated protein, where the level of						
XX	expression of the at least one mRNA or the at least one mRNP complex-						
XX	associated protein is indicative of the metabolic state of the cell. The						
XX	method can be used for assessing the metabolic state in a cell, and for						
XX	identifying and evaluating mRNA and protein targets associated with mRNP						
XX	complexes and implicated in the expression of proteins involved in common						
XX	physiological pathways. The present sequence represents a TGF beta 2 3'-						
XX	UTR consensus sequence, which is used in an example from the present						
XX	invention.						
XX	Sequence 23 BP; 2 A; 1 C; 2 G; 1 T; 16 U; 1 Other;						
Query Match							
Best Local Similarity		0.5%;	Score 21;			DB 1;	Length 23;
Matches		5;	Conservative	16;	Mismatches		
				Indels	0;		
				Gaps	0;		
QY	4078	TTTTTCTTTTAATTGGTTTTT	4098				
DB	1	UUUUUUUUUAUUGGUUUUU	21				
RESULT 22							
ID	ABL41487	standard; DNA; 24 BP.					
XX	ABL41487;						
XX	27-AUG-2002	(first entry)					
XX	Human ATP-dependent serine	protein hydrolase 12 RT-PCR primer, SEQ ID:3.					
XX							

KW Human; ATP-dependent serine protein hydrolase 12; recombinant production;
 KW tumour; cancer; gene therapy; human immunodeficiency virus;
 KW HIV infection; cytostatic; antiviral; reverse transcription-PCR; RT-PCR;
 KW primer; ss.
 XX Homo sapiens.
 OS
 PN CN1331337-A.
 XX
 XX 16-JAN-2002.
 PD
 XX
 XX 26-JUN-2000; 2000CN-00116723.
 PF
 XX
 XX 26-JUN-2000; 2000CN-00116723.
 PR
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 XX WPI; 2002-340680/38.
 DR
 XX
 XX A human ATP dependent serine protein hydrolase 12 polypeptide, and the
 PT polynucleotide encoding it, for treating e.g. cancer and HIV infection.
 PT
 PS Example 2; Page 17 (Disclosure); 32pp; Chinese.
 XX
 XX The invention relates to human ATP-dependent serine protein hydrolase 12
 CC (ABB9561) and nucleic acids encoding it (ABL41486). The protein has a
 CC molecular weight of 12 kD. The invention also relates to a method for the
 CC recombinant production of the protein, an antagonist of the protein, and
 CC the use of the protein, gene and antagonist in therapeutic applications.
 CC ATP-dependent serine protein hydrolase 12 can be used in the treatment of
 CC a variety of diseases such as cancer and HIV (human immunodeficiency
 CC virus) infection. Sequences ABL41487-ABL41488 represent reverse
 CC transcription-PCR (RT-PCR) primers used in an exemplification of the
 CC invention to isolate human ATP-dependent serine protein hydrolase 12 cDNA
 XX
 XX Sequence 24 BP; 4 A; 11 C; 9 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.5%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 78;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 619 GCGCGCACGCGCGCGCACAC 640
 Db 2 GCGCGCACGCGCGCGCGCACAC 23
 RESULT 23
 AAC96323/c
 ID AAC96323 standard; DNA; 25 BP.
 XX
 XX AAC96323;
 AC
 XX
 XX 26-FEB-2001 (first entry)
 DT
 XX
 DE HLA DPB1 gene PCR primer #55.
 XX
 KW DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 XX WO200065088-A2.
 PN
 XX
 XX 02-NOV-2000.
 PD
 XX
 XX 20-APR-2000; 2000WO-EP003636.
 PF
 XX
 XX 26-APR-1999; 99EP-00303215.
 PR
 XX
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

XX Ulfendahl P, Wong K;
 PI
 XX WPI; 2000-679677/66.
 DR
 XX
 XX Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 PT
 XX
 XX Claim 14; Page 49; 66pp; English.
 PS
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 XX
 XX Sequence 25 BP; 3 A; 3 C; 5 G; 14 T; 0 U; 0 Other;
 SQ
 Query Match 0.5%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 94;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 918 TCCCTTCCAGGAGAGAAAAAACA 942
 Db 25 TCCCTTCCAGGAGAGAAAAAACA 1
 RESULT 24
 AAC88273/c
 ID AAC88273 standard; DNA; 25 BP.
 XX
 XX AAC88273;
 AC
 XX
 XX 02-MAR-2001 (first entry)
 DT
 XX
 DE SCDNA102 DNA sequence.
 XX
 KW Drug binding site; viscosity; biomolecule interaction; drug target;
 KW electronic transducer; primer; ds.
 XX
 OS Synthetic.
 OS
 XX WO200068419-A2.
 PN
 XX
 XX 16-NOV-2000.
 PD
 XX
 XX 05-MAY-2000; 2000WO-CA000504.
 PF
 XX
 XX 05-MAY-1999; 99CA-02271179.
 PR
 XX
 PA (SENS-) SENSORCHEM INT CORP.
 XX
 XX McGovern M, Thompson M;
 PI
 XX
 XX WPI; 2001-024875/03.
 DR
 XX
 XX Monitoring/detecting small molecule-biomolecule interactions for drug
 PT screening involves contacting a solution of small molecules with
 PT immobilized biomolecules and measuring the frequency generated with an
 PT acoustic wave device.
 PT
 XX
 XX Example 4; Fig 5; 44pp; English.
 PS
 XX
 XX The present invention describes a device and method for monitoring small
 CC molecule-biomolecule interactions. These involve the measurement of the
 CC oscillation of a liquid when in contact with the biomolecule only
 CC compared with the small molecule-biomolecule complex. This uses a
 CC piezoelectric device and can be used with biomolecules such as DNA. The
 CC present sequence was used as an example. The device can be used to screen

CC for drug candidates, to determine the conditions in which small molecules
CC will not bind to given biomolecules and to obtain information on the
CC tertiary structure of biomolecules

XX SQ Sequence 25 BP; 0 A; 13 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 94;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 614 GGCGCGCGCGACGACGCGCGCAC 638
|||
Db 25 GGCGCGCGCGCGCGCGCGCGCGC 1

RESULT 25
AAV63217
ID AAV63217 standard; DNA; 20 BP.

XX AC AAV63217;

DT 14-JAN-1999 (first entry)

XX Forward PCR primer for human transforming growth factor-beta 2 cDNA.

XX Human transforming growth factor-beta 2; TGF-beta3; oxygen tension;
KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW preeclampsia; pregnancy; choriocarcinoma; PCR primer; ss.

XX OS Synthetic.

OS Homo sapiens.

XX WO9840747-A1.

XX 17-SEP-1998.

XX 05-MAR-1998; 98WO-CA000180.

XX 07-MAR-1997; 97US-0039919P.

XX (MOUN) MOUNT SINAI HOSPITAL CORP.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.

XX Caniggia I, Post M, Lye S;

XX WPI; 1998-520837/44.

XX Regulation of trophoblast invasion - by, e.g. transforming growth factor-
PT beta3 inhibitor, useful for detecting or treating preeclampsia in
PT pregnant women.

XX Example 4; Page 21; 59pp; English.

XX PCR primers AAV63217-18 were used to amplify cDNA encoding human
CC transforming growth factor-beta 2 (TGF-beta2). The specification
CC describes a composition for regulating trophoblast invasion which
CC comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors,
CC hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The
CC composition is used in methods of diagnosing, monitoring, preventing or
CC treating conditions requiring regulation of trophoblast invasion,
CC especially preeclampsia in pregnant women or choriocarcinomas

XX Sequence 20 BP; 1 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1254 CATCTGCTCCCGTGGCGCT 1273
|||
Db 1 CATCTGCTCCCGTGGCGCT 20

RESULT 26
AAV79980/c
ID AAV79980 standard; DNA; 20 BP.
XX AC AAV79980;
DT 24-FEB-1999 (first entry)
XX TGF-beta 2 DNA amplifying primer.
XX Transgenic; osteogenic; core binding factor; CBFA1/PEBP2-alpha-A;
KW polyoma enhancer binding protein; runt; osteoblast; variant; TGF-beta;
KW PCR primer; ss.
XX OS Synthetic.
XX JP10309148-A.
XX 24-NOV-1998.
XX 11-SEP-1997; 97JP-00247346.
XX 10-MAR-1997; 97JP-00074453.
XX (KISH/) KISHIMOTO C.
XX WPI; 1999-063649/06.
XX Transgenic animal with no osteogenic property - has introduced variation
PT in gene encoding core binding factor/polyoma enhancer binding protein.
XX Example 10; Page 7; 19pp; Japanese.

XX The invention provides a transgenic animal devoid of osteogenic property.
CC The transgenic animal has an introduced variation in a gene encoding for
CC core binding factor/polyoma enhancer binding protein (CBFA1/PEBP2-alpha
CC A), particularly in runt region DNA, especially prepared by introduction
CC of a variation devoid of at least a part of gene encoding CBFA1/PEBP2-
CC alpha-A, leading to a disturbance in differentiation and maturation of
CC osteoblast cells. The transgenic animal can be prepared by introducing a
CC variant gene encoding for CBFA1/PEBP2-alpha-A. The animal can be used to
CC elucidate the in vivo mechanism of CBFA1/PEBP2-alpha-A. Sequences
CC AAV79975 to AAV80010 represent PCR primers used during the course of the
CC invention
XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1300 ACATGATCAGTTTATGGC 1319
|||
Db 20 ACATGATCAGTTTATGGC 1

RESULT 27
AAV79979

ID AAV79979 standard; DNA; 20 BP.

XX AC AAV79979;

XX 24-FEB-1999 (first entry)

XX TGF-beta 2 DNA amplifying primer.

XX Transgenic; osteogenic; core binding factor; CBFA1/PEBP2-alpha-A;
KW polyoma enhancer binding protein; runt; osteoblast; variant; TGF-beta;
KW PCR primer; ss.

XX OS Synthetic.

XX

PN JP10309148-A.
XX 24-NOV-1998.
XX 11-SEP-1997; 97JP-00247346.
XX 10-MAR-1997; 97JP-00074453.
XX (KISH/) KISHIMOTO C.
XX WPI; 1999-063649/06.
XX Transgenic animal with no osteogenic property - has introduced variation
PT in gene encoding core binding factor/polyoma enhancer binding protein.
XX
XX Example 10; Page 7; 19pp; Japanese.
XX The invention provides a transgenic animal devoid of osteogenic property.
CC The transgenic animal has an introduced variation in a gene encoding for
CC core binding factor/polyoma enhancer binding protein (CBFA1/PEBP2-alpha
CC A), particularly in runt region DNA, especially prepared by introduction
CC of a variation devoid of at least a part of gene encoding CBFA1/PEBP2-
CC alpha-A, leading to a disturbance in differentiation and maturation of
CC osteoblast cells. The transgenic animal can be prepared by introducing a
CC variant gene encoding for CBFA1/PEBP2-alpha-A. The animal can be used to
CC elucidate the in vivo mechanism of CBFA1/PEBP2-alpha-A. Sequences
CC AAV79975 to AAV80010 represent PCR primers used during the course of the
CC invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1015 GTTGGGAACCGTTGCATTT 1034
Db 1 GTTGGGAACCGTTGCATTT 20
RESULT 28
ADF86265
ID ADF86265 standard; DNA; 20 BP.
XX
AC ADF86265;
XX
DT 26-FEB-2004 (first entry)
XX
DE Mouse TGF-beta 2 PCR primer related to liver regeneration SeqID11.
XX
KW liver regeneration promoter; hepatic disorder; anti-kallikrein antibody;
KW hepatotropic; antiinflammatory; virucide; TGF;
KW transforming growth factor-beta; liver tissue fibrosis; liver cirrhosis;
KW hepatitis; liver regeneration insufficiency; PCR; primer; ss; mouse;
KW murine; TGF-beta 2.
XX
OS Mus sp.
XX
XX JP2003252792-A.
XX
PD 10-SEP-2003.
XX
PF 04-MAR-2002; 2002JP-00057253.
XX
PR 04-MAR-2002; 2002JP-00057253.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
XX WPI; 2003-857283/80.
XX
XX Liver regeneration promoter for treating and preventing hepatic disorder,
PT contains anti-kallikrein antibody as active ingredient.

XX Disclosure; SEQ ID NO 11; 25pp; Japanese.
XX This invention relates to a novel liver regeneration promoter for
CC treating and preventing a hepatic disorder, which contains anti-
CC kallikrein antibody as an active ingredient. The invention may be useful
CC in the development of compositions with hepatotropic, antiinflammatory or
CC virucide activities as a transforming growth factor (TGF)-agonist. The
CC invention may be useful for treating and preventing hepatic disorders
CC resulting from the effect of transforming growth factor-beta, liver
CC tissue fibrosis, liver cirrhosis, hepatitis or liver regeneration
CC insufficiency.
XX
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2048 GACCCACATCTCTGCTAA 2067
Db 1 GACCCACATCTCTGCTAA 20
RESULT 29
ADF86266/c
ID ADF86266 standard; DNA; 20 BP.
XX
AC ADF86266;
XX
DT 26-FEB-2004 (first entry)
XX
DE Mouse TGF-beta 2 PCR primer related to liver regeneration SeqID12.
XX
KW liver regeneration promoter; hepatic disorder; anti-kallikrein antibody;
KW hepatotropic; antiinflammatory; virucide; TGF;
KW transforming growth factor-beta; liver tissue fibrosis; liver cirrhosis;
KW hepatitis; liver regeneration insufficiency; PCR; primer; ss; mouse;
KW murine; TGF-beta 2.
XX
OS Mus sp.
XX
XX JP2003252792-A.
XX
PD 10-SEP-2003.
XX
PF 04-MAR-2002; 2002JP-00057253.
XX
PR 04-MAR-2002; 2002JP-00057253.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
XX WPI; 2003-857283/80.
XX
XX Liver regeneration promoter for treating and preventing hepatic disorder,
PT contains anti-kallikrein antibody as active ingredient.

XX Disclosure; SEQ ID NO 12; 25pp; Japanese.
XX This invention relates to a novel liver regeneration promoter for
CC treating and preventing a hepatic disorder, which contains anti-
CC kallikrein antibody as an active ingredient. The invention may be useful
CC in the development of compositions with hepatotropic, antiinflammatory or
CC virucide activities as a transforming growth factor (TGF)-agonist. The
CC invention may be useful for treating and preventing hepatic disorders
CC resulting from the effect of transforming growth factor-beta, liver
CC tissue fibrosis, liver cirrhosis, hepatitis or liver regeneration
CC insufficiency.
XX
SQ Sequence 20 BP; 2 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 54;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2401 GAAATACGCCCAAGATCGAA 2420		
Db	20 GAAATACGCCCAAGATCGAA 1		
RESULT 30			
AD180093/c			
ID	AD180093 standard; DNA; 20 BP.		
XX	AD180093;		
AC	AD180093;		
XX	22-APR-2004 (first entry)		
DT	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 94.		
DE	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;		
XX	cytostatic; nontropic; neuroprotective; immunosuppressive;		
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;		
KW	immune; ss; mouse; murine.		
XX	Mus musculus.		
OS	US2004006030-A1.		
PN	08-JAN-2004.		
XX	02-JUL-2002; 2002US-00189267.		
PD	02-JUL-2002; 2002US-00189267.		
XX	(ISIS-) ISIS PHARM INC.		
PA	Monia BP, Freier SM, Dobie KW;		
PI	WPI; 2004-081742/08.		
DR	New compounds, particularly antisense oligonucleotides targeted to a		
XX	nucleic acid encoding TGF-beta 2, useful for treating cancer, a		
PT	neurodegenerative disorder, or a disease involving hyperactivation of		
PT	immune response.		
PS	Example 16; SEQ ID NO 94; 135pp; English.		
XX	The invention relates to a novel antisense compound of 8-80 nucleobases		
CC	in length targeted to, and which specifically hybridizes with, a nucleic		
CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and		
CC	inhibits the expression of TGF-beta 2. The invention further relates to:		
CC	a compound 8-80 nucleobases in length that specifically hybridizes with		
CC	at least an 8-nucleobase portion of an active site on a nucleic acid		
CC	molecule encoding TGF-beta 2; a composition comprising the compound and a		
CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or		
CC	tissues by contacting the cells or tissues with the compound so that		
CC	expression of TGF-beta 2 is inhibited; treating an animal having a		
CC	disease or condition associated with TGF-beta 2 by administering to the		
CC	animal a therapeutic or prophylactic amount of the compound so that		
CC	expression of TGF-beta 2 is inhibited; and screening an antisense		
CC	compound. The antisense compound has cytostatic, nontropic,		
CC	neuroprotective, and immunosuppressive activities. The compound,		
CC	composition and methods are useful for treating a disease or condition		
CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.		
CC	cancer, a neurodegenerative disorder, or a disease or condition involving		
CC	hyperactivation of an immune response. This polynucleotide sequence		
CC	represents an antisense oligonucleotide of the invention.		
XX	Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;		
Query Match 0.5%; Score 20; DB 1; Length 20;			
Best Local Similarity 100.0%; Pred. No. 54;			
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	914 CCTCTCCCTTCCAGGAGAAA 933		
Db	20 CCTCTCCCTTCCAGGAGAAA 1		

Best Local Similarity 100.0%; Pred. No. 54;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	133 TAGGCTTTAAAGAGCCATTC 152		
Db	20 TAGGCTTTAAAGAGCCATTC 1		
RESULT 31			
AD180095/c			
ID	AD180095 standard; DNA; 20 BP.		
XX	AD180095;		
AC	AD180095;		
XX	22-APR-2004 (first entry)		
DT	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 96.		
DE	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;		
XX	cytostatic; nontropic; neuroprotective; immunosuppressive;		
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;		
KW	immune; ss; mouse; murine.		
XX	Mus musculus.		
OS	US2004006030-A1.		
PN	08-JAN-2004.		
XX	02-JUL-2002; 2002US-00189267.		
PD	02-JUL-2002; 2002US-00189267.		
XX	(ISIS-) ISIS PHARM INC.		
PA	Monia BP, Freier SM, Dobie KW;		
PI	WPI; 2004-081742/08.		
DR	New compounds, particularly antisense oligonucleotides targeted to a		
XX	nucleic acid encoding TGF-beta 2, useful for treating cancer, a		
PT	neurodegenerative disorder, or a disease involving hyperactivation of		
PT	immune response.		
PS	Example 16; SEQ ID NO 96; 135pp; English.		
XX	The invention relates to a novel antisense compound of 8-80 nucleobases		
CC	in length targeted to, and which specifically hybridizes with, a nucleic		
CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and		
CC	inhibits the expression of TGF-beta 2. The invention further relates to:		
CC	a compound 8-80 nucleobases in length that specifically hybridizes with		
CC	at least an 8-nucleobase portion of an active site on a nucleic acid		
CC	molecule encoding TGF-beta 2; a composition comprising the compound and a		
CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or		
CC	tissues by contacting the cells or tissues with the compound so that		
CC	expression of TGF-beta 2 is inhibited; treating an animal having a		
CC	disease or condition associated with TGF-beta 2 by administering to the		
CC	animal a therapeutic or prophylactic amount of the compound so that		
CC	expression of TGF-beta 2 is inhibited; and screening an antisense		
CC	compound. The antisense compound has cytostatic, nontropic,		
CC	neuroprotective, and immunosuppressive activities. The compound,		
CC	composition and methods are useful for treating a disease or condition		
CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.		
CC	cancer, a neurodegenerative disorder, or a disease or condition involving		
CC	hyperactivation of an immune response. This polynucleotide sequence		
CC	represents an antisense oligonucleotide of the invention.		
XX	Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;		
Query Match 0.5%; Score 20; DB 1; Length 20;			
Best Local Similarity 100.0%; Pred. No. 54;			
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	914 CCTCTCCCTTCCAGGAGAAA 933		
Db	20 CCTCTCCCTTCCAGGAGAAA 1		

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RESULT 32
ADI80105/c
ID ADI80105 standard; DNA; 20 BP.
XX AC ADI80105;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 106.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 106; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1314 ATCGCAAGAGGATCGAGGC 1333
DB 20 ATGCGCAAGAGGATCGAGGC 1
RESULT 33
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ADI80119/c
ID ADI80119 standard; DNA; 20 BP.
XX AC ADI80119;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 120.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 120; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 5 A; 2 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1584 TCACAGCCCTACTTCAGAAAT 1603
DB 20 TACAGACCCTACTTCAGAAAT 1
RESULT 34
ADI80139/c
ID ADI80139 standard; DNA; 20 BP.
XX
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AC ADI80139;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 140.
 XX
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 XX
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR (ISIS-) ISIS PHARM INC.
 XX
 PA Monia BP, Freier SM, Dobie KW;
 XX
 PI WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 140; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 2 A; 2 C; 8 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2292 CAACACCAACCAAGTCTCTAG 2311
 DB |||||||||||||||||||
 20 CAACACCAACCAAGTCTCTAG 1
 RESULT 35
 ADI80140/C
 ID ADI80140 standard; DNA; 20 BP.
 XX
 AC ADI80140;
 XX
 DT 22-APR-2004 (first entry)

XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 141.
 DE
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR (ISIS-) ISIS PHARM INC.
 XX
 PA Monia BP, Freier SM, Dobie KW;
 XX
 PI WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 141; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2349 CCTTCTGTGTGTCTCCAGCA 2368
 DB |||||||||||||||||||
 20 CCTTCTGTGTGTCTCCAGCA 1
 RESULT 36
 ADI80141/C
 ID ADI80141 standard; DNA; 20 BP.
 XX
 AC ADI80141;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 142.
 XX

KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 PN US2004006030-A1.
 XX
 XX 08-JAN-2004.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 142; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2444 GTCTGTAATGACGCTAA 2463
 DB 20 GTCTGTAATGACGCTAA 1
 RESULT 37
 ADI80152/c
 ID ADI80152 standard; DNA; 20 BP.
 XX
 AC ADI80152;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 153.
 DE
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.

KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 PN US2004006030-A1.
 XX
 XX 08-JAN-2004.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 153; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 9 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3279 AATTGTAATGGTCTTTGC 3298
 DB 20 AATTGTAATGGTCTTTGC 1
 RESULT 38
 ADI80159/c
 ID ADI80159 standard; DNA; 20 BP.
 XX
 AC ADI80159;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 160.
 DE
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.

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XX PN US2004006030-A1.
XX XX 08-JAN-2004.
XX PD 02-JUL-2002; 2002US-00189267.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX XX WPI; 2004-081742/08.
XX DR New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 160; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX XX Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
XX SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3737 ATTGCCATTATGACATG 3756
DB 20 ATTGCCATTATGACATG 1
|||||
RESULT 39
ADI80162/c
ID ADI80162 standard; DNA; 20 BP.
XX AC ADI80162;
XX XX 22-APR-2004 (first entry)
XX DT Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 163.
XX DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX XX Mus musculus.
XX OS US2004006030-A1.
XX PN 08-JAN-2004.
XX XX 02-JUL-2002; 2002US-00189267.

PD XX 08-JAN-2004.
XX XX 02-JUL-2002; 2002US-00189267.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX XX WPI; 2004-081742/08.
XX DR New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 163; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX XX Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
XX SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4245 CTTTCAGGCTGATTAAAAA 4264
DB 20 CTTTCAGGCTGATTAAAAA 1
|||||
RESULT 40
ADI80259
ID ADI80259 standard; DNA; 20 BP.
XX AC ADI80259;
XX XX 22-APR-2004 (first entry)
XX DT Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 260.
XX DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX XX Mus musculus.
XX OS US2004006030-A1.
XX PN 08-JAN-2004.
XX XX 02-JUL-2002; 2002US-00189267.
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XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 260; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2226 GAACCCAAAGGGTACAATGC 2245
DB 1 GAACCCAAAGGGTACAATGC 20
RESULT 41
ADI80269
XX ADI80269 standard; DNA; 20 BP.
XX AC ADI80269;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 270.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosstatic; neurotropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
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PA (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 270; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3049 AAACATCATGATGGCTTAAG 3068
DB 1 AAACATCATGATGGCTTAAG 20
RESULT 42
ADI80100/c.
XX ADI80100 standard; DNA; 20 BP.
XX AC ADI80100;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 101.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosstatic; neurotropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
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XX WPI; 2004-081742/08.
XX
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX
XX Example 16; SEQ ID NO 101; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC a nucleic acid encoding TGF-beta 2; a composition comprising the compound and
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 7 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1205 TCCTTTTAAAAACATGCAC 1224
DB 20 TCCTTTTAAAAACATGCAC 1
RESULT 43
ADI80106/c
ID ADI80106 standard; DNA; 20 BP.
XX
XX
XX AC ADI80106;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 107.
DE
DE
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX

PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 107; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1321 AGAGGATCGAGGCCATCCGC 1340
DB 20 AGAGGATCGAGGCCATCCGC 1
RESULT 44
ADI80107/c
ID ADI80107 standard; DNA; 20 BP.
XX
XX AC ADI80107;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 108.
DE
DE
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.

PT	immune response.	
XX	Example 16; SEQ ID NO 108; 135pp; English.	
PS	The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.	
XX	Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;	
SQ	Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 54; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1335 ATCCGCGGCGAGATCCTGAG 1354 	
DB	20 ATCCGCGGCGAGATCCTGAG 1	
RESULT 45		
AD180117/c		
ID	AD180117 standard; DNA; 20 BP.	
XX		
AC	AD180117;	
XX		
DT	22-APR-2004 (first entry)	
XX		
DE	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 118.	
XX		
KW	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; neurotropic; neuroprotective; immunosuppressive;	
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; immune; ss; mouse; murine.	
XX		
OS	Mus musculus.	
XX		
PN	US2004006030-A1.	
XX		
PD	08-JAN-2004.	
XX		
PF	08-JAN-2004.	
XX		
PP	02-JUL-2002; 2002US-00189267.	
XX		
PR	02-JUL-2002; 2002US-00189267.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Monia BP, Freier SM, Dobie KW;	
XX		
DR	WPI; 2004-081742/08.	
XX		
PT	New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.	
XX		
PS	Example 16; SEQ ID NO 118; 135pp; English.	
CC	The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.	
XX	Sequence 20 BP; 5 A; 1 C; 9 G; 5 T; 0 U; 0 Other;	
SQ	Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 54; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1576 CCACCTTCTACAGACCTTAC 1595 	
DB	20 CCACCTTCTACAGACCTTAC 1	
RESULT 46		
AD180134/c		
ID	AD180134 standard; DNA; 20 BP.	
XX		
AC	AD180134;	
XX		
DT	22-APR-2004 (first entry)	
XX		
DE	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 135.	
XX		
KW	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; neurotropic; neuroprotective; immunosuppressive;	
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; immune; ss; mouse; murine.	
XX		
OS	Mus musculus.	
XX		
PN	US2004006030-A1.	
XX		
PD	08-JAN-2004.	
XX		
PF	02-JUL-2002; 2002US-00189267.	
XX		
PR	02-JUL-2002; 2002US-00189267.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Monia BP, Freier SM, Dobie KW;	
XX		
DR	WPI; 2004-081742/08.	
XX		
PT	New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.	
XX		
PS	Example 16; SEQ ID NO 135; 135pp; English.	
CC	The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.	

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 9 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2181 CTTTACATTGATTTAAGAG 2200
 Db 20 CTTTACATTGATTTAAGAG 1
 RESULT 47
 AD180143/c
 ID AD180143 standard; DNA; 20 BP.
 AC AD180143;
 XX
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 144.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 144; 135pp; English.
 CC
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX

CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2487 AAAATCAGCGTGACAATGAC 2506
 Db 20 AAAATCAGCGTGACAATGAC 1
 RESULT 48
 AD180231
 ID AD180231 standard; DNA; 20 BP.
 AC AD180231;
 XX
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 232.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 232; 135pp; English.
 CC
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1269 GCGCTCAGTCTGTCTACCTG 1288
 Db 1 GCGCTCAGTCTGTCTACCTG 20
 RESULT 49
 ADI80240
 ID ADI80240 standard; DNA; 20 BP.
 XX
 AC ADI80240;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 241.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 241; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1507 AGTACTACGCCAAGGAGTT 1526
 Db 1 AGTACTACGCCAAGGAGTT 20
 RESULT 50
 ADI80094/C
 ID ADI80094 standard; DNA; 20 BP.
 XX
 AC ADI80094;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 95.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 95; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 7 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 ACACGAACTCCATTCTTC 879
 DB 20 ACACGAACTCCATTCTTC 1

RESULT 51
 ADI80129/c
 ID ADI80129 standard; DNA; 20 BP.
 XX
 AC ADI80129;
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 130.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PS New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX neurodegenerative disorder, or a disease involving hyperactivation of
 XX immune response.
 XX
 PS Example 16; SEQ ID NO 130; 135pp; English.

CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.

CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTTGTGCCCT 2079
 DB 20 CCTGCTAATGTTGTGCCCT 1

RESULT 52
 ADI80132/c
 ID ADI80132 standard; DNA; 20 BP.
 XX
 AC ADI80132;
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 133.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PS New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX neurodegenerative disorder, or a disease involving hyperactivation of
 XX immune response.
 XX
 PS Example 16; SEQ ID NO 133; 135pp; English.

CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.

```
XX SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2151 AATGTGCAGGATTAATGCTG 2170
|||||
Db 20 AATGTGCAGGATTAATGCTG 1

RESULT 53
ADI80144/c
ID ADI80144 standard; DNA; 20 BP.
XX AC ADI80144;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 145.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosstatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 145; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 9 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2635 GTTCTGTTGTTAAACTGG 2654
|||||
Db 20 GTTCTGTTGTTAAACTGG 1

RESULT 54
ADI80241
ID ADI80241 standard; DNA; 20 BP.
XX AC ADI80241;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 242.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosstatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 242; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 8 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1515	GCCAAGCAGCTTTATAAAAT	1534
Db			
	1	GCCAAGGAGGTTTATAAAAT	20
RESULT	55		
ADI80257			
ID	ADI80257	standard; DNA; 20 BP.	
XX	AC	ADI80257;	
XX	AC		
XX	DT		
XX	DE	22-APR-2004 (first entry)	
XX	DE	Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 258.	
XX	XX	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;	
KW	KW	cytostatic; neurotropic; neuroprotective; immunosuppressive;	
KW	KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;	
KW	KW	immune; ss; mouse; murine.	
XX	XX		
OS	OS	Mus musculus.	
XX	XX		
PN	PN	US2004006030-A1.	
XX	XX		
PD	PD	08-JAN-2004.	
XX	XX		
PF	PF	02-JUL-2002; 2002US-00189267.	
XX	XX		
PR	PR	02-JUL-2002; 2002US-00189267.	
XX	XX		
PA	PA	(ISIS-) ISIS PHARM INC.	
XX	XX		
PI	PI	Monia BP, Freier SM, Dobie KW;	
XX	XX		
DR	DR	WPI; 2004-081742/08.	
XX	XX		
PT	PT	New compounds, particularly antisense oligonucleotides targeted to a	
PT	PT	nucleic acid encoding TGF-beta 2, useful for treating cancer, a	
PT	PT	neurodegenerative disorder, or a disease involving hyperactivation of	
PT	PT	immune response.	
XX	XX		
XX	XX	Example 16; SEQ ID NO 258; 135pp; English.	
XX	XX		
CC	CC	The invention relates to a novel antisense compound of 8-80 nucleobases	
CC	CC	in length targeted to, and which specifically hybridizes with, a nucleic	
CC	CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and	
CC	CC	inhibits the expression of TGF-beta 2. The invention further relates to:	
CC	CC	a compound 8-80 nucleobases in length that specifically hybridizes with	
CC	CC	at least an 8-nucleobase portion of an active site on a nucleic acid	
CC	CC	molecule encoding TGF-beta 2; a composition comprising the compound and a	
CC	CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or	
CC	CC	tissues by contacting the cells or tissues with the compound so that	
CC	CC	expression of TGF-beta 2 is inhibited; treating an animal having a	
CC	CC	disease or condition associated with TGF-beta 2 by administering to the	
CC	CC	animal a therapeutic or prophylactic amount of the compound so that	
CC	CC	expression of TGF-beta 2 is inhibited; and screening an antisense	
CC	CC	compound. The antisense compound has cytostatic, neurotropic,	
CC	CC	neuroprotective, and immunosuppressive activities. The compound,	
CC	CC	composition and methods are useful for treating a disease or condition	
CC	CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.	
CC	CC	cancer, a neurodegenerative disorder, or a disease or condition involving	
CC	CC	hyperactivation of an immune response. This polynucleotide sequence	
CC	CC	represents a preferred target DNA region of TGF-beta 2 of the invention.	
XX	XX		
SQ	SQ	Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;	
	Query Match	0.5%; Score 20; DB 1; Length 20;	
	Best Local Similarity	100.0%; Pred. No. 54;	
	Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	2190	GATTTTAAGAGGATCTTGG	2209

RESULT 57
ADI80011
XX ADI80011 standard; DNA; 20 BP.
XX AC ADI80011;
XX DE 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 forward PCR primer.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; mouse; murine; primer; ss.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 13; SEQ ID NO 12; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a primer used in the exemplification of the invention.
XX Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1757 CACCAGCGCTACATCGATA 1776
DB 1 CACCAGCGCTACATCGATA 20
RESULT 58
ADI80099/c
XX ADI80099 standard; DNA; 20 BP.

XX ADI80099;
XX 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 100.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 100; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 9 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1138 CTGAGATTACTAGTTTCTT 1157
DB 20 CTGAGATTACTAGTTTCTT 1
RESULT 59
ADI80136/c
XX ADI80136 standard; DNA; 20 BP.
XX AC ADI80136;
XX

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DT 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 137.
DE
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 16; SEQ ID NO 137; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TGGATCCATGAACCCAAAGG 2236
DB 20 TGGATCCATGAACCCAAAGG 1

RESULT 60
AD180147/c
ID AD180147 standard; DNA; 20 BP.
XX
XX AC AD180147;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 148.

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XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 16; SEQ ID NO 148; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 8 A; 1 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2977 CTATATAATGAACCTTTTCAT 2996
DB 20 CTATATAATGAACCTTTTCAT 1

RESULT 61
AD180148/c
ID AD180148 standard; DNA; 20 BP.
XX
XX AC AD180148;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 149.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;

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KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
OS Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 149; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 7 A; 2 C; 6 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2988 ACCTTTCATTACCTTGGAA 3007
DB 20 ACCTTTCATTACCTTGGAA 1
RESULT 62
ADI80230
ID ADI80230 standard; DNA; 20 BP.
XX AC ADI80230;
XX 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 231.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX US2004006030-A1.

OS Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 231; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1218 ATGCACTACTGTGTCTGAG 1237
DB 1 ATGCACTACTGTGTCTGAG 20
RESULT 63
ADI80234
ID ADI80234 standard; DNA; 20 BP.
XX AC ADI80234;
XX 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 235.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX US2004006030-A1.

XX 08-JAN-2004.
 XX 02-JUL-2002; 2002US-00189267.
 XX 02-JUL-2002; 2002US-00189267.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 XX New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX neurodegenerative disorder, or a disease involving hyperactivation of
 XX immune response.
 XX Example 16; SEQ ID NO 235; 135pp; English.
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 XX in length targeted to, and which specifically hybridizes with, a nucleic
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
 XX inhibits the expression of TGF-beta 2. The invention further relates to:
 XX a compound 8-80 nucleobases in length that specifically hybridizes with
 XX at least an 8-nucleobase portion of an active site on a nucleic acid
 XX molecule encoding TGF-beta 2; a composition comprising the compound and a
 XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 XX tissues by contacting the cells or tissues with the compound so that
 XX expression of TGF-beta 2 is inhibited; treating an animal having a
 XX disease or condition associated with TGF-beta 2 by administering to the
 XX animal a therapeutic or prophylactic amount of the compound so that
 XX expression of TGF-beta 2 is inhibited; and screening an antisense
 XX compound. The antisense compound has cytostatic, neurotropic,
 XX neuroprotective, and immunosuppressive activities. The compound,
 XX composition and methods are useful for treating a disease or condition
 XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 XX cancer, a neurodegenerative disorder, or a disease or condition involving
 XX hyperactivation of an immune response. This polynucleotide sequence
 XX represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1335 ATCCGCGGCAGATCTCTGAG 1354
 DB 1 ATCCGCGGCAGATCTCTGAG 20
 RESULT 64
 ADI80239
 ID ADI80239 standard; DNA; 20 BP.
 XX AC ADI80239;
 XX 22-APR-2004 (first entry)
 XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 240.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 DE cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX Mus musculus.
 XX US2004006030-A1.
 XX 08-JAN-2004.
 XX 02-JUL-2002; 2002US-00189267.
 XX 02-JUL-2002; 2002US-00189267.

PF 02-JUL-2002; 2002US-00189267.
 XX 02-JUL-2002; 2002US-00189267.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 XX New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX neurodegenerative disorder, or a disease involving hyperactivation of
 XX immune response.
 XX Example 16; SEQ ID NO 240; 135pp; English.
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 XX in length targeted to, and which specifically hybridizes with, a nucleic
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
 XX inhibits the expression of TGF-beta 2. The invention further relates to:
 XX a compound 8-80 nucleobases in length that specifically hybridizes with
 XX at least an 8-nucleobase portion of an active site on a nucleic acid
 XX molecule encoding TGF-beta 2; a composition comprising the compound and a
 XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 XX tissues by contacting the cells or tissues with the compound so that
 XX expression of TGF-beta 2 is inhibited; treating an animal having a
 XX disease or condition associated with TGF-beta 2 by administering to the
 XX animal a therapeutic or prophylactic amount of the compound so that
 XX expression of TGF-beta 2 is inhibited; and screening an antisense
 XX compound. The antisense compound has cytostatic, neurotropic,
 XX neuroprotective, and immunosuppressive activities. The compound,
 XX composition and methods are useful for treating a disease or condition
 XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 XX cancer, a neurodegenerative disorder, or a disease or condition involving
 XX hyperactivation of an immune response. This polynucleotide sequence
 XX represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1463 AAGCCGGAGGCGAGCGCCT 1482
 DB 1 AAGCCGGAGGCGAGCGCCT 20
 RESULT 65
 ADI80245
 ID ADI80245 standard; DNA; 20 BP.
 XX AC ADI80245;
 XX 22-APR-2004 (first entry)
 XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 246.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 DE cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX Mus musculus.
 XX US2004006030-A1.
 XX 08-JAN-2004.
 XX 02-JUL-2002; 2002US-00189267.
 XX 02-JUL-2002; 2002US-00189267.

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XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX XX WPI; 2004-081742/08.
XX DR
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX XX Example 16; SEQ ID NO 246; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 5 A; 7 C; 1 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1580 TTCTACAGACCCCTACTTCA 1599
Db 1 TTCTACAGACCCCTACTTCA 20
RESULT 66
ADI80251
ID ADI80251 standard; DNA; 20 BP.
XX AC
XX AC ADI80251;
XX DT 22-APR-2004 (first entry)
XX DE
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 252.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 08-JAN-2004.
XX PR 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
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PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX XX Example 16; SEQ ID NO 252; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1996 CCAGTGGTGATCAGAAAACCT 2015
Db 1 CCAGTGGTGATCAGAAAACCT 20
RESULT 67
ADI80270
ID ADI80270 standard; DNA; 20 BP.
XX AC
XX AC ADI80270;
XX DT 22-APR-2004 (first entry)
XX DE
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 271.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
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XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 271; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 AATTGTAATGGTCTTTGC 3298
|||||
DB 1 AATTGTAATGGTCTTTGC 20

RESULT 68
ADI80098/c
ID ADI80098 standard; DNA; 20 BP.
XX AC ADI80098;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 99.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 99; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1133 CCGCTCTGAGAATTACTAGT 1152
|||||
DB 20 CCGCTCTGAGAATTACTAGT 1

RESULT 69
ADI80133/c
ID ADI80133 standard; DNA; 20 BP.
XX AC ADI80133;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 134.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.

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PS Example 16; SEQ ID NO 134; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 8 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TGCCTTCGCCCTTTACAT 2188
Db 20 TGCCTTCGCCCTTTACAT 1

RESULT 70
AD180142/C
ID AD180142 standard; DNA; 20 BP.
XX
AC AD180142;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 143.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 143; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 8 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TGCCTTCGCCCTTTACAT 2188
Db 20 TGCCTTCGCCCTTTACAT 1

RESULT 71
AD180224
ID AD180224 standard; DNA; 20 BP.
XX
AC AD180224;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 225.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 225; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
```

CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 ACACGAACTCCATTTCTTC 879
 Db 1 ACACGAACTCCATTTCTTC 20

RESULT 72
 ADI80225
 ID ADI80225 standard; DNA; 20 BP.
 XX
 AC ADI80225;
 XX
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 226.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 226; 135pp; English.
 XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTTCCAGGAGAAA 933
 Db 1 CCTCTCCCTTCCAGGAGAAA 20

RESULT 73
 ADI80243
 ID ADI80243 standard; DNA; 20 BP.
 XX
 AC ADI80243;
 XX
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 244.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 244; 135pp; English.
 XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTCCGAAAATGCCATCCCG 1574
DB 1 CCTCCGAAAATGCCATCCCG 20

RESULT 74
AD180037/c
ID AD180037 standard; DNA; 20 BP.
XX
AC AD180037;
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 38.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 15; SEQ ID NO 38; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 CCGCGGGCAGATCCTGAGCA 1356
DB 20 CCGCGGGCAGATCCTGAGCA 1

RESULT 75
AD180096/c
ID AD180096 standard; DNA; 20 BP.
XX
AC AD180096;
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 97.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 97; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1015 GTTGGGACGCGTTGCATT 1034
DB 20 GTTGGGACGCGTTGCATT 1
RESULT 76
ADI80128/c
ID ADI80128 standard; DNA; 20 BP.
XX
AC ADI80128;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 129.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 129; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence

CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2051 CCCACATCTCTGCTAAATGT 2070
DB 20 CCCACATCTCTGCTAAATGT 1
RESULT 77
ADI80153/c
ID ADI80153 standard; DNA; 20 BP.
XX
AC ADI80153;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 154.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 154; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
XX
SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3292 TCCTTGCAGTTTAAGCAAG 3311
DB 20 TCCTTGCAGTTTAAGCAAG 1

RESULT 78
ADI80253
ID ADI80253 standard; DNA; 20 BP.
XX AC
XX ADI80253;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 254.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 254; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytosolic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX SQ Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2060 CCTGCTAAATGTTGTCCT 2079
DB 1 CCTGCTAAATGTTGTCCT 20

RESULT 79
ADI80255
ID ADI80255 standard; DNA; 20 BP.
XX AC
XX ADI80255;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 256.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 256; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytosolic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX SQ Sequence 20 BP; 6 A; 2 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2142 TGCTTTAGAAATGTCAGGA 2161

```

Db      1  TGCTTTAGAAATGTCAGGA 20
|||||
RESULT 80
ADI80263
ID ADI80263 standard; DNA; 20 BP.
XX
AC ADI80263;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 264.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 264; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2451 AAATGAGCTTAAAGTCTTG 2470
|||||
Db      1  AAATGAGCTTAAAGTCTTG 20
|||||
RESULT 81
ADI80109/c
ID ADI80109 standard; DNA; 20 BP.
XX
AC ADI80109;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 110.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 110; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1409 CCCGAGGTGATTTCATCT 1428
|||||
Db      20  CCCGAGGTGATTTCATCT 1
|||||
RESULT 82
ADI80111/c

```


DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 136.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 136; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GATTTTAAAGGGGATCTTG 2209
DB 20 GATTTTAAAGGGGATCTTG 1

RESULT 85
AD180150/c
ID AD180150 standard; DNA; 20 BP.
XX
AC AD180150;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 151.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW

KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 151; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3073 TTGAACCTCAATAAGCCAGG 3092
DB 20 TTGAACCTCAATAAGCCAGG 1

RESULT 86
AD180171
ID AD180171 standard; DNA; 20 BP.
XX
AC AD180171;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 172.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.

```
XX OS Homo sapiens.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX PS Example 16; SEQ ID NO 172; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1965 TTTGCAGGTATTGTCAC 1984
Db 1 TTTGCAGGTATTGTCAC 20
RESULT 87
ADI80238
ID ADI80238 standard; DNA; 20 BP.
XX AC ADI80238;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 239.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytotatic; neurotropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
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PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX PS Example 16; SEQ ID NO 239; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1422 TCCATCTACAACAGTACCAG 1441
Db 1 TCCATCTACAACAGTACCAG 20
RESULT 88
ADI80242
ID ADI80242 standard; DNA; 20 BP.
XX AC ADI80242;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 243.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytotatic; neurotropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
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XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM, Dobie KW;
PI
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 243; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 TTTTAAATCGACATGCCG 1544
Db 1 TTTTAAATCGACATGCCG 20
RESULT 89
AD180246
ID AD180246 standard; DNA; 20 BP.
XX
XX AD180246;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 247.
DE
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
XX
XX 08-JAN-2004.
PN
XX
XX 02-JUL-2002; 2002US-00189267.
PD
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
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PR 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Freier SM, Dobie KW;
PI
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 247; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 7 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1584 TACAGACCCCTACTTCAGAAAT 1603
Db 1 TACAGACCCCTACTTCAGAAAT 20
RESULT 90
AD180252
ID AD180252 standard; DNA; 20 BP.
XX
XX AD180252;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 253.
DE
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
XX
XX 08-JAN-2004.
PN
XX
XX 02-JUL-2002; 2002US-00189267.
PD
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
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XX
PI Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 16; SEQ ID NO 253; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 9 A; 2 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2000 TGGTGATCAGAAACTATAA 2019
XX DB 1 TGGTGATCAGAAACTATAA 20
XX
XX RESULT 91
XX ADI80264
XX ID ADI80264 standard; DNA; 20 BP.
XX AC
XX ADI80264;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 265.
XX
XX antisease; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX
XX OS Mus musculus.
XX
XX PN US2004006030-A1.
XX
XX PD 08-JAN-2004.
XX
XX PF 02-JUL-2002; 2002US-00189267.
XX
XX PR 02-JUL-2002; 2002US-00189267.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 16; SEQ ID NO 265; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 9 A; 2 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2000 TGGTGATCAGAAACTATAA 2019
XX DB 1 TGGTGATCAGAAACTATAA 20
XX
XX RESULT 92
XX ADI80020/c
XX ID ADI80020 standard; DNA; 20 BP.
XX AC
XX ADI80020;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 21.
XX
XX antisease; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; human.
XX
XX OS Homo sapiens.
XX
XX PN US2004006030-A1.
XX
XX PD 08-JAN-2004.
XX
XX PF 02-JUL-2002; 2002US-00189267.
XX
XX PR 02-JUL-2002; 2002US-00189267.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
```


CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2000 TGGTGATCAGAAACTATAA 2019
 Db 20 TGGTGATCAGAAACTATAA 1

RESULT 95
 AD180146/c
 ID AD180146 standard; DNA; 20 BP.
 AC AD180146;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 147.
 DE
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 XX US2004006030-A1.
 PN
 XX 08-JAN-2004.
 PD
 XX 02-JUL-2002; 2002US-00189267.
 PF
 XX 02-JUL-2002; 2002US-00189267.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Monia BP, Freier SM, Dobie KW;
 PI
 XX WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 PT
 XX Example 16; SEQ ID NO 147; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX

SQ Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2970 TGTGTTACTATATATGAAC 2989
 Db 20 TGTGTTACTATATATGAAC 1

RESULT 96
 AD180244
 ID AD180244 standard; DNA; 20 BP.
 AC AD180244;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 245.
 DE
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 XX US2004006030-A1.
 PN
 XX 08-JAN-2004.
 PD
 XX 02-JUL-2002; 2002US-00189267.
 PF
 XX 02-JUL-2002; 2002US-00189267.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Monia BP, Freier SM, Dobie KW;
 PI
 XX WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 PT
 XX Example 16; SEQ ID NO 245; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3292 TCTTTCAGTTTAAGCAAG 3311
Db 1 TCTTTCAGTTTAAGCAAG 20

RESULT 99
ADI80112/c
ID ADI80112 standard; DNA; 20 BP.
XX
AC ADI80112;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 113.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 113; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1463 AAGCCGGAGGCGAGCGCCT 1482
Db 20 AAGCCGGAGGCGAGCGCCT 1

RESULT 100
ADI80127/c
ID ADI80127 standard; DNA; 20 BP.
XX
AC ADI80127;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 128.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 128; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC	hyperactivation of an immune response. This polynucleotide sequence	SQ	Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
CC	represents an antisense oligonucleotide of the invention.	Query Match	0.5%; Score 20; DB 1; Length 20;
XX		Best Local Similarity	100.0%; Pred. No. 54;
SQ	Sequence 20 BP; 4 A; 3 C; 4 G; 9 T; 0 U; 0 Other;	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2011 AAACATAAGTCCACTAGG 2030	QY	2075 GCCCTCTACAGCTGGAGT 2094
Db	20 AAACATAAGTCCACTAGG 1	Db	20 GCCCTCTACAGCTGGAGT 1
RESULT 101		RESULT 102	
ADI80130/C		ADI80156/C	
ID	ADI80130 standard; DNA; 20 BP.	ID	ADI80156 standard; DNA; 20 BP.
XX		XX	
AC	ADI80130;	AC	ADI80156;
DT	22-APR-2004 (first entry)	DT	22-APR-2004 (first entry)
XX		XX	
DE	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 131.	DE	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 157.
XX		XX	
KW	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;	KW	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW	cytostatic; neutropic; neuroprotective; immunosuppressive;	KW	cytostatic; neutropic; neuroprotective; immunosuppressive;
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;	KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW	immune; ss; mouse; murine.	KW	immune; ss; mouse; murine.
OS	Mus musculus.	OS	Mus musculus.
XX		XX	
PN	US2004006030-A1.	PN	US2004006030-A1.
XX		XX	
PD	08-JAN-2004.	PD	08-JAN-2004.
XX		XX	
PF	02-JUL-2002; 2002US-00189267.	PF	02-JUL-2002; 2002US-00189267.
XX		XX	
PR	02-JUL-2002; 2002US-00189267.	PR	02-JUL-2002; 2002US-00189267.
XX		XX	
PA	(ISIS-) ISIS PHARM INC.	PA	(ISIS-) ISIS PHARM INC.
XX		XX	
PI	Monia BP, Freier SM, Dobie KW;	PI	Monia BP, Freier SM, Dobie KW;
XX		XX	
DR	WPI; 2004-081742/08.	DR	WPI; 2004-081742/08.
XX		XX	
PT	New compounds, particularly antisense oligonucleotides targeted to a	PT	New compounds, particularly antisense oligonucleotides targeted to a
PT	nucleic acid encoding TGF-beta 2, useful for treating cancer, a	PT	nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT	neurodegenerative disorder, or a disease involving hyperactivation of	PT	neurodegenerative disorder, or a disease involving hyperactivation of
PT	immune response.	PT	immune response.
PS	Example 16; SEQ ID NO 131; 135pp; English.	PS	Example 16; SEQ ID NO 157; 135pp; English.
XX		XX	
CC	The invention relates to a novel antisense compound of 8-80 nucleobases	CC	The invention relates to a novel antisense compound of 8-80 nucleobases
CC	in length targeted to, and which specifically hybridizes with, a nucleic	CC	in length targeted to, and which specifically hybridizes with, a nucleic
CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and	CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC	inhibits the expression of TGF-beta 2. The invention further relates to:	CC	inhibits the expression of TGF-beta 2. The invention further relates to:
CC	a compound 8-80 nucleobases in length that specifically hybridizes with	CC	a compound 8-80 nucleobases in length that specifically hybridizes with
CC	at least an 8-nucleobase portion of an active site on a nucleic acid	CC	at least an 8-nucleobase portion of an active site on a nucleic acid
CC	molecule encoding TGF-beta 2; a composition comprising the compound and a	CC	molecule encoding TGF-beta 2; a composition comprising the compound and a
CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or	CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC	tissues by contacting the cells or tissues with the compound so that	CC	tissues by contacting the cells or tissues with the compound so that
CC	expression of TGF-beta 2 is inhibited; treating an animal having a	CC	expression of TGF-beta 2 is inhibited; treating an animal having a
CC	disease or condition associated with TGF-beta 2 by administering to the	CC	disease or condition associated with TGF-beta 2 by administering to the
CC	animal a therapeutic or prophylactic amount of the compound so that	CC	animal a therapeutic or prophylactic amount of the compound so that
CC	expression of TGF-beta 2 is inhibited; and screening an antisense	CC	expression of TGF-beta 2 is inhibited; and screening an antisense
CC	compound. The antisense compound has cytostatic, neutropic,	CC	compound. The antisense compound has cytostatic, neutropic,
CC	neuroprotective, and immunosuppressive activities. The compound,	CC	neuroprotective, and immunosuppressive activities. The compound,
CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.	CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC	cancer, a neurodegenerative disorder, or a disease or condition involving	CC	cancer, a neurodegenerative disorder, or a disease or condition involving
CC	hyperactivation of an immune response. This polynucleotide sequence	CC	hyperactivation of an immune response. This polynucleotide sequence
XX	represents an antisense oligonucleotide of the invention.	XX	represents an antisense oligonucleotide of the invention.

Query Match 0.5%; Score 20; DB 1; Length 20;

QY	1015	GTTCGGACCGTTGCATTT	1034
Db	1	GTTCGGACCGTTGCATTT	20
RESULT 104			
ID	AD180228		
ID	AD180228	standard; DNA; 20 BP.	
XX	AC		
XX	AD180228;		
XX	DT		
XX	22-APR-2004	(first entry)	
XX	DE		
XX	Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 229.		
XX	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;		
KW	cytostatic; nontropic; neuroprotective; immunosuppressive;		
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;		
KW	immune; ss; mouse; murine.		
XX	XX		
XX	Mus musculus.		
OS	XX		
XX	US2004006030-A1.		
PN	08-JAN-2004.		
PD	XX		
XX	02-JUL-2002; 2002US-00189267.		
PF	XX		
PR	02-JUL-2002; 2002US-00189267.		
XX	(ISIS-) ISIS PHARM INC.		
PA	XX		
XX	Monia BP, Freier SM, Dobie KW;		
PI	XX		
XX	WPI; 2004-081742/08.		
DR	XX		
XX	New compounds, particularly antisense oligonucleotides targeted to a		
PT	nucleic acid encoding TGF-beta 2, useful for treating cancer, a		
PT	neurodegenerative disorder, or a disease involving hyperactivation of		
PT	immune response.		
XX	XX		
PS	Example 16; SEQ ID NO 229; 135pp; English.		
XX	XX		
CC	The invention relates to a novel antisense compound of 8-80 nucleobases		
CC	in length targeted to, and which specifically hybridizes with, a nucleic		
CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and		
CC	inhibits the expression of TGF-beta 2. The invention further relates to a		
CC	compound 8-80 nucleobases in length that specifically hybridizes with		
CC	at least an 8-nucleobase portion of an active site on a nucleic acid		
CC	molecule encoding TGF-beta 2; a composition comprising the compound and a		
CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or		
CC	tissues by contacting the cells or tissues with the compound so that		
CC	expression of TGF-beta 2 is inhibited; treating an animal having a		
CC	disease or condition associated with TGF-beta 2 by administering to the		
CC	animal a therapeutic or prophylactic amount of the compound so that		
CC	expression of TGF-beta 2 is inhibited; and screening an antisense		
CC	compound. The antisense compound has cytostatic, nontropic,		
CC	neuroprotective, and immunosuppressive activities. The compound,		
CC	composition and methods are useful for treating a disease or condition		
CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.		
CC	cancer, a neurodegenerative disorder, or a disease or condition involving		
CC	hyperactivation of an immune response. This polynucleotide sequence		
CC	represents a preferred target DNA region of TGF-beta 2 of the invention.		
XX	XX		
XX	Sequence 20 BP; 5 A; 3 C; 3 G; 9 T; 0 U; 0 Other;		
XX	XX		
QY	1138	CTGAGAAATTAAGTTTCTT	1157
Query Match 0.5%; Score 20; DB 1; Length 20;			
Best Local Similarity 100.0%; Pred. No. 54;			
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0			

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RESULT 105
ADI80118/c
ID ADI80118 standard; DNA; 20 BP.
XX AC
XX ADI80118;
XX AC
XX 22-APR-2004 (first entry)
XX DT
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 119.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS
XX Mus musculus.
XX PN
XX US2004006030-A1.
XX PD
XX 08-JAN-2004.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS
XX Example 16; SEQ ID NO 119; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 7 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1580 TTCTACAGACCCCTACTTCA 1599
DB 20 TTCTACAGACCCCTACTTCA 1
RESULT 106
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```
ADI80131/c
ID ADI80131 standard; DNA; 20 BP.
XX AC
XX ADI80131;
XX DT
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 132.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS
XX Mus musculus.
XX PN
XX US2004006030-A1.
XX PD
XX 08-JAN-2004.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS
XX Example 16; SEQ ID NO 132; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2142 TGCCTTAGAATGTCAGGA 2161
DB 20 TGCCTTAGAATGTCAGGA 1
RESULT 107
ADI80137/c
ID ADI80137 standard; DNA; 20 BP.
XX
```



```
AC ADI80137;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 138.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosatic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX
XX Mus musculus.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 16; SEQ ID NO 138; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2226 GAACCCAAAGGGTACAATGC 2245
XX |||||
XX 20 GAACCCAAAGGGTACAATGC 1
XX
XX RESULT 108
XX ADI80157/c
XX ID ADI80157 standard; DNA; 20 BP.
XX
XX AC ADI80157;
XX
XX 22-APR-2004 (first entry)
XX
```

```
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 158.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosatic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX
XX Mus musculus.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 16; SEQ ID NO 158; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3642 GCTGGCCAGTACCTTTGAAT 3661
XX |||||
XX 20 GCTGGCCAGTACCTTTGAAT 1
XX
XX RESULT 109
XX ADI80274
XX ID ADI80274 standard; DNA; 20 BP.
XX
XX AC ADI80274;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 275.
XX
```

KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; nontropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PP 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 XX
 DR New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 275; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, nontropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3520 CATGTAATGCTAGATCTTA 3539
 DB 1 CATGTAATGCTAGATCTTA 20
 RESULT 110
 ADI80114/c
 ID ADI80114 standard; DNA; 20 BP.
 XX
 AC ADI80114;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 115.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; nontropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.

KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PP 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 XX
 DR New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 115; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, nontropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1515 GCCAAGGAGGTTTATAAAT 1534
 DB 20 GCCAAGGAGGTTTATAAAT 1
 RESULT 111
 ADI80116/c
 ID ADI80116 standard; DNA; 20 BP.
 XX
 AC ADI80116;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 117.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; nontropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.

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XX US2004006030-A1.
PN
XX
XX
PD 08-JAN-2004.
XX
XX
XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX 02-JUL-2002; 2002US-00189267.
PA (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 117; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTCCGAAATGCCATCCCG 1574
Db |||||||||||||||||||
20 CTCCGAAATGCCATCCCG 1

RESULT 112
ADI80124/c
ID ADI80124 standard; DNA; 20 BP.
XX
XX AC ADI80124;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 125.
DE
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
PN
XX
XX 02-JUL-2002; 2002US-00189267.
PF
XX

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PD 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 125; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 TGCAGGTATTGATGGCACCT 1986
Db |||||||||||||||||||
20 TGCAGGTATTGATGGCACCT 1

RESULT 113
ADI80149/c
ID ADI80149 standard; DNA; 20 BP.
XX
XX AC ADI80149;
XX
XX 22-APR-2004 (first entry)
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 150.
DE
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
PN
XX
XX 08-JAN-2004.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PF

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XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
PA Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 150; 135pp; English.
PS
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3049 AACTCATGGATGGCTTAAG 3068
DB 20 AACTCATGGATGGCTTAAG 1
RESULT 114
ADI80158/c
ID ADI80158 standard; DNA; 20 BP.
XX
XX ADI80158;
XX 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 159.
DE
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 159.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX

PA (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 159; 135pp; English.
PS
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3673 ATTTTGACTTGCACTACAAA 3692
DB 20 ATTTTGACTTGCACTACAAA 1
RESULT 115
ADI80160/c
ID ADI80160 standard; DNA; 20 BP.
XX
XX ADI80160;
XX 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 161.
DE
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 161.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX

PT immune response.
XX Example 16; SEQ ID NO 234; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1321 AGAGGATCGAGGCATCCGC 1340
DB 1 AGAGGATCGAGGCATCCGC 20
RESULT 118
ADI80247
ID ADI80247 standard; DNA; 20 BP.
XX
AC ADI80247;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 248.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 248; 135pp; English.

XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1593 TACTTCAGAAATCGTCGCTT 1612
DB 1 TACTTCAGAAATCGTCGCTT 20
RESULT 119
ADI80103/c
ID ADI80103 standard; DNA; 20 BP.
XX
AC ADI80103;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 104.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 104; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1239 ACCTTTTGTCTCTGCATCT 1258
 DB 20 ACCTTTTGTCTCTGCATCT 1

RESULT 120
 ADI80104/C
 ID ADI80104 standard; DNA; 20 BP.
 XX
 AC ADI80104;
 XX
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 105.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX

Example 16; SEQ ID NO 105; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1269 GCGCTCAGTCTGTCTACCTG 1288
 DB 20 GCGCTCAGTCTGTCTACCTG 1

RESULT 121
 ADI80110/C
 ID ADI80110 standard; DNA; 20 BP.
 XX
 AC ADI80110;
 XX
 DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 111.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 111; 135pp; English.
 XX

The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCATCTACAAC 1433
 DB 20 AGGTGATTTCCATCTACAAC 1

RESULT 122
 ADI80120/c
 ID ADI80120 standard; DNA; 20 BP.

XX AC ADI80120;
 XX DT 22-APR-2004 (first entry)

DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 121.
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.

OS Mus musculus.
 XX US2004006030-A1.

XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.
 XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.

PS Example 16; SEQ ID NO 121; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TACTTCAGAAATCGTCGCTT 1612
 DB 20 TACTTCAGAAATCGTCGCTT 1

RESULT 123
 ADI80154/c
 ID ADI80154 standard; DNA; 20 BP.

XX AC ADI80154;
 XX DT 22-APR-2004 (first entry)

XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 155.
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.

OS Mus musculus.
 XX US2004006030-A1.

XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.
 XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.

PS Example 16; SEQ ID NO 155; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3505 ACAGTAACACTTACATGT 3524
|||||
Db 20 ACAGTAACACTTACATGT 1

RESULT 124
ADI80189
ID ADI80189 standard; DNA; 20 BP.
XX
XX
AC ADI80189;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 190.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.
XX
PS Example 16; SEQ ID NO 190; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that disease or condition associated with TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents a preferred target DNA region of TGF-beta 2 of the invention.

CC cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GGAGGTGATTCCNCTCTACA 1431
|||||
Db 1 GGAGGTGATTCCNCTCTACA 20

RESULT 125
ADI80229
ID ADI80229 standard; DNA; 20 BP.
XX
XX
AC ADI80229;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 230.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.
XX
PS Example 16; SEQ ID NO 230; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that disease or condition associated with TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents a preferred target DNA region of TGF-beta 2 of the invention.

XX SQ Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match
Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1209 TTTAAACATGCTACTG 1228
Db 1 TTTAAACATGCTACTG 20

RESULT 126
ADI80235
ID ADI80235 standard; DNA; 20 BP.
AC ADI80235;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 236.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer. a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 236; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match
Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 CCCGGAAGACTATCCGAGC 1395
Db 1 CCCGGAAGACTATCCGAGC 20

RESULT 127
ADI80261
ID ADI80261 standard; DNA; 20 BP.
XX
AC ADI80261;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 262.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 262; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2349	CCTTGCTGTGTGTCACGGA 2368	
DB	1	CCTTGCTGTGTGTCACGGA 20	
RESULT 128			
AD180046/c			
ID	AD180046	standard; DNA; 20 BP.	
XX	AC	AD180046;	
XX	DT	22-APR-2004 (first entry)	
XX	DE	Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 47.	
XX	KW	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;	
XX	KW	cytostatic; neurotropic; neuroprotective; immunosuppressive;	
XX	KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;	
XX	OS	immune; ss; human.	
XX	OS	Homo sapiens.	
XX	PN	US2004006030-A1.	
XX	PD	08-JAN-2004.	
XX	PF	02-JUL-2002; 2002US-00189267.	
XX	PR	02-JUL-2002; 2002US-00189267.	
XX	PA	(ISIS-) ISIS PHARM INC.	
XX	PI	Monia BP, Freier SM, Dobie KW;	
XX	DR	WPI; 2004-081742/08.	
XX	PT	New compounds, particularly antisense oligonucleotides targeted to a	
XX	PT	nucleic acid encoding TGF-beta 2, useful for treating cancer, a	
XX	PT	neurodegenerative disorder, or a disease involving hyperactivation of	
XX	PT	immune response.	
XX	PS	Example 15; SEQ ID NO 47; 135pp; English.	
XX	CC	The invention relates to a novel antisense compound of 8-80 nucleobases	
XX	CC	in length targeted to, and which specifically hybridizes with, a nucleic	
XX	CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and	
XX	CC	inhibits the expression of TGF-beta 2. The invention further relates to:	
XX	CC	a compound 8-80 nucleobases in length that specifically hybridizes with	
XX	CC	at least an 8-nucleobase portion of an active site on a nucleic acid	
XX	CC	molecule encoding TGF-beta 2; a composition comprising the compound and a	
XX	CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or	
XX	CC	tissues by contacting the cells or tissues with the compound so that	
XX	CC	expression of TGF-beta 2 is inhibited; treating an animal having a	
XX	CC	disease or condition associated with TGF-beta 2 by administering to the	
XX	CC	animal a therapeutic or prophylactic amount of the compound so that	
XX	CC	disease or condition associated with TGF-beta 2 is inhibited; and screening an antisense	
XX	CC	compound. The antisense compound has cytostatic, neurotropic,	
XX	CC	neuroprotective, and immunosuppressive activities. The compound,	
XX	CC	composition and methods are useful for treating a disease or condition	
XX	CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.	
XX	CC	cancer, a neurodegenerative disorder, or a disease or condition involving	
XX	CC	hyperactivation of an immune response. This polynucleotide sequence	
XX	CC	represents an antisense oligonucleotide of the invention.	
XX	SQ	Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;	
		Query Match 0.5%; Score 20; DB 1; Length 20;	
		Best Local Similarity 100.0%; Pred. No. 54;	
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1412	GGAGGTGATTCCATCTACA 1431	
DB	20	CCAGTGGTGATCAGAAAAC 1	
QY	1996	CCAGTGGTGATCAGAAAAC 2015	
DB	20	CCAGTGGTGATCAGAAAAC 1	
		Query Match 0.5%; Score 20; DB 1; Length 20;	
		Best Local Similarity 100.0%; Pred. No. 54;	
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		Query Match 0.5%; Score 20; DB 1; Length 20;	
		Best Local Similarity 100.0%; Pred. No. 54;	
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

RESULT 130	XX	AD180151;	XX	AD180151;
AD180138/c	XX	AC	XX	AC
ID AD180138 standard; DNA; 20 BP.	XX	DT	XX	DT
XX	XX	22-APR-2004 (first entry)	XX	22-APR-2004 (first entry)
AC AD180138;	XX	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 139.	XX	Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 152.
DE	XX	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;	XX	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
DE	XX	cytostatic; neurotropic; neuroprotective; immunosuppressive;	XX	cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW	XX	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;	XX	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW	XX	immune; ss; mouse; murine.	XX	immune; ss; mouse; murine.
OS	XX	Mus musculus.	XX	Mus musculus.
XX	XX	US2004006030-A1.	XX	US2004006030-A1.
PN	XX	08-JAN-2004.	XX	08-JAN-2004.
XX	XX	02-JUL-2002; 2002US-00189267.	XX	02-JUL-2002; 2002US-00189267.
PF	XX	02-JUL-2002; 2002US-00189267.	XX	02-JUL-2002; 2002US-00189267.
XX	XX	(ISIS-) ISIS PHARM INC.	XX	(ISIS-) ISIS PHARM INC.
PR	XX	Monia BP, Freier SM, Dobie KW;	XX	Monia BP, Freier SM, Dobie KW;
XX	XX	WPI; 2004-081742/08.	XX	WPI; 2004-081742/08.
PI	XX	New compounds, particularly antisense oligonucleotides targeted to a	XX	New compounds, particularly antisense oligonucleotides targeted to a
XX	XX	nucleic acid encoding TGF-beta 2, useful for treating cancer, a	XX	nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT	XX	neurodegenerative disorder, or a disease involving hyperactivation of	XX	neurodegenerative disorder, or a disease involving hyperactivation of
PT	XX	immune response.	XX	immune response.
PS	XX	Example 16; SEQ ID NO 139; 135pp; English.	XX	Example 16; SEQ ID NO 152; 135pp; English.
CC	XX	The invention relates to a novel antisense compound of 8-80 nucleobases	XX	The invention relates to a novel antisense compound of 8-80 nucleobases
CC	XX	in length targeted to, and which specifically hybridizes with, a nucleic	XX	in length targeted to, and which specifically hybridizes with, a nucleic
CC	XX	acid molecule encoding transforming growth factor (TGF)-beta 2, and	XX	acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC	XX	inhibits the expression of TGF-beta 2. The invention further relates to:	XX	inhibits the expression of TGF-beta 2. The invention further relates to:
CC	XX	a compound 8-80 nucleobases in length that specifically hybridizes with	XX	a compound 8-80 nucleobases in length that specifically hybridizes with
CC	XX	at least an 8-nucleobase portion of an active site on a nucleic acid	XX	at least an 8-nucleobase portion of an active site on a nucleic acid
CC	XX	molecule encoding TGF-beta 2; a composition comprising the compound and a	XX	molecule encoding TGF-beta 2; a composition comprising the compound and a
CC	XX	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or	XX	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC	XX	tissues by contacting the cells or tissues with the compound so that	XX	tissues by contacting the cells or tissues with the compound so that
CC	XX	expression of TGF-beta 2 is inhibited; treating an animal having a	XX	expression of TGF-beta 2 is inhibited; treating an animal having a
CC	XX	disease or condition associated with TGF-beta 2 by administering to the	XX	disease or condition associated with TGF-beta 2 by administering to the
CC	XX	animal a therapeutic or prophylactic amount of the compound so that	XX	animal a therapeutic or prophylactic amount of the compound so that
CC	XX	expression of TGF-beta 2 is inhibited; and screening an antisense	XX	expression of TGF-beta 2 is inhibited; and screening an antisense
CC	XX	compound. The antisense compound has cytostatic, neurotropic,	XX	compound. The antisense compound has cytostatic, neurotropic,
CC	XX	neuroprotective, and immunosuppressive activities. The compound,	XX	neuroprotective, and immunosuppressive activities. The compound,
CC	XX	composition and methods are useful for treating a disease or condition	XX	composition and methods are useful for treating a disease or condition
CC	XX	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.	XX	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC	XX	cancer, a neurodegenerative disorder, or a disease or condition involving	XX	cancer, a neurodegenerative disorder, or a disease or condition involving
CC	XX	hyperactivation of an immune response. This polynucleotide sequence	XX	hyperactivation of an immune response. This polynucleotide sequence
CC	XX	represents an antisense oligonucleotide of the invention.	XX	represents an antisense oligonucleotide of the invention.
XX	XX	Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;	XX	Sequence 20 BP; 7 A; 6 C; 1 G; 6 T; 0 U; 0 Other;
SQ	XX	Query Match 0.5%; Score 20; DB 1; Length 20;	SQ	Query Match 0.5%; Score 20; DB 1; Length 20;
	XX	Best Local Similarity 100.0%; Pred. No. 54;		Best Local Similarity 100.0%; Pred. No. 54;
	XX	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2238	TACATGCTAACTCTGTGC 2257	QY	3122 GTGAGTTGTTATAGGACTAA 3141
DB	20	TACATGCTAACTCTGTGC 1	DB	20 GTGAGTTGTTATAGGACTAA 1
RESULT 131	XX	AD180151/c	XX	AD180151/c
ID AD180151 standard; DNA; 20 BP.	XX	AD180151	XX	AD180237
AD180151/c	XX	AD180151	XX	AD180237
ID AD180151 standard; DNA; 20 BP.	XX	AD180151	XX	AD180237

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DT 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 238.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosstatic; neutropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 238; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neutropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1414 AGGTGATTTCCTACCTCAAC 1433
DB 1 AGGTGATTTCCTACCTCAAC 20
RESULT 133
ADI80248
ID ADI80248 standard; DNA; 20 BP.
XX AC ADI80248;
XX AC ADI80248;
XX 22-APR-2004 (first entry)
DT Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 249.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosstatic; neutropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 238; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neutropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
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XX Query Match 0.5%; Score 20; DB 1; Length 20;
KW Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1854 CACAAAGACAGAACCTGGG 1873
DB 1 CACAAAGACAGAACCTGGG 20
RESULT 134
ADI80256
ID ADI80256 standard; DNA; 20 BP.
XX AC ADI80256;
XX AC ADI80256;
XX 22-APR-2004 (first entry)
DT Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 257.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosstatic; neutropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 249; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neutropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 8 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
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KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
OS Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 257; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2169 TGCCTTCGCCCTTTACAT 2188
Db 1 TGCCTTCGCCCTTTACAT 20
RESULT 135
AD180260
ID AD180260 standard; DNA; 20 BP.
XX AC AD180260;
XX 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 261.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX

OS Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 261; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2238 TACAATGCTTAACCTCTGTGC 2257
Db 1 TACAATGCTTAACCTCTGTGC 20
RESULT 136
AD180262
ID AD180262 standard; DNA; 20 BP.
XX AC AD180262;
XX 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 263.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX US2004006030-A1.

XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PR 02-JUL-2002; 2002US-00189267.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Freier SM, Dobie KW;
 XX DR WPI; 2004-081742/08.
 XX PT New compounds, particularly antisense oligonucleotides targeted to a
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of
 XX PT immune response.
 XX PS Example 16; SEQ ID NO 263; 135pp; English.
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2444 GTCTGTAATGAGCTAAA 2463
 DB 1 GTCTGTAATGAGCTAAA 20
 RESULT 137
 ADI80265
 ID ADI80265 standard; DNA; 20 BP.
 XX AC ADI80265;
 XX DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 266.
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX OS Mus musculus.
 XX PN US2004006030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PR 02-JUL-2002; 2002US-00189267.

PF 02-JUL-2002; 2002US-00189267.
 XX 02-JUL-2002; 2002US-00189267.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Freier SM, Dobie KW;
 XX DR WPI; 2004-081742/08.
 XX PT New compounds, particularly antisense oligonucleotides targeted to a
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of
 XX PT immune response.
 XX PS Example 16; SEQ ID NO 266; 135pp; English.
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX SQ Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2635 GTTCTGTTTGTAAACTGG 2654
 DB 1 GTTCTGTTTGTAAACTGG 20
 RESULT 138
 ADI80272
 ID ADI80272 standard; DNA; 20 BP.
 XX AC ADI80272;
 XX DT 22-APR-2004 (first entry)
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 273.
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 XX OS Mus musculus.
 XX PN US2004006030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PR 02-JUL-2002; 2002US-00189267.

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XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 273; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3505 ACAGTAACACTTTACATGT 3524
Db 1 ACAGTAACACTTTACATGT 20
RESULT 139
AD180097/c
ID AD180097 standard; DNA; 20 BP.
XX AC AD180097;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 98.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 273; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3505 ACAGTAACACTTTACATGT 3524
Db 1 ACAGTAACACTTTACATGT 20
RESULT 140
AD180102/c
ID AD180102 standard; DNA; 20 BP.
XX AC AD180102;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 103.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 98; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 9 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1094 CTTTCGAAAAGTTTCGTATT 1113
Db 20 CTTTCGAAAAGTTTCGTATT 1
RESULT 140
AD180102/c
ID AD180102 standard; DNA; 20 BP.
XX AC AD180102;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 103.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
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XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 103; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1218 ATGCACTACTGTGCTGTGAG 1237
DB 20 ATGCACTACTGTGCTGTGAG 1
RESULT 141
ADI80115/c
ID ADI80115 standard; DNA; 20 BP.
XX AC ADI80115;
XX DT 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 116.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX OS US2004006030-A1.
XX PN 08-JAN-2004.
XX PD 02-JUL-2002; 2002US-00189267.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.

PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 116; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 TTTATAAAATCGACATGCCG 1544
DB 20 TTTATAAAATCGACATGCCG 1
RESULT 142
ADI80123/c
ID ADI80123 standard; DNA; 20 BP.
XX AC ADI80123;
XX DT 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 124.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX OS US2004006030-A1.
XX PN 08-JAN-2004.
XX PD 02-JUL-2002; 2002US-00189267.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.

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PS Example 16; SEQ ID NO 124; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1962 AGATTTCAGGTATTCATGG 1981
DB 20 AGATTTCAGGTATTCATGG 1

RESULT 143
ADI80145/c
ID ADI80145 standard; DNA; 20 BP.
XX
AC ADI80145;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 146.
DE
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 146; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTTGTTAAACTGGCATCT 2659
DB 20 GTTTGTTAAACTGGCATCT 1

RESULT 144
ADI80161/c
ID ADI80161 standard; DNA; 20 BP.
XX
AC ADI80161;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 162.
DE
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 162; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:

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CC a compound e-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.,
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 7 C; 1 G; 6 T; 0 U; 0 Other;

CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC	tissues by contacting the cells or tissues with the compound so that
CC	expression of TGF-beta 2 is inhibited; treating an animal having a
CC	disease or condition associated with TGF-beta 2 by administering to the
CC	animal a therapeutic or prophylactic amount of the compound so that
CC	expression of TGF-beta 2 is inhibited; and screening an antisense
CC	compound. The antisense compound has cytostatic, nontropic,
CC	neuroprotective, and immunosuppressive activities. The compound,
CC	composition and methods are useful for treating a disease or condition
CC	associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC	cancer, a neurodegenerative disorder, or a disease or condition involving
CC	hyperactivation of an immune response. This polynucleotide sequence
CC	represents a preferred target DNA region of TGF-beta 2 of the invention.
XX	
SQ	Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
	Query Match 0.5%; Score 20; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 54;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1877 TAAATAAGTTTACACTGCC 1896
Db	1 TAAATAAGTTTACACTGCC 20
RESULT 146	
ADI80258	
ID	ADI80258 standard; DNA; 20 BP.
XX	
AC	ADI80258;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 259.
XX	
KW	antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW	cytostatic; nontropic; neuroprotective; immunosuppressive;
KW	hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW	immune; ss; mouse; murine.
OS	Mus musculus.
XX	
PN	US2004006030-A1.
XX	
PD	08-JAN-2004.
XX	
PJ	02-JUL-2002; 2002US-00189267.
PF	
PR	02-JUL-2002; 2002US-00189267.
XX	(ISIS-) ISIS PHARM INC.
PA	
PI	Monia BP, Freier SM, Dobie KW;
XX	
DR	WPI; 2004-081742/08.
XX	
PT	New compounds, particularly antisense oligonucleotides targeted to a
PT	nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT	neurodegenerative disorder, or a disease involving hyperactivation of
PT	immune response.
XX	
PS	Example 16; SEQ ID NO 259; 135pp; English.
XX	
CC	The invention relates to a novel antisense compound of 8-80 nucleobases
CC	in length targeted to, and which specifically hybridizes with, a nucleic
CC	acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC	inhibits the expression of TGF-beta 2. The invention further relates to:
CC	a compound 8-80 nucleobases in length that specifically hybridizes with
CC	at least an 8-nucleobase portion of an active site on a nucleic acid
CC	molecule encoding TGF-beta 2; a composition comprising the compound and a
CC	carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC	tissues by contacting the cells or tissues with the compound so that
CC	expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TGGATCCATGAACCCAAAGG 2236
 |||||
 DB 1 TGGATCCATGAACCCAAAGG 20

RESULT 147

AD180121/c
 ID AD180121 standard; DNA; 20 BP.

XX AC AD180121;

XX DT 22-APR-2004 (first entry)

XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 122.

XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 XX KW immune; ss; mouse; murine.

XX OS Mus musculus.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX DR WPI; 2004-081742/08.

XX PT New compounds, particularly antisense oligonucleotides targeted to a
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of
 XX PT immune response.

XX PS Example 16; SEQ ID NO 122; 135pp; English.

XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 1 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1854 CACAAAGACAGGAACCTGGG 1873

DB 20 CACAAAGACAGGAACCTGGG 1

RESULT 148

AD180183
 ID AD180183 standard; DNA; 20 BP.

XX AC AD180183;

XX DT 22-APR-2004 (first entry)

XX DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 184.

XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

XX KW immune; ss; human.

XX OS Homo sapiens.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX DR WPI; 2004-081742/08.

XX PT New compounds, particularly antisense oligonucleotides targeted to a
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of
 XX PT immune response.

XX PS Example 16; SEQ ID NO 184; 135pp; English.

XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 CCGCGGCGAGATCCTGAGCA 1356
1 CCGCGGCGAGATCCTGAGCA 20

Db

RESULT 149
ADI80236
ID ADI80236 standard; DNA; 20 BP.
XX
AC ADI80236;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 237.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 237; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence

CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CCGGAGGTGATTTCCATCT 1428
1 CCGGAGGTGATTTCCATCT 20

Db

RESULT 150
ADI80250
ID ADI80250 standard; DNA; 20 BP.
XX
AC ADI80250;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 251.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 251; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

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Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1967 TGCAGGTATTGATGGCACCT 1986
Db 1 TGCAGGTATTGATGGCACCT 20

RESULT 151
ADI80266
ID ADI80266 standard; DNA; 20 BP.
XX AC
XX AC
XX ADI80266;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 267.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosatic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 267; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3512 CTACTTACATGTAATGTGT 3531
```

Db 1 C T A C T T T A C A T G T A A T G T G T 20
|||||

RESULT 153
ADI80275
ID ADI80275 standard; DNA; 20 BP.
XX AC ADI80275;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 276.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 276; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3642 GCTGGCCAGTACCTTTGAAT 3661
|||||
Db 1 GCTGGCCAGTACCTTTGAAT 20

RESULT 154
ADI80276
ID ADI80276 standard; DNA; 20 BP.
XX AC ADI80276;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 277.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 277; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4245 CTTTGCGGCTGATTAAAAA 4264
|||||
Db 1 CTTTGCGGCTGATTAAAAA 20

RESULT 155
ADI80108/c

```

ID ADI80108 standard; DNA; 20 BP.
XX AC
XX ADI80108;
XX DT
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 109.
XX KW
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX KW
XX Mus musculus.
XX OS
XX US2004006030-A1.
XX PN
XX 08-JAN-2004.
XX PD
XX 02-JUL-2002; 2002US-00189267.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Monia BP, Freier SM, Dobie KW;
XX PI
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX PS
XX Example 16; SEQ ID NO 109; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX SQ
XX Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1376 CCGGAAGACTATCCGAGC 1395
DB 20 CCGGAAGACTATCCGAGC 1
XX
RESULT 156
ADI80113/c
ID ADI80113 standard; DNA; 20 BP.
XX AC
XX ADI80113;
XX DT
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 109.
XX KW
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX KW
XX Mus musculus.
XX OS
XX US2004006030-A1.
XX PN
XX 08-JAN-2004.
XX PD
XX 02-JUL-2002; 2002US-00189267.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Monia BP, Freier SM, Dobie KW;
XX PI
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX PS
XX Example 16; SEQ ID NO 109; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX SQ
XX Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1376 CCGGAAGACTATCCGAGC 1395
DB 20 CCGGAAGACTATCCGAGC 1
XX
RESULT 156
ADI80113/c
ID ADI80113 standard; DNA; 20 BP.
XX AC
XX ADI80113;
XX DT
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 114.
XX KW
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX KW
XX Mus musculus.
XX OS
XX US2004006030-A1.
XX PN
XX 08-JAN-2004.
XX PD
XX 02-JUL-2002; 2002US-00189267.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Monia BP, Freier SM, Dobie KW;
XX PI
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX PS
XX Example 16; SEQ ID NO 114; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX SQ
XX Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1507 AGTACTACGCCAAGAGGTT 1526
DB 20 AGTACTACGCCAAGAGGTT 1
XX
RESULT 157
ADI80155/c
ID ADI80155 standard; DNA; 20 BP.
XX AC
XX ADI80155;
XX DT
XX 22-APR-2004 (first entry)
XX DE
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DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 156.
 XX antisense; transforming growth factor; TGF-beta 2; TGF-beta 2;
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 OS
 XX Mus musculus.
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 156; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 9 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3512 CTACTTTACATGTAATGTGT 3531
 DB 20 CTACTTTACATGTAATGTGT 1
 RESULT 158
 ADI80227
 ID ADI80227 standard; DNA; 20 BP.
 AC
 XX ADI80227;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 228.
 KW antisense; transforming growth factor; TGF-beta 2; TGF-beta 2;
 XX antisense; transforming growth factor; TGF-beta 2; TGF-beta 2;
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.

KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.
 OS
 XX Mus musculus.
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 DR
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 228; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1133 CCGCTCTGAGAATTACTAGT 1152
 DB 1 CCGCTCTGAGAATTACTAGT 20
 RESULT 159
 ADI80267
 ID ADI80267 standard; DNA; 20 BP.
 AC
 XX ADI80267;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 268.
 KW antisense; transforming growth factor; TGF-beta 2; TGF-beta 2;
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; mouse; murine.

XX OS Mus musculus.
 XX PN US2004006030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PR 02-JUL-2002; 2002US-00189267.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Freier SM, Dobie KW;
 XX DR WPI; 2004-081742/08.
 XX PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX Example 16; SEQ ID NO 268; 135pp; English.
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX SQ Sequence 20 BP; 7 A; 2 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2970 TGTGTTACTATATAATGAAC 2989
 Db 1 TGTGTTACTATATAATGAAC 20
 RESULT 160
 AAQ41618
 ID AAQ41618 standard; cDNA; 21 BP.
 AC AAQ41618;
 XX 25-MAR-2003 (revised)
 DT 26-AUG-1993 (first entry)
 XX TGF-beta2 sense strand (nucleotides 111-131) PCR primer.
 XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;
 KW cancer treatment; bone repair; growth regulation;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 OS

PN EP542679-A1.
 XX 19-MAY-1993.
 XX PF 03-NOV-1992; 92EP-00810845.
 XX PR 11-NOV-1991; 91EP-00810870.
 XX PA (CIBA) CIBA GEIGY AG.
 XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
 XX DR WPI; 1993-161126/20.
 XX PT New hybrid transforming growth factor-beta molecules - comprise portions
 PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,
 PT antiinflammatory and immunosuppressive agents etc.
 XX Example 1; Page 36; 48pp; English.
 XX CC The invention covers hybrid TGF-beta molecules consisting of parts of the
 CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600
 CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-
 CC beta polypeptides were constructed from the appropriate, PCR-amplified
 CC segments of the wild-type isoforms. For the construction of hybrid DNA
 CC molecules encoding TGF-beta hybrids all having the hinge points between
 CC amino acids 44 and 45, the primers AAQ41614-Q41619 (corresp. to the hinge
 CC regions) were used with the appropriate primers (see AAQ41608-Q41613)
 CC which flank the regions coding for each of the three full-length mature
 CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 78;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2234 AGGGTACAAATGCTAACTTCTG 2254
 Db 1 AGGGTACAAATGCCAACTTCTG 21
 RESULT 161
 AAQ41619/c
 ID AAQ41619 standard; cDNA; 21 BP.
 AC AAQ41619;
 XX 25-MAR-2003 (revised)
 DT 26-AUG-1993 (first entry)
 XX TGF-beta2 antisense strand (nucleotides 111-131) PCR primer.
 XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;
 KW cancer treatment; bone repair; growth regulation;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 OS EP542679-A1.
 XX 19-MAY-1993.
 XX PF 03-NOV-1992; 92EP-00810845.
 XX PR 11-NOV-1991; 91EP-00810870.
 XX PA (CIBA) CIBA GEIGY AG.
 XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
 XX DR WPI; 1993-161126/20.

XX New hybrid transforming growth factor-beta molecules - comprise portions
 PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,
 PT antiinflammatory and immunosuppressive agents etc.
 XX
 PS Example 1; Page 37; 48pp; English.
 XX
 CC The invention covers hybrid TGF-beta molecules consisting of parts of the
 CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600
 CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-
 CC beta polypeptides were constructed from the appropriate, PCR-amplified
 CC segments of the wild-type isoforms. For the construction of hybrid DNA
 CC molecules encoding TGF-beta hybrids all having the hinge points between
 CC amino acids 44 and 45, the primers AAQ41614-Q41619 (corresp. to the hinge
 CC regions) were used with the appropriate primers (see AAQ41608-Q41613)
 CC which flank the regions coding for each of the three full-length mature
 CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 78;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2234 AGGTACAATGCTAACTTCTG 2254
 |||||
 DB 21 AGGTACAATGCCAATTCTG 1

RESULT 162
 ADM92728/C
 ID ADM92728 standard; DNA; 21 BP.
 XX
 AC ADM92728;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE SNP-containing cardiovascular associated gene primer #58.
 XX
 KW SNP; single nucleotide polymorphism; cardiovascular associated gene;
 KW allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;
 KW restenosis; arterial inflammation; myocardial infarction; stroke; primer;
 KW ss.
 XX Homo sapiens.
 XX
 PN WO2003057911-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 07-JAN-2003; 2003WO-EP000060.
 XX
 PR 08-JAN-2002; 2002EP-00000153.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Stropp U, Schwes S, Kallabis H;
 XX
 DR WPI; 2003-577532/54.
 XX
 CC New isolated polynucleotides comprising single nucleotide polymorphisms
 PT of the cardiovascular gene, useful for assessing predisposition or
 PT susceptibility to a cardiovascular disease, e.g. atherosclerosis,
 PT restenosis or stroke.
 XX
 PS Disclosure; Page 68; 187pp; English.
 XX
 CC The invention relates an isolated polynucleotide (I) encoded by a
 CC cardiovascular associated (CA) gene, having allelic variation contained
 CC in a functional surrounding like full length cDNA for CA gene
 CC polypeptide, and with or without the CA gene promoter sequence. (I) is a
 CC polynucleotide comprising single nucleotide polymorphisms predicting

CC cardiovascular disease. The polynucleotides are useful for assessing
 CC predisposition or susceptibility to a cardiovascular disease, e.g.
 CC atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial
 CC inflammation, myocardial infarction, and stroke. These may also be used
 CC to predict personal medication schemes omitting adverse drug reactions,
 CC or as probes for detecting genetic polymorphisms and as templates for the
 CC recombinant production of normal or variant peptides/polypeptides encoded
 CC by the genes. This sequence corresponds to a PCR primer to amplify one of
 CC the genes of the invention.

SQ Sequence 21 BP; 10 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 78;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3283 GTAAATGGTTCTTTCACGTT 3303
 |||||
 DB 21 GTAAATGGTTCTTTCACGTT 1

RESULT 163
 AAX59725
 ID AAX59725 standard; DNA; 24 BP.
 XX
 AC AAX59725;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE DNA target used for the modified oligodeoxyribonucleotides.
 XX
 KW Oligodeoxyribonucleotide; intersubunit linkage;
 KW phosphoramidate intersubunit; antisense activity; nuclease resistant;
 KW in-vitro cell growth inhibition assay; infection;
 KW smooth muscle cell proliferation disorder; inflammatory process;
 KW genetic disorder; cancer; ss.

OS Synthetic.

PN WO9525814-A1.

PD 28-SEP-1995.

PF 20-MAR-1995; 95WO-US003575.

PR 18-MAR-1994; 94US-00210505.

PR 18-MAR-1994; 94US-00214599.

PA (LYNX-) LYNX THERAPEUTICS INC.

PI Gryaznov SM, Schultz RG, Chen J;

PI WPI; 1995-344627/44.

PT Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance
 PT toward phosphodiesterase digestion, and form stable duplexes with DNA and
 PT RNA strands.

PS Disclosure; Page 61; 101pp; English.

XX The specification describes oligodeoxyribonucleotides having contiguous
 CC nucleoside subunits joined by intersubunit linkages, where at least 3
 CC contiguous subunits are joined by phosphoramidate intersubunits. The
 CC oligodeoxyribonucleotides has a sequence of nucleoside subunits effective
 CC to form a duplex with a target nucleic acid molecule. The
 CC oligodeoxyribonucleotides are more resistant to nuclease digestion and
 CC have improved RNA and dsDNA hybridisation characteristics, relative to
 CC oligonucleotides not containing N3'-P5' phosphoramidate linkages. They
 CC also have excellent antisense activity against complementary mRNA targets
 CC in in-vitro cell growth inhibition assays. They also exhibit low
 CC cytotoxicity. They may be used in diagnostic and therapeutic
 CC applications, e.g., in combatting infections agents such as bacteria,
 CC viruses, etc. or in treatment of smooth muscle cell proliferation

This sequence represents a synthetic polyguanosine tract PCR primer #22, used with primer #21 (AAZ19841) to generate a vector to the substitute a polyguanosine tract for the plastid atpB gene 3' untranslated region (3' UTR). This vector was then used in the generation of transgenic plants which can inducibly express a trehalose biosynthetic enzyme in a plastid. Trehalose is a disaccharide (a-D-glucopyranosyl-[1,1]-a-D-glucopyranoside) commonly found in organisms such as bacteria, fungi and insects which acts as a protectant against the deleterious effects of various stresses such as heat, desiccation and the deleterious effects of biosynthesis requires two enzymic activities; a trehalose-6-phosphate synthase catalyses the condensation of UDP-glucose and glucose-6-phosphate to trehalose-6-phosphate; and a trehalase-6-phosphate phosphatase phosphorylates trehalose-6-phosphate to trehalose. Previous attempts have been made to express trehalase biosynthetic enzymes in plants; however, certain deleterious effects appear to be associated with constitutive trehalase production in the cytosol, particularly when expression occurs in root tissue or during early development. These adverse effects include stunted growth, abnormal leaves and undeveloped roots. The use of an inducible promoter prevents these effects. Transformation with constructs containing trehalase biosynthetic enzymes under the control of an inducible promoter can provide plants protected against drought, high salinity, osmotic stress and temperature extremes. They can also be used for increasing the storage properties of plants,

RESULT 166
AAD21596
ID AAD21596 standard; DNA; 24 BP.
XX
AC AAD21596;
XX
DT 28-JAN-2002 (first entry)
XX
DE Kinase oligo #2 to construct pAT222 vector using polyguanosine tract.
XX
KW Transgenic plant; antibacterial; immunosuppressive; virucide; therapy;
KW antiparasitic; allergy; autoimmune disease; immune response; PCR primer;
KW transplantation; ss.
XX
OS Unidentified.
XX
FN WO200177353-A2.
XX
PD 18-OCT-2001.
XX
PF 03-APR-2001; 2001WO-BP003788.
XX
PR 05-APR-2000; 2000US-00543619.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Heifetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;
XX
DR WPI; 2001-657175/75.
XX
PT Novel plant useful for treating or preventing allergy, comprising a DNA
PT molecule encoding a mature ragweed pollen allergen in its plasmid genome
PT and capable of expressing the pollen allergen.
XX
PS Example 10; Page 47; 99pp; English.
XX
CC The invention relates to a transgenic plant comprising in its plasmid
CC genome a DNA molecule encoding a mature ragweed pollen allergen, which is
CC capable of expressing the pollen allergen. The plant or plant matter
CC derived from the transgenic plant such as tobacco, tomato, soybean, rice
CC or maize is useful for treating or preventing an allergy. The plant is
CC also useful as a pharmaceutical and as a medical food. The plant is
CC useful for suppressing and reducing undesired immune response, and
CC production of an antigen for determination of immunological activity. The
CC plant is useful for treating and preventing bacterial, parasitic and
CC viral diseases, allergies, autoimmune diseases and transplantations. The
CC present sequence is an oligonucleotide used for constructing pAT222
CC vector using polyguanosine tract as a substitute for 3' UTR
XX
SQ Sequence 24 BP; 2 A; 19 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 968 AGATTCCCCCCCCACCCGCCCA 991
DB 1 AGCTTCCCCCCCCCCCCCCCCCA 24
RESULT 167
ADD29304
ID ADD29304 standard; DNA; 24 BP.
XX
AC ADD29304;
XX
DT 15-JAN-2004 (first entry)
XX
DE Molecular and biological process inhibiting oligonucleotide seq id 67.
XX
KW molecular process inhibition; monomeric unit;

KW oligonucleotide interaction; polynucleotide interaction;
KW enzyme interaction; local interaction; ss.
XX
OS Synthetic.
XX
FN US6548251-B1.
XX
PD 15-APR-2003.
XX
PF 05-SEP-2000; 2000US-00655804.
XX
PR 05-SEP-2000; 2000US-00655804.
XX
PA (FIDE-) FIDELITY SYSTEMS INC.
XX
PI Kozyavkin SA, Malykh AG, Polouchine NN, Slesarev AI;
XX
DR WPI; 2003-786284/74.
XX
PT Inhibiting nucleic acid hybridization and/or extension in a sample
PT comprises administering to the sample a modified oligonucleotide or
PT polynucleotide that contains at least one monomeric unit.
XX
PS Disclosure; SEQ ID NO 67; 38pp; English.
XX
CC The invention describes a method of inhibiting a molecular process
CC involving the interaction between nucleic acids in a sample capable of
CC undergoing the molecular process. The method comprises administering to
CC the sample an oligonucleotide or polynucleotide that contains at least
CC one monomeric unit having a specific formula. The method is useful in
CC inhibiting undesired molecular interaction between oligonucleotides and
CC their complexes with polynucleotides and enzymes, including local
CC interactions between their chemical units (nucleotides or amino acids).
CC This sequence represents an oligonucleotide used to inhibit undesired
CC molecular interaction between oligonucleotides and their complexes with
XX polynucleotides and enzymes.
XX
SQ Sequence 24 BP; 11 A; 3 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2730 CAAAGAGAAACATCTTTTTTTT 2753
DB 1 CAAAAAAAACACCTTTTTTTT 24
RESULT 168
ADH34300
ID ADH34300 standard; DNA; 24 BP.
XX
AC ADH34300;
XX
DT 11-MAR-2004 (first entry)
XX
DE Hairpin oligonucleotide.
XX
KW Nucleoside analogue; oligonucleotide synthesis; antisense therapy;
KW antigen method; hairpin oligonucleotide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT stem_loop 1..24
FT /*tag= a
XX
PN WO2003068795-A1.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-JF001485.
XX

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PR 13-FEB-2002; 2002JP-00035706.
XX (IMAN/) IMANISHI T.
PA Imanishi T, Obika S;
PI WPI; 2003-689651/65.
XX New nucleoside analogs for producing oligonucleotide analogs useful e.g.
PT as antisense compounds.
XX Example 2; Page 48; 74pp; Japanese.
CC The invention relates to nucleoside analogues and their salts. The
CC invention also encompasses oligonucleotides and their salts comprising at
CC least one nucleoside analogue of the invention. The nucleoside analogues
CC are produced by reducing an nucleoside azide derivative and optionally
CC further interconverting, or by reacting a nucleoside derivative with
CC formaldehyde and optionally deprotecting and/or interconverting. The
CC nucleoside analogues can be used for producing oligonucleotides useful
CC as antisense compounds and in antisense methods. The present sequence
CC represents a hairpin oligonucleotide used in an example of the invention.
XX
XX Sequence 24 BP; 10 A; 4 C; 0 G; 10 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2731 AAAAAGAAAACATCTTTTTTTT 2754
DB 1 AAAAAAAAAACCCCTTTTTTTTTT 24

RESULT 169
ADH63059
ID ADH63059 standard; DNA; 24 BP.
XX AC
XX ADH63059;
XX 25-MAR-2004 (first entry)
XX Murine fibroblast growth factor receptor 2 probe, SEQ ID 13.
XX Cytostatic; Vulnary; Gene Therapy; Antisense;
XX fibroblast growth factor receptor 2; FGF receptor 2;
XX hyperproliferative disorder; cancer; developmental disorder;
XX wound healing; murine; probe; ss.
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Labelled with FAM"
FT modified_base 24
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Labelled with FAM"
XX
XX WO2003024987-A1.
XX
XX 27-MAR-2003.
XX
XX 12-SEP-2002; 2002WO-US029149.
XX
XX 14-SEP-2001; 2001US-00954556.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Cooper SR;
XX

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DR WPI; 2003-354582/33.
XX New antisense oligonucleotides for modulating expression of genes
PT encoding fibroblast growth factor receptor 2, useful for treating
PT hyperproliferative (e.g. cancer of the colon, lung, breast or skin) or
PT developmental disorders.
XX Example 13; SEQ ID NO 13; 200pp; English.
XX The present invention relates to antisense oligonucleotides (ADH63077-
CC ADH63154) targeted to fibroblast growth factor (FGF) receptor 2 coding
CC sequences (ADH63049 and ADH63056), which specifically hybridize with and
CC inhibit FGF receptor 2 expression. The antisense oligonucleotides are
CC useful for treating or preventing diseases or conditions associated with
CC FGF receptor 2 in an animal, e.g. hyperproliferative disorders
CC (particularly cancer of the colon, lung, breast or skin), or
CC developmental disorders. The antisense compound may also be used in wound
CC healing. The antisense compounds are useful for diagnostics,
CC therapeutics, prophylaxis, or as research reagents or kits. ADH63059 is a
CC probe for FGF receptor 2 coding sequence.
XX
XX Sequence 24 BP; 5 A; 13 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2927 CTTCCCGTCCTTCTCTCAAGCT 2950
DB 1 CCACACCGTCCTCATCTCCAAGCT 24

RESULT 170
AAC88273
ID AAC88273 standard; DNA; 25 BP.
XX AC
XX AAC88273;
XX 02-MAR-2001 (first entry)
XX SCDNA102 DNA sequence.
XX Drug binding site; viscosity; biomolecule interaction; drug target;
XX electronic transducer; primer; ds.
XX Synthetic.
XX WO200068419-A2.
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-CA000504.
XX 05-MAY-1999; 99CA-02271179.
XX (SENS-) SENSORCHEM INT CORP.
XX McGovern M, Thompson M;
XX WPI; 2001-024875/03.
XX
XX Monitoring/detecting small molecule-biomolecule interactions for drug
PT screening involves contacting a solution of small molecules with
PT immobilized biomolecules and measuring the frequency generated with an
PT acoustic wave device.
XX Example 4; Fig 5; 44pp; English.
XX The present invention describes a device and method for monitoring small
CC molecule-biomolecule interactions. These involve the measurement of the
CC oscillation of a liquid when in contact with the biomolecule only
CC compared with the small molecule-biomolecule complex. This uses a
CC piezoelectric device and can be used with biomolecules such as DNA. The

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CC present sequence was used as an example. The device can be used to screen
 CC for drug candidates, to determine the conditions in which small molecules
 CC will not bind to given biomolecules and to obtain information on the
 CC tertiary structure of biomolecules

XX Sequence 25 BP; 0 A; 13 C; 12 G; 0 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 19.2; DB 1; Length 25;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 615 GCGGCGCGCGCGCGCGCGCGCGAC 638
 DB 1 GCGGCGCGCGCGCGCGCGCGCGCGCGCGC 24

RESULT 171
 AAV48956/c
 ID AAV48956 standard; DNA; 19 BP.
 XX AC AAV48956;
 XX DT 15-OCT-1998 (first entry)
 XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-27.
 XX KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 XX modulate; gene expression; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN EP856579-A1.
 XX PD 05-AUG-1998.
 XX PF 31-JAN-1997; 97EP-00101531.
 XX PR 31-JAN-1997; 97EP-00101531.
 XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX PI Schlingensiepen K, Brysch W;
 XX WPI; 1998-400910/35.
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX Claim 10; Fig 8a; 286pp; English.

XX AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for

CC stimulating the immune system
 XX Sequence 19 BP; 5 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2149 GAAATGTGCAGGATAATTG 2167
 DB 19 GAAATGTGCAGGATAATTG 1

RESULT 172
 AAZ65459/c
 ID AAZ65459 standard; DNA; 19 BP.
 XX AC AAZ65459;
 XX DT 30-MAR-2000 (first entry)
 XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-19.
 XX KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 XX prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 XX glomerulonephritis; acute respiratory distress syndrome; ss;
 XX atherosclerosis.
 XX OS Unidentified.
 XX OS WO9963975-A2.
 XX PN 16-DEC-1999.
 XX PD 10-JUN-1999; 99WO-EP004013.
 XX PF 10-JUN-1999; 98EP-00110709.
 XX PR 25-JUL-1998; 98EP-00113974.
 XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX PI Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX WPI; 2000-097470/08.
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX

Query Match 0.4%; Score 19; DB 1; Length 19;

CC specific and efficacious small double-stranded oligonucleotides (SDSO),
 CC antisense oligonucleotide molecules or short interfering RNA (siRNA)
 CC (comprising identifying a special pattern that can be localised in any
 CC position of an oligonucleotide sequence evaluating the specificity of a
 CC selected sequence). The short interfering RNA (siRNA) are targeted
 CC against genes involved in viral infection, malignant tumours, genetic and
 CC metabolic diseases. The methods are useful for designing and selecting
 CC short double-stranded oligonucleotides as a gene drug that can
 CC specifically inactivate a group of corresponding genes. The composition
 CC may be used for treating diseases or disorders associated with abnormal
 CC expression of genes in cells or tissues of humans or animals, such as
 CC viral infections, cancer, or genetic or metabolic diseases. The present
 CC sequence is a target region for an SDSO from an human CDNA.
 XX
 SQ Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1338 CGCGGCGAGATCTCTGAGCA 1356
 Db 1 CGCGGCGAGATCTCTGAGCA 19
 |||||

RESULT 175
 ADI80213
 ID ADI80213 standard; DNA; 20 BP.
 XX
 AC ADI80213;
 DT 22-APR-2004 (first entry)
 XX
 DE Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 214.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytosolic; nontropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004006030-A1.
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 16; SEQ ID NO 214; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, nontropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1354 GCAAGCTGAAGCTCACCAG 1372
 Db 1 GCAAGCTGAAGCTCACCAG 19
 |||||

RESULT 176
 ADI80073/C
 ID ADI80073 standard; DNA; 20 BP.
 XX
 AC ADI80073;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID NO 74.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytosolic; nontropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004006030-A1.
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 PS Example 15; SEQ ID NO 74; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, nootropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.

XX
SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 GCAAGCTGAAGCTCACCG 1372
|||||
DB 20 GCAAGCTGAAGCTCACCG 2

RESULT 177
AAV48947/c
ID AAV48947 standard; DNA; 20 BP.
XX
AC AAV48947;
XX
DT 15-OCT-1998 (first entry)
XX
DE TGF-beta2 antisense oligonucleotide TGF-beta2-18.

KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
KW modulate; gene expression; ss.

XX Synthetic.
OS Homo sapiens.
XX
XN EP856579-A1.
XX
PD 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen K, Brysch W;
XX WPI; 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of residues
PT able to form two or three hydrogen bonds, have greater activity and
PT reduced toxicity, used therapeutically or to modulate growth of cells in
PT culture.

PS Claim 10; Fig 8a; 286pp; English.
XX
XX AAV48930-49007 represent antisense oligonucleotides directed against
XX transforming growth factor-beta2 (TGF-beta2). Of these, only
XX oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
XX beta 2 protein expression, while oligonucleotides AAV48968-49007 had
XX little effect. The oligonucleotides exemplify the invention. The
XX specification describes oligonucleotides that contain 8-30 nucleotides,
XX which contain at most 8 nucleotides that can each form three hydrogen
XX bonds to cytosine; do not contain four consecutive nucleotides able to
XX form three H-bonds each to four consecutive cytosines; do not contain two
XX sequences of three consecutive nucleotides each able to form three H-
XX bonds to three consecutive cytosines, and the ratio between residues able
XX to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of
XX genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
XX beta 2 to control proliferation of primary cell cultures (e.g. bone
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or

CC keratinocytes). The oligonucleotides can also be used to analyse function
CC of proteins (by altering their expression or activity) and
CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
CC stimulating the immune system

XX
SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1853 CCACAAAGACAGGAACCTGG 1872
|||||
DB 20 CCATAAAGACAGGAACCTGG 1

RESULT 178
ABA91534
ID ABA91534 standard; DNA; 20 BP.
XX
AC ABA91534;
XX
DT 23-APR-2002 (first entry)
XX
DE DNA oligonucleotide AGT02022 used to test RNase H cleavage.

KW Nucleic acid detection; probe; mismatch; ss.

OS Synthetic.

XX
FH Key Location/Qualifiers
FT misc_feature 12 /tag= a
FT /note= "mismatch to target DNA"
FT misc_feature 13 /tag= b
FT /note= "mismatch to target DNA"

XX WO200206531-A2.

XX 24-JAN-2002.

XX 12-JUL-2001; 2001WO-US022166.

XX 14-JUL-2000; 2000US-00616761.

XX 30-MAR-2001; 2001US-00823647.

XX (GENE-) APPLIED GENE TECHNOLOGIES INC.

XX Dattagupta N;

XX WPI; 2002-171819/22.

PT Probes for detecting target nucleotide sequence in sample, has sequence
PT that forms hairpin structure having a double-stranded segment and single-
PT stranded loop collectively forming region complementary to target
PT sequence.

XX Example 5; Page 50; 72pp; English.

XX The present sequence is that of oligonucleotide AGT02022, which contains
XX a single mismatch with a target DNA oligonucleotide (see ABA91531). It is
XX one of a set of oligonucleotides (see ABA91532-37) containing
XX mismatch(es) to the target DNA that were tested in a hybridisation/RNase
XX H cleavage assay. The results showed that 2 mismatches between the target
XX and the probe ablated RNase H cleavage. The invention provides probes for
XX nucleic acid hybridisation. The probes form a hairpin structure
XX comprising a double-stranded stem and a single-stranded loop, and are
XX capable of both intramolecular and intermolecular hybridisation. The
XX double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that
XX is resistant to RNase H cleavage. When the probe hybridises with a target
XX DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H
XX treatment and can be removed. Arrays and methods for nucleic acid

CC hybridisation using the probes are provided

XX Sequence 20 BP; 16 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

SQ Query Match 0.4%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 98;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGGAGAAAA 2599

|||||

1 AAAAAAAATTGGAGAAAA 20

RESULT 179

ADI80077/C

ID ADI80077 standard; DNA; 20 BP.

XX AC ADI80077;

XX DT 22-APR-2004 (first entry)

DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 78.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytotatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; human.

XX OS Homo sapiens.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 15; SEQ ID NO 78; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

XX represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 98;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2240 CAATGCTAACTCTGTGCTG 2259

|||||

20 CAATGCCAACTCTGTGCTG 1

RESULT 180

ADI80049/C

ID ADI80049 standard; DNA; 20 BP.

XX AC ADI80049;

XX DT 22-APR-2004 (first entry)

DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 50.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytotatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; human.

XX OS Homo sapiens.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 15; SEQ ID NO 50; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

XX represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 7 A; 5 C; 2 G; 6 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.4%; Score 18.4; DB 1; Length 20;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2187 ATTGATTTTAAGAGGATCT 2206
    ||||| ||||| ||||| |||||
Db 20 ATTGATTTCAAGAGGATCT 1
    ||||| ||||| ||||| |||||

RESULT 181
ADI80199
ID ADI80199 standard; DNA; 20 BP.
XX
AC ADI80199;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 200.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 200; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
    Query Match 0.4%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 98;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1310 GTTATGCGCAGAGGATCG 1329
    ||||| ||||| ||||| |||||
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Db 1 GTTCATGCCGACAGGATCG 20
    ||||| ||||| ||||| |||||

RESULT 182
ADI80075/c
ID ADI80075 standard; DNA; 20 BP.
XX
AC ADI80075;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID NO 76.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 15; SEQ ID NO 76; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 2 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
    Query Match 0.4%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 98;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1851 CACCACAAAGACAGGAACCT 1870
    ||||| ||||| ||||| |||||
Db 20 CACCATAAAGACAGGAACCT 1
    ||||| ||||| ||||| |||||
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RESULT 183
ADI80215
ID ADI80215 standard; DNA; 20 BP.
XX
AC
XX ADI80215;
XX
AC ADI80215;
XX
DT 22-APR-2004 (first entry)
XX
DE
XX Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 216.
XX
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US200406030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 216; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound, the antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2240 CAATGCTAACTTCTGTGCTG 2259
Db 1 CAATGCCAACTTCTGTGCTG 20
RESULT 184
ADI80191
ID ADI80191 standard; DNA; 20 BP.
XX
AC
XX ADI80191;
XX
DT 22-APR-2004 (first entry)
XX
DE
XX Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 192.
XX
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US200406030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 192; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound, the antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 9 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2224 ATGACCCCAAGGGTACAAT 2243
Db 1 ACGACCCCAAGGGTACAAT 20
RESULT 185
ADI80041/C
ID ADI80041 standard; DNA; 20 BP.
XX
AC ADI80041;
```

XX
DT 22-APR-2004 (first entry)
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 42.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 15; SEQ ID NO 42; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2442 AGCTCTTGAATGCGAGCTA 2461
DB 20 AGCTCTTGAATGCGAGCTA 1

RESULT 186
ADI80179
ID ADI80179 standard; DNA; 20 BP.
XX
AC ADI80179;
XX
DT 22-APR-2004 (first entry)
XX

DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 180.
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 180; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACTCTGCAGCACCCTCGA 1300
DB 1 TCTACTCTGCAGCACCCTCGA 20

RESULT 187
ADI80030/c
ID ADI80030 standard; DNA; 20 BP.
XX
AC ADI80030;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 31.
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 OS Homo sapiens.
 XX US2004006030-A1.
 PN 08-JAN-2004.
 PD 02-JUL-2002; 2002US-00189267.
 PF 02-JUL-2002; 2002US-00189267.
 PR 02-JUL-2002; 2002US-00189267.
 XX (ISIS-) ISIS PHARM INC.
 PA Monia BP, Freier SM, Dobie KW;
 PI WPI; 2004-081742/08.
 DR New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 PS Example 15; SEQ ID NO 31; 135pp; English.
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 PS in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 98;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1281 TCTACTCTGACGACCTCGA 1300
 DB 20 TCTACTCTGACGACCTCGA 1
 RESULT 188
 ADI80056/c
 ID ADI80056 standard; DNA; 20 BP.
 XX ADI80056;
 AC ADI80056;
 XX 22-APR-2004 (first entry)
 DT Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 57.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.

XX Homo sapiens.
 OS US2004006030-A1.
 PN 08-JAN-2004.
 PD 02-JUL-2002; 2002US-00189267.
 PF 02-JUL-2002; 2002US-00189267.
 PR 02-JUL-2002; 2002US-00189267.
 XX (ISIS-) ISIS PHARM INC.
 PA Monia BP, Freier SM, Dobie KW;
 PI WPI; 2004-081742/08.
 DR New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 PS Example 15; SEQ ID NO 57; 135pp; English.
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 PS in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 98;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1310 GTTTATGCGCAAGAGGATCG 1329
 DB 20 GTTATGCGCAAGAGGATCG 1
 RESULT 189
 ADI80192
 ID ADI80192 standard; DNA; 20 BP.
 XX ADI80192;
 AC ADI80192;
 XX 22-APR-2004 (first entry)
 DT Human transforming growth factor-beta 2 target DNA region, SEQ ID No 193.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX Homo sapiens.
 OS

PN US2004006030-A1.
 XX 08-JAN-2004.
 PD
 XX 02-JUL-2002; 2002US-00189267.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 PI
 XX New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of
 XX PT immune response.
 XX
 XX Example 16; SEQ ID NO 193; 135pp; English.
 PS
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 XX Sequence 20 BP; 6 A; 2 C; 5 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 98;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2187 ATTGATTTTAAGAGGGATCT 2206
 Db 1 ATTGATTTCAAGAGGGATCT 20
 RESULT 190
 ADI80038/c
 ID ADI80038 standard; DNA; 20 BP.
 XX
 AC ADI80038;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 39.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 XX cytosstatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.

XX 02-JUL-2002; 2002US-00189267.
 PF
 XX 02-JUL-2002; 2002US-00189267.
 XX
 PR (ISIS-) ISIS PHARM INC.
 PA
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 PI
 XX New compounds, particularly antisense oligonucleotides targeted to a
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of
 XX PT immune response.
 XX
 XX Example 15; SEQ ID NO 39; 135pp; English.
 PS
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 XX Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 98;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1419 ATTTCATCTACACAGTAC 1438
 Db 20 ATTTCATCTACACAGCAC 1
 RESULT 191
 ADI80048/c
 ID ADI80048 standard; DNA; 20 BP.
 XX
 AC ADI80048;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 49.
 XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 XX cytosstatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX


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PR 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 15; SEQ ID NO 49; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 2 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2224 ATGAACCCAAAGGTTCAAT 2243
Db | | | | | | | | | | | | | | | | | | | | | |
20 ACGAACCCAAAGGTTCAAT 1
RESULT 192
AD023091
ID ADO23091 standard; cDNA; 20 BP.
XX
XX ADO23091;
AC
XX 01-JUL-2004 (first entry)
DE
DE Human transforming growth factor beta 2 SDO target region #2.
XX
XX Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
XX viral infection; malignant tumour; genetic disease; metabolic disease;
XX gene chip; protein chip; microarray; gene drug; Dermogene; Lungene;
XX Hepatogene; Leukogene; Lymphogene; Prostagene; Breastogene;
XX Brainumogene; Skin-whitogene; short interfering RNA; siRNA; cancer;
XX RNA interference.
XX
XX Homo sapiens.
OS
XX US2004072769-A1.
PN
XX 15-APR-2004.
PD
XX 16-SEP-2002; 2002US-00016490.
PF
XX 16-SEP-2002; 2002US-00016490.
PR
```

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XX (YINJ/) YIN J Q.
PA
XX Yin JQ;
PI
XX WPI; 2004-355427/33.
XX
XX Designing and selecting short double-stranded oligonucleotides for
PT treating viral infections, cancer and genetic or metabolic diseases,
PT comprises using gene chip and protein chip microarrays to identify
PT specific DNA sequences.
XX
XX Example 1; Page 18; 58pp; English.
XX
XX The invention relates to screening, identifying or predicting, and
CC assembling 19-25 nt double-stranded oligonucleotides (termed short double
CC stranded oligonucleotides, SDO) as active pharmaceutical compositions and
CC for the treatment of viral infections, malignant tumours, and genetic and
CC metabolic diseases, comprising screening and identifying a specific DNA
CC sequence in an abnormal gene encoding a protein with gene chip and
CC protein chip microarrays. The above method comprises screening the
CC disease-causing genes, over-expressing in cells and/or tissues, with the
CC gene chip and protein chip microarrays, identifying a specific DNA
CC sequence within the abnormal gene encoding a protein or playing other
CC biological roles with the assistance of computer and specific software,
CC predicting efficacious 19-25 nt double-stranded oligonucleotides with a
CC 5'-AU(T)CCG-3' or 5'-U(T)CCG-3' special pattern complementary to at
CC least a portion of an RNA molecule and making sure that selected sequence
CC is not localised within the stem-loop of target mRNA with any related
CC software. Also included are pharmaceutical compositions of gene drugs
CC (such as Dermogene, Lungene, Hepatogene, Leukogene, Lymphogene,
CC Prostagene, Breastogene, Brainumogene and Skin-whitogene including but
CC being not limited to part or all of the following components: single or a
CC group of specific 19-25 nt dsRNA, 19-25 nt sRNA-cDNA, 19-25 nt dsRNA
CC and/or single-stranded RNA and/or DNA with the special pattern, 5'-
CC CCGAT(U)-3' or its derivatives, one or more nucleic acid condensation
CC agents (or none), one or more pharmaceutical carriers, one or more
CC specific cell-targeting proteins and other active agents and selecting a
CC material) and a simplified method for predicting and selecting a
CC specific and efficacious small double-stranded oligonucleotides (SDSO),
CC antisense oligonucleotide molecules or short interfering RNA (siRNA)
CC (comprising identifying a special pattern that can be localised in any
CC position of an oligonucleotide sequence evaluating the specificity of a
CC selected sequence). The Short interfering RNA (siRNA) are targeted
CC against genes involved in viral infection, malignant tumours, genetic and
CC metabolic diseases. The methods are useful for designing and selecting
CC short double-stranded oligonucleotides as a gene drug that can
CC specifically inactivate a group of corresponding genes. The composition
CC may be used for treating diseases or disorders associated with abnormal
CC expression of genes in cells or tissues of humans or animals, such as
CC viral infections, cancer, or genetic or metabolic diseases. The present
CC sequence is a target region for an SDO from an human cDNA.
XX
XX Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2418 GAACAGCTTTCCAAATATGAT 2437
Db | | | | | | | | | | | | | | | | | | | | | |
1 GAACAGCTTTCCAAATATGAT 20
RESULT 193
AAA80353
ID AAA80353 standard; DNA; 21 BP.
XX
XX AAA80353;
AC
XX 22-NOV-2000 (first entry)
DT
XX Human ASTH1I 5' region polymorphic site, SEQ ID NO:100 (a).
DE
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RESULT 195
AAQ78455/c
ID  AAQ78455 standard; DNA; 18 BP.
XX
XX  AAQ78455;
AC
XX
XX  25-MAR-2003 (revised)
DT  27-JUN-1995 (first entry)
DE
DE  TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
XX  Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW  angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW  carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW  immunosuppression; oligonucleotide; ss.
XX
XX  Synthetic.
OS
XX  WO9425588-A2.
PN
XX  10-NOV-1994.
PD
XX  29-APR-1994; 94WO-EP001362.
PF
XX  30-APR-1993; 93EP-00107089.
PR  13-MAY-1993; 93EP-00107849.
XX
XX  Synthetic.
OS
XX  WO9425588-A2.
PN
XX  10-NOV-1994.
PD
XX  29-APR-1994; 94WO-EP001362.
PF
XX  30-APR-1993; 93EP-00107089.
PR  13-MAY-1993; 93EP-00107849.
XX
XX  (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA
XX  Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI  Bogdahn U;
PI
XX  WPI; 1994-358266/44.
DR
XX  New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT  treating immunosuppression, tumours, etc.
PT
XX  Claim 6; Page 54; 74pp; English.
PS
XX  The antisense oligonucleotides are useful in the treatment of tumours in
CC  which expression of TGF-beta is of relevance for pathogenicity and/or
CC  inhibition of pathological angiogenesis. They are used especially for the
CC  treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC  the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC  hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC  and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC  of skin carcinogenesis, and treatment of oesophageal and gastric
CC  carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC  AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC  beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC  oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC  analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX  Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031
DB 18 CTATAAGTCCACTAGGA 1

RESULT 196
AAQ78418/c
ID  AAQ78418 standard; DNA; 18 BP.
XX
XX  AAQ78418;
AC
XX
XX  25-MAR-2003 (revised)
DT  27-JUN-1995 (first entry)
DE
DE  Reverse PCR primer for human transforming growth factor-beta 2 cDNA.
XX
XX  Human transforming growth factor-beta 2; TGF-beta3; oxygen tension;
KW  trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW  TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW  preeclampsia; pregnancy; choriocarcinoma; PCR primer; ss.
XX
XX  Synthetic.
OS
XX  Homo sapiens.
OS
XX

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DE
XX  TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
XX  Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW  angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW  carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW  immunosuppression; oligonucleotide; ss.
XX
XX  Synthetic.
OS
XX  WO9425588-A2.
PN
XX  10-NOV-1994.
PD
XX  29-APR-1994; 94WO-EP001362.
PF
XX  30-APR-1993; 93EP-00107089.
PR  13-MAY-1993; 93EP-00107849.
XX
XX  (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA
XX  Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI  Bogdahn U;
PI
XX  WPI; 1994-358266/44.
DR
XX  New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT  treating immunosuppression, tumours, etc.
PT
XX  Claim 6; Page 43; 74pp; English.
PS
XX  The antisense oligonucleotides are useful in the treatment of tumours in
CC  which expression of TGF-beta is of relevance for pathogenicity and/or
CC  inhibition of pathological angiogenesis. They are used especially for the
CC  treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC  the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC  hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC  and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC  of skin carcinogenesis, and treatment of oesophageal and gastric
CC  carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC  AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC  beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC  oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC  analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX  Sequence 18 BP; 6 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCATCTACA 1431
DB 18 AGGTGATTTCCATCTACA 1

RESULT 197
AAV63218/c
ID  AAV63218 standard; DNA; 18 BP.
XX
XX  AAV63218;
AC
XX
XX  14-JAN-1999 (first entry)
DT
XX
XX  Reverse PCR primer for human transforming growth factor-beta 2 cDNA.
DE
XX
XX  Human transforming growth factor-beta 2; TGF-beta3; oxygen tension;
KW  trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW  TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW  preeclampsia; pregnancy; choriocarcinoma; PCR primer; ss.
XX
XX  Synthetic.
OS
XX  Homo sapiens.
OS
XX

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PN WO9840747-A1.
 PD 17-SEP-1998.
 XX
 PF 05-MAR-1998; 98WO-CA000180.
 XX
 PR 07-MAR-1997; 97US-0039919P.
 XX
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 XX
 PI Caniggia I, Post M, Iye S;
 XX
 DR WPI; 1998-520837/44.
 XX
 XX Regulation of trophoblast invasion - by, e.g. transforming growth factor-
 PT beta3 inhibitor, useful for detecting or treating preeclampsia in
 PT pregnant women.
 XX
 PS Example 4; Page 21; 59pp; English.
 XX
 CC PCR primers AAV63217-18 were used to amplify cDNA encoding human
 CC transforming growth factor-beta 2 (TGF-beta2). The specification
 CC describes a composition for regulating trophoblast invasion which
 CC comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors,
 CC hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The
 CC composition is used in methods of diagnosing, monitoring, preventing or
 CC treating conditions requiring regulation of trophoblast invasion,
 CC especially preeclampsia in pregnant women or choriocarcinomas
 XX
 SQ Sequence 18 BP; 5 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1590 CCTACTTCAGATCGTC 1607
 Db 18 CCTACTTCAGATCGTC 1
 RESULT 198
 AAV48953/c
 ID AAV48953 standard; DNA; 18 BP.
 XX
 AC AAV48953;
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-24.
 XX
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN EP856579-A1.
 XX
 XX 05-AUG-1998.
 XX
 XX 31-JAN-1997; 97EP-00101531.
 PF
 XX 31-JAN-1997; 97EP-00101531.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA Schlingensiepen K, Brysch W;
 XX
 PI WPI; 1998-400910/35.
 XX
 DR Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT

PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 PS Claim 10; Fig 8a; 286pp; English.
 XX
 CC AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive cytosines, and the ratio between residues able
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, ERB-2, JunB, JunD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 18 BP; 3 A; 2 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.4%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2007 CAGAAACTATATAAGTCC 2024
 Db 18 CAGAAACTATATAAGTCC 1
 RESULT 199
 AAZ65457/c
 ID AAZ65457 standard; DNA; 18 BP.
 XX
 AC AAZ65457;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-17.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 OS
 XX WO9963975-A2.
 PN
 XX 16-DEC-1999.
 PD
 XX 10-JUN-1999; 99WO-EP004013.
 PF
 XX 10-JUN-1998; 98EP-00110709.
 PR
 XX 25-JUL-1998; 98EP-00113974.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX
 PI WPI; 2000-097470/08.
 DR
 XX Composition containing immune stimulant and inhibitor of agent that

PT adversely affects the immune response, for treating cancers and
 PT infections.

PS Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031

Db 18 CTATAAGTCCACTAGGA 1

RESULT 200

AAQ05124/C
 ID AAQ05124 standard; DNA; 20 BP.

AC AAQ05124;

XX 25-MAR-2003 (revised)

DT 02-NOV-1990 (first entry)

DE Probe used to screen cDNA library for human TGF-Beta2 precursor.

XX Human TGF-Beta2 precursor; cancer; tumorigenic; ss.

XX Synthetic.

PN EP376785-A.

XX 04-JUL-1990.

PF 14-DEC-1989; 89EP-00403480.

XX 16-DEC-1988; 88US-00285140.

PR 05-DEC-1989; 89US-00446020.

XX (ONCO) ONCOGEN LP.

XX Purchio AF, Madisen L, Webb N;

DR WPI; 1990-203127/27.

XX Cloning and expression of transforming growth factor beta 2 - used for
 PT treatment of tumours or for augmenting wound healing.

XX Example 6; Page 13; 58pp; English.

XX TGF-Beta2 may be used in treatment of tumors at effective doses, and may
 CC also be useful in augmenting wound healing by stimulating cell

CC proliferation. The growth factor can be produced at high levels from a
 CC CHO expression system. (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 20 BP; 3 A; 5 C; 3 G; 5 T; 0 U; 4 Other;

Query Match 0.4%; Score 18; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2211 TGGAAATGGATCCATGAAC 2230

Db 20 TGGAAATGGATCCATGAAC 1

RESULT 201

AAF97183/C

ID AAF97183 standard; DNA; 21 BP.

XX AAF97183;

XX 18-NOV-2004 (revised)

DT 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #1944.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

KW polymorphism; vascular disease; coronary artery disease; forensics;

KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

KW pulmonary embolism; paternity test; ds.

XX Homo sapiens.

OS Unidentified.

XX Key

FT Location/Qualifiers

FT Variation

FT /*tag= a

FT /standard_name= "Single nucleotide polymorphism"

XX WO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000WO-US024503.

XX 10-SEP-1999; 99US-0153357P.

PR 26-JUL-2000; 2000US-0220947P.

PR 16-AUG-2000; 2000US-0225724P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

PA (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.

XX Example; Page 180; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification

CC Revised record issued on 18-NOV-2004 : The variantion feature was
CC incorrectly given a captial V
XX Sequence 21 BP; 2 A; 7 C; 11 G; 1 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 588 CCGCGCGCTCGCAGGCTCG 608
DB 21 CCGCGGGCTCCCGAGGCTCG 1

RESULT 202
AAS17230
ID AAS17230 standard; DNA; 21 BP.
XX AC
XX AAS17230;
XX
DT 12-MAR-2002 (first entry)
XX
DE DNA sequence #3 from reusable P-chip streptavidin-ds-DNA construct.
XX
KW Reusable protein chip microarray; P-chip; streptavidin-ds-DNA construct;
KW Ab1-P-Ab2 sandwich; thermally decoupled linker; ss.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "Biotinylayted"
XX
XX WO200181924-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-US013025.
XX
PR 23-APR-2001; 2001WO-US013025.
XX
PA (BIOT-) BIOTRACES INC.
XX
PI Drukier AK;
XX
DR WPI; 2002-041425/05.
XX
PF Novel reusable protein chip useful for protein extraction, and protein
PT quantification, can quantitate proteins with very high sensitivity.
XX
PS Example; Page 52; 68pp; English.
XX
CC The present invention relates to a new reusable protein chip (P-chip)
CC microarray which can quantitate at least a few hundred proteins with a
CC sensitivity not less than 10 pg/ml. The invention is useful for
CC quantitating low abundance proteins and the P-chip is suitable for Ab1-P-
CC Ab2 sandwich format with sensitivity better than 100 fg/ml for a majority
CC of targets. The P-chip microarray of the invention is capable of
CC detecting low abundance proteins from physiologic fluids that exist in
CC concentrations smaller than 0.1 pg/ml. This superior sensitivity of P-
CC chips allows them to be low cost, reliable and reusable. The present
CC nucleic acid sequence forms a streptavidin-ds-DNA construct along with
CC DNA sequence #4 (AAS17231). This construct was used in the invention to
CC produce a reusable P-chip with a thermally decoupled linker
XX
SQ Sequence 21 BP; 0 A; 11 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CCGCGCGCGCACGACCGCGCGC 636
DB 1 CCGCGCGCGCGCGCGCGCGC 21

RESULT 203
AAS17230/C
ID AAS17230 standard; DNA; 21 BP.
XX AC
XX AAS17230;
XX
DT 12-MAR-2002 (first entry)
XX
DE DNA sequence #3 from reusable P-chip streptavidin-ds-DNA construct.
XX
KW Reusable protein chip microarray; P-chip; streptavidin-ds-DNA construct;
KW Ab1-P-Ab2 sandwich; thermally decoupled linker; ss.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "Biotinylayted"
XX
XX WO200181924-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-US013025.
XX
PR 23-APR-2001; 2001WO-US013025.
XX
PA (BIOT-) BIOTRACES INC.
XX
PI Drukier AK;
XX
DR WPI; 2002-041425/05.
XX
PF Novel reusable protein chip useful for protein extraction, and protein
PT quantification, can quantitate proteins with very high sensitivity.
XX
PS Example; Page 52; 68pp; English.
XX
CC The present invention relates to a new reusable protein chip (P-chip)
CC microarray which can quantitate at least a few hundred proteins with a
CC sensitivity not less than 10 pg/ml. The invention is useful for
CC quantitating low abundance proteins and the P-chip is suitable for Ab1-P-
CC Ab2 sandwich format with sensitivity better than 100 fg/ml for a majority
CC of targets. The P-chip microarray of the invention is capable of
CC detecting low abundance proteins from physiologic fluids that exist in
CC concentrations smaller than 0.1 pg/ml. This superior sensitivity of P-
CC chips allows them to be low cost, reliable and reusable. The present
CC nucleic acid sequence forms a streptavidin-ds-DNA construct along with
CC DNA sequence #4 (AAS17231). This construct was used in the invention to
CC produce a reusable P-chip with a thermally decoupled linker
XX
SQ Sequence 21 BP; 0 A; 11 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 CCGCGCGCGCACGACCGCGCGC 635
DB 21 CCGCGCGCGCGCGCGCGCGC 1

RESULT 204
AAV48945/C
ID AAV48945 standard; DNA; 19 BP.

```

XX AAV48945;
XX
XX 15-OCT-1998 (first entry)
XX
XX TGF-beta2 antisense oligonucleotide TGF-beta2-16.
XX
XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
XX modulate; gene expression; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX EP856579-A1.
XX
XX 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Brysch W;
XX
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX
XX Claim 10; Fig 8a; 286pp; English.
XX
XX AAV48930-49007 represent antisense oligonucleotides directed against
XX transforming growth factor-beta2 (TGF-beta2). Of these, only
XX oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
XX beta 2 protein expression, while oligonucleotides AAV48968-49007 had
XX little effect. The oligonucleotides exemplify the invention. The
XX specification describes oligonucleotides that contain 8-30 nucleotides,
XX which contain at most 8 nucleotides that can each form three hydrogen
XX bonds to cytosine; do not contain four consecutive nucleotides able to
XX form three H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of
XX genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
XX beta 2 to control proliferation of primary cell cultures (e.g. bone
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
XX keratinocytes). The oligonucleotides can also be used to analyse function
XX of proteins (by altering their expression or activity) and
XX therapeutically, e.g. in cases of cancer or (targeting TGF) for
XX stimulating the immune system
XX
XX Sequence 19 BP; 5 A; 1 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 17.4; DB 1; Length 19;
XX Best Local Similarity 94.7%; Pred. No. 1.2e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1738 CCAAAGACTTAACTCTCC 1756
XX ||||| ||||| ||||| |||||
XX Db 19 CCAAAGATTAACTCTCC 1
XX
XX RESULT 205
XX AAV48966/c
XX ID AAV48966 standard; DNA; 19 BP.
XX
XX AC AAV48966;
XX
XX

```

```

DT 15-OCT-1998 (first entry)
XX
XX TGF-beta2 antisense oligonucleotide TGF-beta2-37.
XX
XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
XX modulate; gene expression; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX EP856579-A1.
XX
XX 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Brysch W;
XX
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX
XX Claim 10; Fig 8a; 286pp; English.
XX
XX AAV48930-49007 represent antisense oligonucleotides directed against
XX transforming growth factor-beta2 (TGF-beta2). Of these, only
XX oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
XX beta 2 protein expression, while oligonucleotides AAV48968-49007 had
XX little effect. The oligonucleotides exemplify the invention. The
XX specification describes oligonucleotides that contain 8-30 nucleotides,
XX which contain at most 8 nucleotides that can each form three hydrogen
XX bonds to cytosine; do not contain four consecutive nucleotides able to
XX form three H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of
XX genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
XX beta 2 to control proliferation of primary cell cultures (e.g. bone
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
XX keratinocytes). The oligonucleotides can also be used to analyse function
XX of proteins (by altering their expression or activity) and
XX therapeutically, e.g. in cases of cancer or (targeting TGF) for
XX stimulating the immune system
XX
XX Sequence 19 BP; 7 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 17.4; DB 1; Length 19;
XX Best Local Similarity 94.7%; Pred. No. 1.2e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 2383 CCATTCCTCTATTACATTGG 2401
XX ||||| ||||| ||||| |||||
XX Db 19 CCATTCCTCTACTACATTGG 1
XX
XX RESULT 206
XX ADO23060
XX ID ADO23060 standard; cDNA; 19 BP.
XX
XX AC ADO23060;
XX
XX
XX 01-JUL-2004 (first entry)
XX
XX Human transforming growth factor beta 2 SDO target region #7.
XX

```

XX Human; ss; SDSO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;
KW gene chip; protein chip; microarray; gene drug; Dermogene; Lungene;
KW Hepatogene; Leukogene; Lymphogene; Prostogene; Breastogene;
KW Braintumogene; Skin-whitogene; short interfering RNA; siRNA; cancer;
KW RNA interference.
XX
XX Homo sapiens.
XX
XX US2004072769-A1.
XX
XX PD 15-APR-2004.
XX
XX PF 16-SEP-2002; 2002US-00016490.
XX
XX PR 16-SEP-2002; 2002US-00016490.
XX
XX PA (YINJ/) YIN J Q.
XX
XX PI Yin JQ;
XX
XX DR WPI; 2004-355427/33.
XX
XX PT Designing and selecting short double-stranded oligonucleotides for
PT treating viral infections, cancer and genetic or metabolic diseases,
PT comprises using gene chip and protein chip microarrays to identify
PT specific DNA sequences.
XX
XX Example 1; Page 18; 59pp; English.
XX
XX The invention relates to screening, identifying or predicting, and
XX assembling 19-25 nt double-stranded oligonucleotides (termed short double
XX stranded oligonucleotides, SDSO) as active pharmaceutical compositions
XX for the treatment of viral infections, malignant tumours, and genetic and
XX metabolic diseases, comprising screening and identifying a specific DNA
XX sequence in an abnormal gene encoding a protein with gene chip and
XX protein chip microarrays. The above method comprises screening the
XX disease-causing genes, over-expressing in cells and/or tissues, with the
XX gene chip and protein chip microarrays, identifying a specific DNA
XX sequence within the abnormal gene encoding a protein or playing other
XX biological roles with the assistance of computer and specific software,
XX predicting efficacious 19-25 nt double-stranded oligonucleotides with a
XX 5'-AU(T)CCG-3' or 5'-U(T)CCC-3', special pattern complementary to at
XX least a portion of an RNA molecule and making sure that selected sequence
XX is not localised within the stem-loop of target mRNA with any related
XX software. Also included are pharmaceutical compositions of gene drugs
XX (such as Dermogene, Lungene, Hepatogene, Leukogene, Lymphogene,
XX Prostogene, Breastogene, Braintumogene and Skin-whitogene including but
XX being not limited to part or all of the following components: single or a
XX group of specific 19-25 nt dsRNA, 19-25 nt sRNA-cDNA, 19-25 nt dsRNA
XX and/or single-stranded RNA and/or DNA with the special pattern, 5'-
XX CCGAT(U)-3' or its derivatives, one or more nucleic acid condensation
XX agents (or none), one or more pharmaceutical carriers, one or more
XX specific cell-targeting proteins and other active agents and additional
XX materials) and a simplified method for predicting and selecting a
XX specific and efficacious small double-stranded oligonucleotides (SDSO),
XX antisense oligonucleotide molecules or short interfering RNA (siRNA)
XX (comprising identifying a special pattern that can be localised in any
XX position of an oligonucleotide sequence evaluating the specificity of a
XX selected sequence). The short interfering RNA (siRNA) are targeted
XX against genes involved in viral infection, malignant tumours, genetic and
XX metabolic diseases. The methods are useful for designing and selecting
XX short double-stranded oligonucleotides as a gene drug that can
XX specifically inactivate a group of corresponding genes. The composition
XX may be used for treating diseases or disorders associated with abnormal
XX expression of genes in cells or tissues of humans or animals, such as
XX viral infections, cancer, or genetic or metabolic diseases. The present
XX sequence is a target region for an SDO from an human cDNA.
XX
XX Sequence 19 BP; 8 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 17.4; DB 1; Length 19;

Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2036 AACCACTGGGAAGACCCCA 2054
DB 1 AAACACTGGGAAGACCCCA 19
RESULT 207
AAA80354
ID AAA80354 standard; DNA; 20 BP.
XX
XX AC AAA80354;
XX
XX DT 22-NOV-2000 (first entry)
XX
XX DE Human ASTH11 5' region polymorphic site, SEQ ID NO:100 (b).
XX
XX KW ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma;
KW bronchial hyperreactivity; ets family; transcription factor;
KW splice variant; genetic predisposition; polymorphism; antibody;
KW drug screening; prophylaxis; therapy; diagnosis;
KW single nucleotide polymorphism; SNP; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT variation replace(10..11,TTA)
FT /*tag= a
XX
XX PN US6087485-A.
XX
XX PD 11-JUL-2000.
XX
XX PF 21-JAN-1998; 98US-00009913.
XX
XX PR 21-JAN-1997; 97US-0035663P.
XX
XX PR 01-JUL-1997; 97US-0051432P.
XX
XX PA (AXYS-) AXYS PHARM INC.
XX
XX PI Galvin M, Miller A, North M, Cardon L, Buckler A;
XX Brooks-Wilson AR, Carey AH;
XX WPI; 2000-505109/45.
XX
XX PT New nucleic acids other than naturally occurring chromosomes encoding
XX ASTH1 protein, for e.g. screening compositions that modulate expression
XX or function of ASTH1 proteins or as diagnostics for genetic
XX predisposition to asthma.
XX
XX Example; Col 41-42; 131pp; English.
XX
XX The invention relates to the ASTH1 locus on the short arm of human
XX chromosome (11p). This locus comprises the ASTH11 and ASTH1J genes, which
XX are associated with a genetic predisposition to asthma and bronchial
XX hyperreactivity. The ASTH11 and ASTH1J genes are oriented in opposite
XX directions with the ASTH1 locus, and have similar patterns of expression
XX and common sequence motifs. They are both expressed in trachea, lung and
XX several other tissues. ASTH11 and ASTH1J are novel members of the ets
XX family of transcription factors, which have been implicated in the
XX activation of a variety of genes including the TCRA gene and cytokine
XX genes known to be important in the aetiology of asthma. Both ASTH11 and
XX ASTH1J mRNAs are alternatively spliced. Alternative splicing of
XX transcripts has no effect on the open reading frame of ASTH1J, as the
XX exons involved are all 5' to the start codon in exon b. In contrast,
XX alternative splicing of ASTH11 transcripts results in 3 different ASTH11
XX isoforms. The invention also encompasses mouse asth1j protein. The ASTH11
XX nucleic acids are useful as diagnostics to identify a hereditary
XX predisposition to asthma, as probes for identifying ASTH1 related genes,
XX for identifying expression of the gene in a biological specimen, and for
XX generating genetically modified non-human animals or site specific gene
XX modifications in cell lines. The encoded ASTH1 proteins are useful as

CC immunogens to raise specific antibodies; in drug screening for
CC compositions that mimic or modulate activity or expression of ASTH11
CC and/or ASTH1J (including altered forms of these proteins); and as a
CC therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
CC ASTH1 genomic regulatory regions, and anti-ASTH11 and anti-ASTH1J
CC antibodies are useful in the identification of individuals predisposed to
CC development of asthma, and for modulation of gene activity in vivo for
CC prophylactic and therapeutic purposes. The intact ASTH11 or ASTH1J
CC proteins or active fragments thereof may be used to modulate or reduce
CC bronchial hyperactivity. Sequences AAA80260-A80261 and AAA80264-A80416
CC represent polymorphic sites within the ASTH1J or ASTH11 genes

SQ Sequence 20 BP; 8 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
XX

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2747 TTTT TTTT TTTT TTTT AAGG AAAAAA 2765
||||| ||||| ||||| ||||| |||||
Db 2 TTTT TTTT TTTT AAGG AAAAAA 20

RESULT 208
ADI80042/c
ID ADI80042 standard; DNA; 20 BP.
XX
AC ADI80042;
XX
XX 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 43.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 15; SEQ ID NO 43; 135pp; English.

CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,

CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.

XX
SQ Sequence 20 BP; 3 A; 4 C; 5 G; 8 T; 0 U; 0 Other;
XX

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2084 CAGACTGGAGTGCACACACAG 2102
||||| ||||| ||||| ||||| |||||
Db 20 CAGACTTGAGTCACACACAG 2

RESULT 209
ADI80069/c
ID ADI80069 standard; DNA; 20 BP.
XX
AC ADI80069;
XX
XX 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 70.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 15; SEQ ID NO 70; 135pp; English.

CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX

SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3027 TCGAGACCAAACTACTTGC 3045
 | | | | | | | | | | | | | | | | | | | |
 Db 19 TGGAGACCAAACTACTTGC 1

RESULT 210
 ADI80210
 ID ADI80210 standard; DNA; 20 BP.
 XX
 AC ADI80210;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 211.
 XX
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX

Example 16; SEQ ID NO 211; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX

CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3027 TCGAGACCAAACTACTTGC 3045
 | | | | | | | | | | | | | | | | | | | |
 Db 2 TGGAGACCAAACTACTTGC 20

RESULT 211
 ADI80200
 ID ADI80200 standard; DNA; 20 BP.
 XX
 AC ADI80200;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 201.
 XX
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004006030-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-JUL-2002; 2002US-00189267.
 XX
 PR 02-JUL-2002; 2002US-00189267.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-081742/08.
 XX
 PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX

Example 16; SEQ ID NO 201; 135pp; English.
 XX
 CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX

QY 800 TCTGTCCTCTTTGGCCG 818
 Db 19 TCTCTTCCCTTTGGCCG 1

RESULT 214

ADI80186

ID ADI80186 standard; DNA; 20 BP.

XX ADI80186;

XX 22-APR-2004 (first entry)

XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 187.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

XX cytosatic; nontropic; neuroprotective; immunosuppressive;

XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

XX immune; ss; human.

XX Homo sapiens.

OS US2004006030-A1.

PN 08-JAN-2004.

XX 02-JUL-2002; 2002US-00189267.

XX 02-JUN-2002; 2002US-00189267.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a

XX neurodegenerative disorder, or a disease involving hyperactivation of

XX immune response.

XX Example 16; SEQ ID NO 187; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

XX in length targeted to, and which specifically hybridizes with, a nucleic

XX acid molecule encoding transforming growth factor (TGF)-beta 2, and

XX inhibits the expression of TGF-beta 2. The invention further relates to:

XX a compound 8-80 nucleobases in length that specifically hybridizes with

XX at least an 8-nucleobase portion of an active site on a nucleic acid

XX molecule encoding TGF-beta 2; a composition comprising the compound and a

XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

XX tissues by contacting the cells or tissues with the compound so that

XX expression of TGF-beta 2 is inhibited; treating an animal having a

XX disease or condition associated with TGF-beta 2 by administering to the

XX animal a therapeutic or prophylactic amount of the compound so that

XX expression of TGF-beta 2 is inhibited; and screening an antisense

XX compound. The antisense compound has cytostatic, nontropic,

XX neuroprotective, and immunosuppressive activities. The compound,

XX composition and methods are useful for treating a disease or condition

XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

XX cancer, a neurodegenerative disorder, or a disease or condition involving

XX hyperactivation of an immune response. This polynucleotide sequence

XX represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 17.4; DB 1; Length 20;

XX Best Local Similarity 94.7%; Pred. No. 1.4e+02;

XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2084 CAGACTGGAGTCACACAG 2102

Db 1 CAGACTTGAGTCACACAG 19

RESULT 215
 ADL58461/c
 ID ADL58461 standard; DNA; 20 BP.
 XX ADL58461;
 XX 03-JUN-2004 (first entry)
 XX Human ESM-1 antisense oligonucleotide seqid 710.
 XX cytosatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
 XX gene therapy; endothelial specific molecule-1; ESM-1;
 XX ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
 XX angiogenic disorder; immunological disorder; cardiovascular disorder;
 XX neurological disorder; antisense technology; ss.
 XX Homo sapiens.

XX Key Location/Qualifiers
 PH modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone. All cytidine
 residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 XX WO2004021978-A2.

XX 18-MAR-2004.
 XX 19-AUG-2003; 2003WO-US025833.
 XX 19-AUG-2002; 2002US-0404495P.
 XX (PHAA) PHARMACIA CORP.
 XX Weinstein EJ, Griggs DW;
 XX WPI; 2004-248358/23.
 XX New antisense compound, having a sequence targeted to a nucleic acid
 XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
 XX composition for treating e.g., diabetes, cancer or cardiovascular
 XX disorder.

XX Claim 3; SEQ ID NO 710; 555pp; English.
 XX The invention describes a new antisense compound, having a sequence
 XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
 XX specific molecule-1 (ESM-1), that specifically hybridises with the
 XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
 XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
 XX treating an animal having a disease or condition associated with ESM-1.
 XX The compound is useful for preparing a composition for treating diabetes,
 XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
 XX cardiovascular or neurological disorder. This sequence represents an
 XX antisense oligonucleotide that can be used to modulate expression of
 XX endothelial specific molecule-1 (ESM-1).

XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
 XX Query Match 0.4%; Score 17.4; DB 1; Length 20;
 XX Best Local Similarity 94.7%; Pred. No. 1.4e+02;
 XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 362 TGGCCGCTGGAGCAAGAA 380
|||||
Db 19 TGGCCGCTGGAGCAATAA 1

RESULT 216
ADL58256/c
ID ADL58256 standard; DNA; 20 BP.
XX AC ADL58256;
XX DT 03-JUN-2004 (first entry)
XX DE Human ESM-1 antisense oligonucleotide seqid 505.
XX KW cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW gene therapy; endothelial specific molecule-1; ESM-1;
KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW angiogenic disorder; immunological disorder; cardiovascular disorder;
KW neurological disorder; antisense technology; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone. All cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2004021978-A2.
XX 18-MAR-2004.
XX 19-AUG-2003; 2003WO-US025833.
XX 19-AUG-2002; 2002US-0404495P.
XX (PHAA) PHARMACIA CORP.
XX Weinstein EJ, Griggs DW;
XX WPI; 2004-248358/23.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX composition for treating e.g., diabetes, cancer or cardiovascular
XX disorder.
XX Claim 3; SEQ ID NO 505; 555pp; English.
XX The invention describes a new antisense compound, having a sequence
XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX specific molecule-1 (ESM-1), that specifically hybridises with the
XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX treating an animal having a disease or condition associated with ESM-1.
XX The compound is useful for preparing a composition for treating diabetes,
XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX cardiovascular or neurological disorder. This sequence represents an
XX antisense oligonucleotide that can be used to modulate expression of
XX endothelial specific molecule-1 (ESM-1).

Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 362 TGGCCGCTGGAGCAAGAA 380
|||||
Db 20 TGGCCGCTGGAGCAATAA 2

RESULT 217
ADQ90968
ID ADQ90968 standard; DNA; 20 BP.
XX AC ADQ90968;
XX DT 21-OCT-2004 (first entry)
XX DE Human fibrillin-like protein-specific cloning/sequencing primer #2.
XX KW human; fibrillin-like protein; skin damage; multiple sclerosis; cancer;
KW osteoarthritis; rheumatoid arthritis; osteoporosis;
KW cardiovascular disease; fibrosis; liver fibrosis; kidney fibrosis;
KW renal disorder; hepatitis; bone reconstruction; joint reconstruction;
KW ligament reconstruction; fracture; lesion; cloning; sequencing; primer;
KW ss.
XX OS Homo sapiens.
XX WO2004063226-A2.
XX 29-JUL-2004.
XX 22-DEC-2003; 2003WO-BP051089.
XX 27-DEC-2002; 2002US-0436935P.
XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX Mcallister G, Bienkowska J;
XX WPI; 2004-544073/52.
XX New isolated polypeptide having fibrillin-like activity, useful for
XX manufacturing a medicament for treating e.g., skin damage, multiple
XX sclerosis, cancer, osteoarthritis, cardiovascular disease and hepatitis.
XX Example 3; Page 50; 150pp; English.
XX The invention comprises the amino acid and coding sequences of human
XX fibrillin-like proteins. The DNA and protein sequences of the invention
XX are useful for characterising ligands which bind to fibrillin-like
XX proteins. The DNA and protein sequences of the invention are useful for
XX the treatment of diseases and conditions in which fibrillin-like proteins
XX are implicated, such as: skin damage (e.g. through ageing, injuries or
XX sun exposure), multiple sclerosis, cancer, osteoarthritis, rheumatoid
XX arthritis, osteoporosis, cardiovascular diseases and fibrosis (e.g. liver
XX fibrosis or kidney fibrosis), renal disorders and hepatitis. The DNA and
XX protein sequences of the invention are also useful for bone, joint or
XX ligament reconstruction after fractures or lesions. The present DNA
XX sequence represents a primer that was used in an example of the
XX invention.
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4241 CATTCTTTTCAGGCTGATT 4259
|||||
Db 2 CATTCTTCGAGGCTGATT 20

```

RESULT 218
AAZ26584
ID  AAZ26584 standard; DNA; 21 BP.
XX  AC
XX  AAZ26584;
XX  AC
XX  30-NOV-1999 (first entry)
XX  DE
XX  Human polymorphic region 773.
XX  KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX  KW cell viability; loss of heterozygosity; precancerous condition; ASI;
XX  KW allele specific inhibitor; somatic cell; diagnosis; prevention;
XX  KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX  KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX  KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX  OS
XX  Homo sapiens.
XX  KW
XX  WO9841648-A2.
XX  PN
XX  24-SEP-1998.
XX  PD
XX  19-MAR-1998; 98WO-US005419.
XX  PF
XX  20-MAR-1997; 97US-0041057P.
XX  PR
XX  (VARI-) VARTAGENICS INC.
XX  PA
XX  Housman D, Ledley FD, Stanton VP;
XX  PI
XX  WPI; 1998-521232/44.
XX  DR
XX  Identifying target genes for allele-specific drugs - used for diagnosis,
XX  PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX  PT dysplastic lesions, endometriosis or graft versus host disease.
XX  PS
XX  Disclosure; Fig 7; 605pp; English.
XX  CC
XX  This invention describes a novel method for identifying an inhibitor
XX  CC potentially useful for treatment of cancer, where the inhibitor is active
XX  CC on a gene vital for cell growth or viability, and where the gene is
XX  CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX  CC used for preventing the development of cancer in a patient having a
XX  CC precancerous condition, by administering to the patient a first allele
XX  CC specific inhibitor (ASI) targeted to an allele of a first essential gene
XX  CC present in cells of the precancerous condition, where the normal somatic
XX  CC cells of the patient are heterozygous for the first gene, the inhibitor
XX  CC is active on at least one but less than all allelic forms of the gene
XX  CC present in a population and targets only one allelic form present in the
XX  CC normal somatic cells, and the first gene. The products and methods can be
XX  CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX  CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX  CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX  CC graft versus host disease. The method can also be used to remove
XX  CC malignant cells from bone marrow transplants. AAZ25812-226825 represent
XX  CC human polymorphic sites described in the method of the invention
XX  SQ
XX  Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2570 GTGTTTAAAAA 2588
DB 1 GTTTTAAAAA 19

RESULT 219
AAZ18450
ID  AAZ18450 standard; DNA; 21 BP.
XX  AC
XX  AAZ18450;
XX  AC
XX  19-OCT-1999 (first entry)
XX  DE
XX  Polymorphic fragment in region 5' to ASTH1I.
XX  KW
XX  ASTH1; asthma; human; chromosome 11p; ASTH1I; ASTH1J; genetic locus;
XX  KW therapeutic; immunogen; polymorphism; ss.
XX  OS
XX  Homo sapiens.
XX  KW
XX  WO9937809-A1.
XX  PN
XX  29-JUL-1999.
XX  PD
XX  21-JAN-1998; 98WO-US001260.
XX  PF
XX  21-JAN-1998; 98WO-US001260.
XX  PR
XX  (AXYS-) AXYS PHARM INC.
XX  PA
XX  Brooks-Wilson AR, Buckler A, Cardon L, Carey AH, Galvin M;
XX  PI Miller A, North M;
XX  PI WPI; 1999-479058/40.
XX  DR
XX  Mammalian asthma related genes, useful for diagnosis of a predisposition
XX  PT to development of asthma.
XX  PS
XX  Disclosure; Page 63; 195pp; English.
XX  CC
XX  The invention identifies a genetic locus ASTH1, associated with asthma,
XX  CC mapped to human chromosome 11p. ASTH1I and ASTH1J are genes present
XX  CC within the locus, located close to each other on human chromosome 11p,
XX  CC and have similar patterns of expression, and common sequence motifs. The
XX  CC ASTH1 genes and fragments, encoded protein, genomic regulatory regions
XX  CC and anti-ASTH1 antibodies are useful in the identification of individuals
XX  CC predisposed to development of asthma, and for the modulation of gene
XX  CC activity in vivo for prophylactic and therapeutic purposes. The ASTH1
XX  CC protein is useful as an immunogen to raise specific antibodies, in drug
XX  CC screening for compositions that mimic or modulate ASTH1 activity or
XX  CC expression, including altered forms of ASTH1 protein, and as a
XX  CC therapeutic. Sequences AAZ18366-218509 represent polymorphisms in the
XX  CC ASTH1I and ASTH1J genes
XX  SQ
XX  Sequence 21 BP; 8 A; 0 C; 2 G; 10 T; 0 U; 1 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTT TTTT TTTT TAAGGAAAAA 2765
DB 2 TTTT TTTT TTTT TAAGGAAAAA 21

RESULT 220
AAZ04118/c
ID  AAZ04118 standard; DNA; 20 BP.
XX  AC
XX  AAZ04118;
XX  AC
XX  25-MAR-2003 (revised)
XX  DT 26-MAR-1996 (first entry)
XX  DT
XX  Human transforming growth factor-beta2 precursor degenerate probe.
XX  DE
XX  TGF-beta2; TGF-beta2; transforming growth factor; protein;
XX  KW cell differentiation; cell proliferation; CHO; Chinese hamster; ovary;
XX  KW COS; monkey kidney; animal; mammal; DNA probe; ss.
XX  OS
XX  Synthetic.

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XX EP676474-A1.
 PN XX
 PD 11-OCT-1995.
 XX
 XX PF 14-DEC-1989; 95EP-00104223.
 XX
 PR 16-DEC-1988; 88US-00285140.
 PR 05-DEC-1989; 89US-00446020.
 XX
 PA (ONCO) ONCOGEN LP.
 XX
 XX Purchio AF, Madisen L, Webb N;
 PI
 DR WPI; 1995-346094/45.
 XX
 XX Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used to
 PT produce biologically active, mature TGF-beta-2.
 PT
 XX Example 6; Page 13; 52pp; English.
 PS
 XX This probe is used during a procedure for the cloning of TGF-beta2
 CC precursor from human prostate adenocarcinoma cell line PC-3. DS cDNA was
 CC synthesized from polyadenylated RNACC isolated from PC-3 cells treated
 CC with tamoxifen for 24 hr. cDNA fractions larger than 1000 bases were
 CC cloned into phage lambda gt10. The library was first screened in duplicate
 CC with this 32P-labelled 24-mer degenerate probe complementary to DNA
 CC encoding AA WKWHEP which are conserved between TGF-beta1 and TGF-beta2.
 CC Positive clones were then screened with 2nd degenerate probe (AAT04119).
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 3 G; 5 T; 0 U; 4 Other;
 Query Match 0.4%; Score 17.2; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2211 TGGAAATGGATCCCATGAACC 2230
 DB 20 TGGAAATGGATCCATGARGCC 1
 RESULT 221
 AAV48933/C
 ID AAV48933 standard; DNA; 17 BP.
 XX
 XX AAV48933;
 AC
 XX 15-OCT-1998 (first entry)
 DT
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-4.
 XX
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; 88.
 KW
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX EP856579-A1.
 PN
 XX 05-AUG-1998.
 PD
 XX 31-JAN-1997; 97EP-00101531.
 PF
 XX 31-JAN-1997; 97EP-00101531.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Brysch W;
 PI
 XX WPI; 1998-400910/35.
 DR
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT

PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 XX Claim 10; Fig 8a; 286pp; English.
 PS
 XX AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1343 GCAGATCCTGAGCAAGC 1359
 DB 17 GCAGATCCTGAGCAAGC 1
 RESULT 222
 AA265508/C
 ID AA265508 standard; DNA; 17 BP.
 XX
 XX AA265508;
 AC
 XX 30-MAR-2000 (first entry)
 DT
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta-17-c-2260.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; as;
 XX atherosclerosis.
 XX Unidentified.
 OS
 XX WO963975-A2.
 PN
 XX 16-DEC-1999.
 PD
 XX 10-JUN-1999; 99WO-EP004013.
 PF
 XX 10-JUN-1998; 98EP-00110709.
 PR 25-JUL-1998; 98EP-00113974.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI
 XX WPI; 2000-097470/08.
 DR
 XX

```

PT Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
XX
XX Claim 10; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1509 TACTAGCCCAAGGAGGT 1525
DB 17 TACTAGCCCAAGGAGGT 1
RESULT 223
AAZ65443/C
ID AAZ65443 standard; DNA; 17 BP.
XX
XX AAZ65443;
XX
XX 30-MAR-2000 (first entry)
XX
XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-3.
XX
XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
XX prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
XX glomerulonephritis; acute respiratory distress syndrome; ss;
XX atherosclerosis.
XX
XX Unidentified.
XX
XX WO963975-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-EP004013.
XX
XX 10-JUN-1998; 98EP-00110709.
XX
XX 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
XX adversely affects the immune response, for treating cancers and
PT

```

```

PT infections.
XX
XX Claim 5; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1343 GCAGATCCTGTGAGCAAGC 1359
DB 17 GCAGATCCTGTGAGCAAGC 1
RESULT 224
ADJ76724
ID ADJ76724 standard; DNA; 17 BP.
XX
XX ADJ76724;
XX
XX 20-MAY-2004 (first entry)
XX
XX TGFbeta reverse PCR primer SEQ ID NO:1976.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX gene therapy; marker; PCR; primer; ss.
XX
XX Mus musculus.
XX Synthetic.
XX
XX EP1394274-A2.
XX
XX 03-MAR-2004.
XX
XX 04-AUG-2003; 2003EP-00254857.
XX
XX 06-AUG-2002; 2002JP-00229312.
XX
XX 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX
XX Example 11; SEQ ID NO 1976; 241pp; English.
PS

```


QY 2142 TGCTTTAGAAATGTGCAGGA 2161
 DE 20 TGYTTAGRAAYGTNCARGA 1

RESULT 227
 AA205389/c
 ID AA205389 standard; DNA; 20 BP.
 XX
 AC AA205389;
 XX
 DT 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritheatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS Chlamydia trachomatis.
 XX
 PN WO9928475-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 27-NOV-1998; 98WO-IB001939.
 XX
 PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-371125/31.
 XX
 PT Genome sequence of Chlamydia trachomatis.
 XX
 PS Disclosure; Page 1766; 1755pp; English.
 XX
 CC PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
 CC encode polypeptides (see AA206754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conjunctival trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;
 CC epididymitis, cervicitis, salpingitis, peritheatitis, bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases
 XX
 SQ Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 GCGGAGAGCGCGCTT 2127
 DE 17 GCGGAGAGCGCGCTT 1

RESULT 228
 AAF87713/c
 ID AAF87713 standard; DNA; 20 BP.
 XX
 AC AAF87713;
 XX

DT 06-JUL-2001 (first entry)
 XX Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.
 XX
 KW Human; glutathione S-transferase pi; GSTP1; CpG island; diagnosis;
 KW hepatic cell proliferative disorder; liver cancer; anticancer;
 KW tumorigenesis; detection; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200126536-A2.
 PD 19-APR-2001.
 XX
 PF 12-OCT-2000; 2000WO-US028427.
 XX
 PR 13-OCT-1999; 99US-0159168P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Nelson WG, Lin X, Tchou JC, Bakker J;
 XX WPI; 2001-290647/30.
 DR
 XX
 PT Detecting hepatic cell proliferative disorder useful for detecting
 PT hepatocellular carcinoma comprises detecting a methylated CpG-containing
 PT glutathione-S-transferase nucleic acid.
 XX
 PS Claim 83; Page 42; 64pp; English.
 XX
 CC The present invention describes a method for detecting hepatic cell
 CC proliferative disorders. The method comprises detecting a methylated CpG-
 CC containing glutathione-S-transferase (GST) nucleic acid (I) in a hepatic
 CC specimen or a biological fluid, where a methylated GST nucleic acid is
 CC indicative of a hepatic cell proliferative disorder. The method can be
 CC used to diagnose hepatocellular carcinoma, and to monitor progress of its
 CC treatment. Increasing the level of GST is useful in the treatment of
 CC liver cancer, in humans or animals. The method can detect the early
 CC stages of tumorigenesis in liver cells simply. The present sequence
 CC represents a PCR primer which is used in the amplification of the human
 CC glutathione S-transferase pi gene (GSTP1) promoter in an example from the
 CC present invention for mapping somatic GSTP1 CpG island DNA
 CC hypermethylation changes by genomic sequencing after bisulfite treatment
 XX
 SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
 Query Match 0.4%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAAATT 2590
 DE 19 TTAAAAAATAAAAAAATT 3

RESULT 229
 AAD55457/c
 ID AAD55457 standard; DNA; 20 BP.
 XX
 AC AAD55457;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Human FGFR-3 antisense oligonucleotide, ISIS #125161.
 XX
 KW Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
 KW developmental disorder; hyperproliferative disorder; antisense therapy;
 KW FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT modified_base 1. .20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1. .5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16. .20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT WQ2003023004-A2.
 PN 20-MAR-2003.
 PD
 XX
 XX 06-SEP-2002; 2002WO-US028549.
 XX 10-SEP-2001; 2001US-00953047.
 XX (ISIS-) ISIS PHARM INC.
 PA Monia BP, Wyatt JR;
 PI WPI; 2003-313244/30.
 DR
 XX
 XX Novel compound targetted to a nucleic acid molecule encoding fibroblast
 PT growth factor receptor 3, useful for inhibiting the expression of the
 PT receptor and for treating an animal having cancer or developmental
 PT disorder.
 PS Claim 3; Page 79; 120pp; English.
 XX
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC molecule encoding fibroblast growth factor (FGF) receptor 3 (also known
 CC as FGFR-3, ACH, JTK4 and CER2) to inhibit its expression. Antisense
 CC compounds of the invention are useful for treating diseases or conditions
 CC associated with FGFR-3 such as developmental disorders or
 CC hyperproliferative disorders, especially cancer of colorectal, bladder,
 CC bone, lung, cervical, breast or skin. They are useful as research
 CC reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools
 CC in differential and/or combinatorial analyses to elucidate expression
 CC patterns of a portion of the genes expressed within cells and tissues.
 CC They are also useful in antisense therapy. The present sequence is an
 CC antisense oligonucleotide targetted to human FGFR-3
 SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2351 TTGCTGTGTGTCACG 2367
 DB 17 TTGCTGTGTGTCACG 1
 RESULT 230
 AAQ75726/C
 ID AAQ75726 standard; DNA; 21 BP.
 XX
 AC AAQ75726;
 XX
 XX 04-AUG-1995 (first entry)
 DT
 XX Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.

XX JP06303997-A.
 PN 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-00112515.
 PF 16-APR-1993; 93JP-00112515.
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 PT Disclosure; Page 8; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 0.4%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2572 GTTTAAAAA 2588
 DB 21 GTTTAAAAA 5
 RESULT 231
 AAQ78450/C
 ID AAQ78450 standard; DNA; 20 BP.
 XX
 AC AAQ78450;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUN-1995 (first entry)
 XX
 DE TGF-beta gene phosphorothioate antisense oligonucleotide.
 XX
 KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX
 OS Synthetic.
 XX
 PN WO9425588-A2.
 XX
 PD 10-NOV-1994.
 XX
 PF 29-APR-1994; 94WO-EF001362.
 XX
 PR 30-APR-1993; 93EP+00107089.
 PR 13-MAY-1993; 93EP-00107849.
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 XX Bogdahn U;
 PI WPI; 1994-358266/44,
 XX
 XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for

PT treating immunosuppression, tumours, etc.
XX Claim 6; Page 52; 74pp; English.
XX
CC The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1928 CATCATCCCGAATAAAGCG 1947
Db ||||||| |||||||
20 CATCATCCCAATAAAGTG 1
RESULT 232
AAT48166
ID AAT48166 standard; DNA; 20 BP.
XX
AC AAT48166;
XX
DT 19-SEP-1997 (first entry)
XX
DE Escherichia coli chromosomal PCR primer beta21079.
XX
KW Escherichia coli; heterologous non-bacterial protein; host cell;
KW IGF-I fusion gene; chromosomal transfer DNA; polymerase chain reaction;
KW ss.
XX
OS Synthetic.
XX
PN WO9640722-A1.
XX
PD 19-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US009006.
XX
PR 07-JUN-1995; 95US-00482182.
XX
PR (CEL-T-) CELTRIX PHARM INC.
XX
PI Mascarenhas D, Olson PS;
XX
XX WPI; 1997-065167/06.
XX
XX Prodn. of heterologous non-bacterial protein in bacteria - using a
PT chromosomal transfer DNA contg. a gene which has not been cloned in a
PT multi-copy vector.
XX
XX Example 6; Page 40; 80pp; English.
PS
XX A method has been produced for the production of a heterologous,
CC preferably non-bacterial, protein in a bacterial host cell such as
CC Escherichia coli. The method involves: transferring a chromosomal DNA
CC into a bacterial host cell preferably comprising a chromosome, where the
CC chromosomal DNA contains at least one copy of a gene encoding the
CC heterologous protein and a selectable marker; selecting for integration
CC of the chromosomal DNA into the cell resulting in a host cell chromosome
CC comprising a gene encoding the heterologous protein operably linked to a

CC promoter functional in the host cell and a selectable marker flanked by
CC duplicate DNA: and expressing the gene, where the gene is at no time
CC operably linked to a promoter, functional in the host cell, on a
CC multicopy number plasmid vector during construction of the transfer DNA
CC and where the heterologous protein accumulates within the host cell to a
CC level in excess of 0.1% of total cell protein. The present sequence is
CC PCR primer beta21079, which is part of a primer pair used to confirm the
CC proper integration of intact chromosomal transfer DNA. The method is
CC especially useful for producing eukaryotic protein, especially mammalian
CC protein. The method of construction avoids the generation of low or high
CC multicopy plasmid where expression of a small amount of the foreign
CC protein may be toxic to the cell. The method allows high accumulation of
CC the foreign protein (about 20% of total cell protein) from low
CC (approximately 2) copies of the gene encoding the heterologous protein
XX
SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2212 GGAATGGATCCATCAACCC 2231
Db ||||||| |||||||
1 GGAATGGATACACGAACCC 20
RESULT 233
AAV47680
ID AAV47680 standard; DNA; 20 BP.
XX
AC AAV47680;
XX
DT 20-NOV-1998 (first entry)
XX
DE Unmethylated CpG dinucleotide 1631.
XX
KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
KW pulmonary disorder; asthma; environmentally induced airway disease;
KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
KW inflammatory bowel disease; ss.
XX
OS Synthetic.
XX
PN WO9837919-A1.
XX
PD 03-SEP-1998.
XX
PF 25-FEB-1998; 98WO-US003678.
XX
PR 28-FEB-1997; 97US-0039405P.
XX
PR (IOWA) UNIV IOWA RES FOUND.
XX
PI Schwartz DA, Krieg AM;
XX
XX WPI; 1998-480941/41.
XX
XX Use of nucleic acids containing an unmethylated CpG - for treating a
PT subject having or at risk of having an acute decrement in air flow or
PT inhibiting an inflammatory response.
XX
XX Claim 35; Page 27; 65pp; English.
PS
XX This sequence represents an unmethylated CpG dinucleotide, and can be
CC used in the method of the invention. The method is for treating a subject
CC having, or at risk of having an acute decrement in air flow, comprising
CC administering a nucleic acid sequence containing at least one
CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
CC dinucleotide affect an immune response in a subject by activating natural
CC killer cells (NK) or redirecting a subject's immune response from a Th2
CC to a Th1 response by inducing monocytic and other cells to produce Th1
CC cytokines. They can be used to treat pulmonary disorders having an

CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with Gram-
 CC positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide

XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
 Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 234
 AAV47680/c
 ID AAV47680 standard; DNA; 20 BP.
 XX
 AC AAV47680;
 XX
 DT 20-NOV-1998 (first entry)
 XX
 DE Unmethylated CpG dinucleotide 1631.
 XX
 KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
 KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 KW pulmonary disorder; asthma; environmentally induced airway disease;
 KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 KW inflammatory bowel disease; ss.
 XX
 OS Synthetic.
 XX
 PN WO9837919-A1.
 XX
 PD 03-SEP-1998.
 XX
 PF 25-FEB-1998; 98WO-US003678.
 XX
 PR 28-FEB-1997; 97US-0039405P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Schwartz DA, Krieg AM;
 XX
 PS WPI; 1998-480941/41.
 XX
 DR Use of nucleic acids containing an unmethylated CpG - for treating a
 PT subject having or at risk of having an acute decrement in air flow or
 PT inhibiting an inflammatory response.
 XX
 PS Claim 35; Page 27; 65pp; English.
 XX
 CC This sequence represents an unmethylated CpG dinucleotide, and can be
 CC used in the method of the invention. The method is for treating a subject
 CC having, or at risk of having an acute decrement in air flow, comprising
 CC administering a nucleic acid sequence containing at least one
 CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
 CC dinucleotide affect an immune response in a subject by activating natural
 CC killer cells (NK) or redirecting a subject's immune response from a Th2
 CC to a Th1 response by inducing monocytic and other cells to produce Th1
 CC cytokines. They can be used to treat pulmonary disorders having an
 CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with Gram-
 CC positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease,
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide

XX
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
 Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 235
 AAV48940/c
 ID AAV48940 standard; DNA; 20 BP.
 XX
 AC AAV48940;
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-11.
 XX
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN EP856579-A1.
 XX
 PD 05-AUG-1998.
 XX
 PF 31-JAN-1997; 97EP-00101531.
 XX
 PR 31-JAN-1997; 97EP-00101531.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Brysch W;
 XX
 DR WPI; 1998-400910/35.
 XX
 PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 PS Claim 10; Fig 8a; 286pp; English.
 XX
 CC AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, ErbB-2, JunB, JunD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system

XX Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

```
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1523 GGTTTATAAATCGACATGC 1542
DB 20 GGTTCACAAAATAGACATGC 1

RESULT 236
AAV74258
ID AAV74258 standard; DNA; 20 BP.
XX
AC AAV74258;
XX
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; ss.
XX
OS Synthetic.
XX
PN WO9852581-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US010408.
XX
PR 20-MAY-1997; 97US-0047209P.
XX
PR 20-MAY-1997; 97US-0047233P.
XX
PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (IOWA ) UNIV IOWA RES FOUND.
PA (QIAG-) QIAGEN GMBH.
XX
PI Davis HL, Krieg AM, Schorr J, Wu T;
XX WPI; 1999-059712/05.
XX
DR Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
PT enhancing the immunostimulatory effect of an antigen or enhancing the
PT expression of a therapeutic polypeptide.
XX
PS Example 5; Page 73; 109pp; English.
XX
CC AAV74254-V74261 are oligonucleotides used to describe a method for
CC enhancing the immunostimulatory effect of an antigen encoded by nucleic
CC acid contained in a nucleic acid construct. The method involves
CC determining the CpG-N and CpG-S motifs present in the construct, removing
CC neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG
CC (CpG-S) motifs in the construct, thereby producing a nucleic acid
CC construct having enhanced immunostimulatory efficacy. The method can be
CC used for immunisation against viral antigens, e.g. from hepatitis B virus
CC (HBV), bacterial antigens or an antigen derived from a parasite. They can
CC also be used for expression of a therapeutic polypeptide, e.g. growth
CC factors, toxins, tumour suppressors, cytokines, apoptotic proteins,
CC interferons, hormones, clotting factors, ligands and receptors. (Updated
CC on 20-MAR-2003 to correct PA field.)
XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
DB 1 GCGCGCGCGCGCGCGCGC 20

RESULT 238
AAZ65448/c
ID AAZ65448 standard; DNA; 20 BP.
XX
AC AAZ65448;
```

```
RESULT 237
AAV74258/c
ID AAV74258 standard; DNA; 20 BP.
XX
AC AAV74258;
XX
KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW hormone; clotting factor; ligand; receptor; ss.
XX
OS Synthetic.
XX
PN WO9852581-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US010408.
XX
PR 20-MAY-1997; 97US-0047209P.
XX
PR 20-MAY-1997; 97US-0047233P.
XX
PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA (IOWA ) UNIV IOWA RES FOUND.
PA (QIAG-) QIAGEN GMBH.
XX
PI Davis HL, Krieg AM, Schorr J, Wu T;
XX WPI; 1999-059712/05.
XX
DR Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
PT enhancing the immunostimulatory effect of an antigen or enhancing the
PT expression of a therapeutic polypeptide.
XX
PS Example 5; Page 73; 109pp; English.
XX
CC AAV74254-V74261 are oligonucleotides used to describe a method for
CC enhancing the immunostimulatory effect of an antigen encoded by nucleic
CC acid contained in a nucleic acid construct. The method involves
CC determining the CpG-N and CpG-S motifs present in the construct, removing
CC neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG
CC (CpG-S) motifs in the construct, thereby producing a nucleic acid
CC construct having enhanced immunostimulatory efficacy. The method can be
CC used for immunisation against viral antigens, e.g. from hepatitis B virus
CC (HBV), bacterial antigens or an antigen derived from a parasite. They can
CC also be used for expression of a therapeutic polypeptide, e.g. growth
CC factors, toxins, tumour suppressors, cytokines, apoptotic proteins,
CC interferons, hormones, clotting factors, ligands and receptors. (Updated
CC on 20-MAR-2003 to correct PA field.)
XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
DB 20 GCGCGCGCGCGCGCGCGC 1

RESULT 238
AAZ65448/c
ID AAZ65448 standard; DNA; 20 BP.
XX
AC AAZ65448;
```

XX 30-MAR-2000 (first entry)
 XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-8.
 DE
 XX
 XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 XX Unidentified.
 OS
 XX
 XX WO963975-A2.
 PN
 XX
 XX 16-DEC-1999.
 PD
 XX
 XX 10-JUN-1999; 99WO-EP004013.
 PF
 XX
 XX 10-JUN-1998; 98EP-00110709.
 PR
 XX
 XX 25-JUL-1998; 98EP-00113974.
 PR
 XX
 XX (BIOG-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI
 XX
 XX WPI; 2000-097470/08.
 DR
 XX
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 PT
 XX
 XX Claim 5; Fig 1; 30pp; English.
 PS
 XX
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 XX Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1523 GGTATTATAAATGCACATGC 1542
 DB 20 GGTATTACAAATGACATGC 1
 RESULT 239
 AAZ57138
 ID AAZ57138 standard; DNA; 20 BP.
 XX
 AC AAZ57138;
 XX
 XX 24-MAR-2000 (first entry)
 DT
 XX
 XX Self complementary intermolecular duplex SEQ ID NO:13.
 DE
 XX
 XX Quadruplex DNA; antibody; binding; detection; isolation; purification;
 KW ss.
 XX
 XX Synthetic.
 OS
 XX
 XX US6001657-A.
 PN
 XX
 XX 14-DEC-1999.
 PD
 XX
 XX 11-OCT-1996; 96US-00729598.
 PF
 XX
 XX 12-OCT-1995; 95US-0005242P.
 PR
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA (JACK-) JACKSON LAB.
 XX
 XX Roberts JF, Pelsue SC, Hardin CC, Brown BA;
 PI
 XX
 XX WPI; 2000-096139/08.
 DR
 XX
 XX Quadruplex nucleic acid and antibody binding assay useful for detecting
 PT and purifying antibodies and nucleic acids from a biological sample.
 PT
 XX
 XX Example 4; Col 10; 11pp; English.
 PS
 XX
 XX A method has been developed for binding quadruplex nucleic acids. The
 CC method comprises contacting a quadruplex nucleic acid with a monoclonal
 CC antibody that selectively binds to quadruplex nucleic acid to form an
 CC antibody-quadruplex nucleic acid complex. The method can be used for
 CC detecting antibodies that bind to quadruplex nucleic acids and to collect
 CC antibodies that bind to quadruplex nucleic acids. The method is also
 CC suitable for detecting, isolating and purifying quadruplex nucleic acids.
 CC The detecting step can be carried out on a biological sample such as
 CC cerebrospinal fluid, tissues samples, blood samples or other sample
 CC suspected of containing quadruplex nucleic acids. The method can be used
 CC for the purification of quadruplex nucleic acids from solutions and to
 CC purify aptamers from combinatorial libraries or heterogeneous solutions,
 CC in particular to purify or detect DNA aptamers that specifically bind the
 CC thrombin molecule critical in the thrombin-catalysed, fibrin-clot
 CC formation cascade of blood platelets. The antibodies can then be used to
 CC detect levels of a known therapeutic aptamer in a patient and monitor
 CC clearance and dosage levels in a treatment protocol involving the
 CC aptamer. The present sequence represents an oligonucleotide used in the
 CC exemplification of the present invention
 XX
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 616 CGCGCGCGCACGCGCGCG 635
 DB 1 CGCGCGCGCGCGCGCGCG 20
 RESULT 240
 AAZ57138/C
 ID AAZ57138 standard; DNA; 20 BP.
 XX
 AC AAZ57138;
 XX
 XX 24-MAR-2000 (first entry)
 DT
 XX
 XX Self complementary intermolecular duplex SEQ ID NO:13.
 DE
 XX
 XX Quadruplex DNA; antibody; binding; detection; isolation; purification;
 KW ss.
 XX
 XX Synthetic.
 OS

```
XX US6001657-A.
PN
XX
XX
PD 14-DEC-1999.
XX
XX PF 11-OCT-1996; 96US-00729598.
XX
XX PR 12-OCT-1995; 95US-0005242P.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA (JACK-) JACKSON LAB.
XX
XX Roberts JF, Pelsue SC, Hardin CC, Brown BA;
PI WPI; 2000-096139/08.
XX
XX Quadruplex nucleic acid and antibody binding assay useful for detecting
PT and purifying antibodies and nucleic acids from a biological sample.
XX
XX Example 4; Col 10; 11pp; English.
XX
XX A method has been developed for binding quadruplex nucleic acids. The
CC method comprises contacting a quadruplex nucleic acid with a monoclonal
CC antibody that selectively binds to quadruplex nucleic acid to form an
CC antibody-quadruplex nucleic acid complex. The method can be used for
CC detecting antibodies that bind to quadruplex nucleic acids and to collect
CC antibodies that bind to quadruplex nucleic acids. The method is also
CC suitable for detecting, isolating and purifying quadruplex nucleic acids.
CC The detecting step can be carried out on a biological sample such as
CC cerebrospinal fluid, tissues samples, blood samples or other sample
CC suspected of containing quadruplex nucleic acids. The method can be used
CC for the purification of quadruplex nucleic acids from solutions and to
CC purify aptamers from combinatorial libraries or heterogeneous solutions.
CC In particular to purify or detect DNA aptamers that specifically bind the
CC thrombin molecule critical in the thrombin-catalysed, fibrin-clot
CC formation cascade of blood platelets. The antibodies can then be used to
CC detect levels of a known therapeutic aptamer in a patient and monitor
CC clearance and dosage levels in a treatment protocol involving the
CC aptamer. The present sequence represents an oligonucleotide used in the
CC exemplification of the present invention
XX
XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCACGCACGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1
RESULT 241
AAF99391
ID AAF99391 standard; DNA; 20 BP.
XX
AC AAF99391;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #507.
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XX WO200122972-A2.
XX
XX 05-APR-2001.
XX
XX 25-SEP-2000; 2000WO-US026383.
XX
XX 25-SEP-1999; 99US-0156113P.
XX
XX 27-SEP-1999; 99US-0156135P.
XX
XX 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
PA
```

```
PF 25-SEP-2000; 2000WO-US026383.
XX
XX 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Schetter C, Vollmer J;
PI WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
XX Claim 101; Page 48; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCACGCACGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20
RESULT 242
AAF99391/c
ID AAF99391 standard; DNA; 20 BP.
XX
AC AAF99391;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #507.
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XX WO200122972-A2.
XX
XX 05-APR-2001.
XX
XX 25-SEP-2000; 2000WO-US026383.
XX
XX 25-SEP-1999; 99US-0156113P.
XX
XX 27-SEP-1999; 99US-0156135P.
XX
XX 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
PA
```


XX Krieg AM, Schetter C, Vollmer J;
 PI WPI; 2001-273485/28.
 XX
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX
 PS Claim 101; Page 48; 338pp; English.
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 616 CGCGCGCGCACGCACGCGCG 635
 DB 20 CGCGCGCGCGCGCGCGCG 1
 |||||
 RESULT 243
 AAF99569
 ID AAF99569 standard; DNA; 20 BP.
 XX
 AC AAF99569;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Immunostimulatory nucleic acid #685.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO200122972-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 25-SEP-2000; 2000WO-US026383.
 XX
 PR 25-SEP-1999; 99US-0156113P.
 PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 XX
 DR WPI; 2001-273485/28.
 XX
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX

PS Claim 101; Page 53; 338pp; English.
 XX
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 616 CGCGCGCGCACGCACGCGCG 635
 DB 1 CGCGCGCGCGCGCGCGCG 20
 |||||
 RESULT 244
 AAF99569/c
 ID AAF99569 standard; DNA; 20 BP.
 XX
 AC AAF99569;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Immunostimulatory nucleic acid #685.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO200122972-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 25-SEP-2000; 2000WO-US026383.
 XX
 PR 25-SEP-1999; 99US-0156113P.
 PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 XX
 DR WPI; 2001-273485/28.
 XX
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX
 PS Claim 101; Page 53; 338pp; English.
 XX
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX

CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC hemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone

XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 CGCGCGCGCGACGCGCGCG 635
||||||| ||| |||||
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 245

ABA91532

ID ABA91532 standard; DNA; 20 BP.

XX AC ABA91532;

XX 23-APR-2002 (first entry)

XX DNA oligonucleotide AGT02020 used to test RNase H cleavage.

XX Nucleic acid detection; probe; mismatch; ss.

XX Synthetic.

XX Key misc_feature 13 Location/Qualifiers

XX /tag= a

XX /note= "mismatch to target DNA"

XX WO200206531-A2.

XX 24-JAN-2002.

XX 12-JUL-2001; 2001WO-US022166.

XX 14-JUL-2000; 2000US-00616761.

XX 30-MAR-2001; 2001US-00823647.

XX (GENE-) APPLIED GENE TECHNOLOGIES INC.

XX Dattagupta N;

XX WPI; 2002-171819/22.

XX Probes for detecting target nucleotide sequence in sample, has sequence

XX that forms hairpin structure having a double-stranded segment and single-

XX stranded loop collectively forming region complementary to target

XX sequence.

XX Example 5; Page 49; 72pp; English.

XX The present sequence is that of oligonucleotide AGT02020, which contains

XX a single mismatch with a target DNA oligonucleotide (see ABA91531). It is

XX one of a set of oligonucleotides (see ABA91532-37) containing

XX mismatch(es) to the target DNA that were tested in a hybridisation/RNase

XX H cleavage assay. The results showed that 2 mismatches between the target

XX and the probe ablated RNase H cleavage. The effect of one mismatch site

XX was less than that of two mismatch sites, and showed a polarity effect,

XX with stronger inhibition shown in assays with AGT02020 than in assays

XX using an oligonucleotide in which the mismatch was at an adjacent

XX position. The invention provides probes for nucleic acid hybridisation.

XX The probes form a hairpin structure comprising a double-stranded stem and

XX a single-stranded loop, and are capable of both intramolecular and

CC intermolecular hybridisation. The double-stranded stem may comprise a

CC methylphosphonate DNA:RNA hybrid that is resistant to RNase H cleavage.

CC When the probe hybridises with a target DNA, the RNA strand in the

CC DNA:RNA duplex becomes sensitive to RNase H treatment and can be removed.

CC Arrays and methods for nucleic acid hybridisation using the probes are

CC provided

XX
SQ Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2580 AAAAAAAAAATTCGACGAAAAA 2599
||||||| ||| |||||
Db 1 AAAAAAAAAATTCGAAAAAA 20

RESULT 246

ABA91533

ID ABA91533 standard; DNA; 20 BP.

XX AC ABA91533;

XX 23-APR-2002 (first entry)

XX DNA oligonucleotide AGT02021 used to test RNase H cleavage.

XX Nucleic acid detection; probe; mismatch; ss.

XX Synthetic.

XX Key misc_feature 12 Location/Qualifiers

XX /tag= a

XX /note= "mismatch to target DNA"

XX WO200206531-A2.

XX 24-JAN-2002.

XX 12-JUL-2001; 2001WO-US022166.

XX 14-JUL-2000; 2000US-00616761.

XX 30-MAR-2001; 2001US-00823647.

XX (GENE-) APPLIED GENE TECHNOLOGIES INC.

XX Dattagupta N;

XX WPI; 2002-171819/22.

XX Probes for detecting target nucleotide sequence in sample, has sequence

XX that forms hairpin structure having a double-stranded segment and single-

XX stranded loop collectively forming region complementary to target

XX sequence.

XX Example 5; Page 50; 72pp; English.

XX The present sequence is that of oligonucleotide AGT02021, which contains

XX a single mismatch with a target DNA oligonucleotide (see ABA91531). It is

XX one of a set of oligonucleotides (see ABA91532-37) containing

XX mismatch(es) to the target DNA that were tested in a hybridisation/RNase

XX H cleavage assay. The results showed that 2 mismatches between the target

XX and the probe ablated RNase H cleavage. The effect of one mismatch site

XX was less than that of two mismatch sites, and showed a polarity effect,

XX with weaker inhibition shown in assays with AGT02021 than in assays

XX using an oligonucleotide in which the mismatch was at an adjacent

XX position. The invention provides probes for nucleic acid hybridisation.

XX The probes form a hairpin structure comprising a double-stranded stem and

XX a single-stranded loop, and are capable of both intramolecular and

XX intermolecular hybridisation. The

CC double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that
 CC is resistant to RNase H cleavage. When the probe hybridises with a target
 CC DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H
 CC treatment and can be removed. Arrays and methods for nucleic acid
 CC hybridisation using the probes are provided
 XX
 SQ Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAA 2599
 Db 1 AAAAAAAAAATTGAAAAAAAA 20
 |||||

RESULT 247
 ABS78285
 ID ABS78285 standard; DNA; 20 BP.

XX AC ABS78285;
 XX DT 13-DEC-2002 (first entry)
 XX DE Angiogenesis inhibitory oligonucleotide #769.
 XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Oeler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.

XX OS Synthetic.
 XX PN WO200253141-A2.
 XX PD 11-JUL-2002.
 XX PF 14-DEC-2001; 2001WO-US048458.
 XX PR 14-DEC-2000; 2000US-0255534P.
 XX PA (COLE-) COLEY PHARM GROUP INC.
 XX PI Bratzler RL;
 XX WPI; 2002-566690/60.

DR Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX Claim 2; Page 33; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Oeler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention

XX SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCG 635
 Db 1 CGCGCGCGCGCGCGCG 20
 |||||

RESULT 248
 ABS78285/c
 ID ABS78285 standard; DNA; 20 BP.

XX AC ABS78285;
 XX DT 13-DEC-2002 (first entry)
 XX DE Angiogenesis inhibitory oligonucleotide #769.
 XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Oeler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.

XX OS Synthetic.
 XX PN WO200253141-A2.
 XX PD 11-JUL-2002.
 XX PF 14-DEC-2001; 2001WO-US048458.
 XX PR 14-DEC-2000; 2000US-0255534P.
 XX PA (COLE-) COLEY PHARM GROUP INC.
 XX PI Bratzler RL;
 XX WPI; 2002-566690/60.

DR Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.

XX Claim 2; Page 33; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Oeler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention

XX SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCG 635
 |||||

Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 249

ABS78036

ID ABS78036 standard; DNA; 20 BP.

AC ABS78036;

XX 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #520.

DE Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;

KW plaque neovascularisation; telangiectasia; haemophiliac joint;

KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

KW scleroderma; hypertrophic scar.

XX Synthetic.

OS WO200253141-A2.

PN 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.

XX 14-DEC-2000; 2000US-0255534P.

XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

PI WPI; 2002-566690/60.

DR Inhibiting angiogenesis in a subject, involves administering at least one

XX antiangiogenic nucleic acid molecule to the subject.

XX Claim 2; Page 28; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic

XX acid of the invention

SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 616 CGCGCGCGCGCGCGCGCG 635

Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 250

ABS78036/c

ID ABS78036 standard; DNA; 20 BP.

XX

AC ABS78036;

XX 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #520.

DE Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;

KW plaque neovascularisation; telangiectasia; haemophiliac joint;

KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

KW scleroderma; hypertrophic scar.

XX Synthetic.

OS WO200253141-A2.

PN 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.

XX 14-DEC-2000; 2000US-0255534P.

XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

PI WPI; 2002-566690/60.

DR Inhibiting angiogenesis in a subject, involves administering at least one

XX antiangiogenic nucleic acid molecule to the subject.

XX Claim 2; Page 28; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic

XX acid of the invention

SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 616 CGCGCGCGCGCGCGCGCG 635

Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 251

ABL38812

ID ABL38812 standard; DNA; 20 BP.

XX

AC ABL38812;

XX 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 193.

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;

DR WPI; 2002-154611/20.
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
XX Disclosure; Page 144; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCGCG 20
RESULT 254
ID ABL38811/c
XX ABL38811 standard; DNA; 20 BP.
AC ABL38811;
XX
XX 16-APR-2002 (first entry)
DE Immunostimulatory nucleic acid SEQ ID NO: 192.
DE
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "phosphorothioate backbone"
XX
XX WO200197843-A2.
PN
XX
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US020154.
PF
XX
XX 22-JUN-2000; 2000US-0213346P.
XX
XX (IOWA) UNIV IOWA RES FOUND.
PA
XX
XX Weiner G, Hartmann G;
PI
XX WPI; 2002-154611/20.
DR
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer.
XX
XX Disclosure; Page 144; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCGCG 1
RESULT 255
ID ABA97650/c
XX ABA97650 standard; DNA; 20 BP.
AC ABA97650;
XX
XX 11-APR-2002 (first entry)
DE probe u.
DE
XX ss; fluorochrome; nucleic acid probe; fluorescence.
XX
XX Unidentified.
XX
XX JP2001286300-A.
PN
XX 16-OCT-2001.
PD
XX
XX 20-APR-2000; 2000JP-00120097.
PF
XX
XX 20-APR-1999; 99JP-00111601.
PR
XX 24-AUG-1999; 99JP-00236666.
PR
XX 30-AUG-1999; 99JP-00242693.
PR
XX 01-FEB-2000; 2000JP-00028896.
PR
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
XX WPI; 2002-134193/18.
DR
XX
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
PT
XX
XX Example 6; Page 18; 34pp; Japanese.
PS
XX This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 15 A; 0 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATATATTT 1171
 DB 20 TTTTATATATATATAT 1

RESULT 256
 ACH03107
 ID ACH03107 standard; DNA; 20 BP.
 XX AC ACH03107;
 XX DT 25-SEP-2003 (first entry)
 XX DE Immunostimulatory nucleic acid #742.
 XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX OS Synthetic.
 XX PN US2003050268-A1.
 XX PD 13-MAR-2003.
 XX PF 29-MAR-2002; 2002US-00112653.
 XX PR 29-MAR-2001; 2001US-0279642P.
 XX PA (KRIE/) KRIEG A M.
 XX PI (BERG/) BERG D J.
 XX PI Krieg AM, Berg DJ;
 XX DR WPI; 2003-521815/49.
 XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX PS Disclosure; Page 29; 229pp; English.
 XX CC The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 XX SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
 DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 257
 ACH03107/c
 ID ACH03107 standard; DNA; 20 BP.
 XX AC ACH03107;

XX DT 25-SEP-2003 (first entry)
 XX DE Immunostimulatory nucleic acid #742.
 XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX OS Synthetic.
 XX PN US2003050268-A1.
 XX PD 13-MAR-2003.
 XX PF 29-MAR-2002; 2002US-00112653.
 XX PR 29-MAR-2001; 2001US-0279642P.
 XX PA (KRIE/) KRIEG A M.
 XX PI (BERG/) BERG D J.
 XX PI Krieg AM, Berg DJ;
 XX DR WPI; 2003-521815/49.
 XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX PS Disclosure; Page 29; 229pp; English.
 XX CC The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 XX SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
 DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 258
 ACD99811
 ID ACD99811 standard; DNA; 20 BP.
 XX AC ACD99811;
 XX DT 25-SEP-2003 (first entry)
 XX DE Immunostimulatory nucleic acid #497.
 XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX OS Synthetic.
 XX PN US2003050268-A1.
 XX PD 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.
 XX
 XX 29-MAR-2001; 2001US-0279642P.
 XX
 XX (KRIE/) KRIEG A M.
 XX (BERG/) BERG D J.
 XX
 XX Krieg AM, Berg DJ;
 XX WPI; 2003-521815/49.
 XX
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
 XX disease by administering an immunostimulatory nucleic acid.
 XX
 XX Disclosure; Page 22; 229pp; English.
 XX
 XX The invention describes a method of treating non-allergic inflammatory
 XX disease comprising administering to a subject having or at risk of
 XX developing a non-allergic inflammatory disease an immunostimulatory
 XX nucleic acid for prevention or treatment of the disease. The method is
 XX useful for treating non-allergic inflammatory diseases, such as
 XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 XX This sequence represents an immunostimulatory nucleic acid
 XX
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 16.8; DB 1; Length 20;
 XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 616 CGCGCGCGCAGCAGCGCG 635
 XX 1 CGCGCGCGCGCGCGCGCG 20
 XX
 XX RESULT 259
 XX ACD9811/c
 XX ID ACD9811 standard; DNA; 20 BP.
 XX
 XX ACD9811;
 XX
 XX 25-SEP-2003 (first entry)
 XX
 XX Immunostimulatory nucleic acid #497.
 XX
 XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
 XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX
 XX Synthetic.
 XX
 XX US2003050268-A1.
 XX
 XX 13-MAR-2003.
 XX
 XX 29-MAR-2002; 2002US-00112653.
 XX
 XX 29-MAR-2001; 2001US-0279642P.
 XX
 XX (KRIE/) KRIEG A M.
 XX (BERG/) BERG D J.
 XX
 XX Krieg AM, Berg DJ;
 XX WPI; 2003-521815/49.
 XX
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
 XX disease by administering an immunostimulatory nucleic acid.

XX
 XX Disclosure; Page 22; 229pp; English.
 XX
 XX The invention describes a method of treating non-allergic inflammatory
 XX disease comprising administering to a subject having or at risk of
 XX developing a non-allergic inflammatory disease an immunostimulatory
 XX nucleic acid for prevention or treatment of the disease. The method is
 XX useful for treating non-allergic inflammatory diseases, such as
 XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 XX This sequence represents an immunostimulatory nucleic acid
 XX
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 16.8; DB 1; Length 20;
 XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 616 CGCGCGCGCAGCAGCGCG 635
 XX 20 CGCGCGCGCGCGCGCGCG 1
 XX
 XX RESULT 260
 XX ADB37071
 XX ID ADB37071 standard; DNA; 20 BP.
 XX
 XX ADB37071;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX Immunostimulatory nucleic acid #685.
 XX
 XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 XX hypo-responsive subject; immunostimulatory.
 XX
 XX Synthetic.
 XX
 XX US2003087848-A1.
 XX
 XX 08-MAY-2003.
 XX
 XX 02-FEB-2001; 2001US-00776479.
 XX
 XX 03-FEB-2000; 2000US-0179991P.
 XX
 XX (BRAT/) BRATZLER R L.
 XX (PETE/) PETERSEN D M.
 XX (FOUR/) FOURON Y.
 XX
 XX Bratzler RL, Petersen DM, Fouron Y;
 XX WPI; 2003-657977/62.
 XX
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 XX nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 XX Disclosure; Page 16; 221pp; English.
 XX
 XX The invention relates to a method of treating or preventing allergy or
 XX asthma which comprises administering to a subject a poly-G nucleic acid
 XX in an aerosol formulation. The methods and compositions of the present
 XX invention are useful for diagnosing and/or treating asthma and allergy
 XX especially in a hypo-responsive subject. The present sequence represents
 XX an immunostimulatory nucleic acid of the invention.
 XX
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 16.8; DB 1; Length 20;
 XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 616 CGCGCGCGCAGCAGCGCG 635


```

Db      1 CGCGCGCGCGCGCGCGCGCG 20
|||||
RESULT 261
ADB37071/c
ID      ADB37071 standard; DNA; 20 BP.
XX
AC      ADB37071;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Immunostimulatory nucleic acid #685.
XX
KW      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX      hypo-responsive subject; immunostimulatory.
XX
OS      Synthetic.
XX
PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
Disclosure; Page 16; 22ipp; English.
XX
The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCGCGCG 635
Db      20 CGCGCGCGCGCGCGCGCGCG 1
|||||

RESULT 262
ADB36893
ID      ADB36893 standard; DNA; 20 BP.
XX
AC      ADB36893;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Immunostimulatory nucleic acid #507.
XX
KW      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX      hypo-responsive subject; immunostimulatory.
XX
OS      Synthetic.
XX
PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
Disclosure; Page 16; 22ipp; English.
XX
The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCGCGCG 635
Db      20 CGCGCGCGCGCGCGCGCGCG 1
|||||

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PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
Disclosure; Page 12; 22ipp; English.
XX
The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCGCGCG 635
Db      1 CGCGCGCGCGCGCGCGCGCG 20
|||||

RESULT 263
ADB36893/c
ID      ADB36893 standard; DNA; 20 BP.
XX
AC      ADB36893;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Immunostimulatory nucleic acid #507.
XX
KW      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX      hypo-responsive subject; immunostimulatory.
XX
OS      Synthetic.
XX
PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX

```

```

PS Disclosure; Page 12; 22lpp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCACGCGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1
RESULT 264
ADF86263
ID ADF86263 standard; DNA; 20 BP.
XX
AC ADF86263;
XX
DT 26-FEB-2004 (first entry)
XX
DE Rat TGF-beta 2 PCR primer related to liver regeneration SeqID9.
XX
KW liver regeneration promoter; hepatic disorder; anti-kallikrein antibody;
KW hepatotropic; antiinflammatory; virucide; TGF;
KW transforming growth factor-beta; liver tissue fibrosis; liver cirrhosis;
KW hepatitis; liver regeneration insufficiency; PCR; primer; ss; rat;
KW TGF-beta 2.
XX
OS Rattus sp.
XX
PN JP2003252792-A.
XX
PD 10-SEP-2003.
XX
PF 04-MAR-2002; 2002JP-00057253.
XX
PR 04-MAR-2002; 2002JP-00057253.
XX
PA (RIKA ) RIKAGAKU KENKYUSHO.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
DR WPI; 2003-857283/80.
XX
OS
PT Liver regeneration promoter for treating and preventing hepatic disorder,
PT contains anti-kallikrein antibody as active ingredient.
XX
PN JP2003252792-A.
XX
PD 10-SEP-2003.
XX
PF 04-MAR-2002; 2002JP-00057253.
XX
PR 04-MAR-2002; 2002JP-00057253.
XX
PA (RIKA ) RIKAGAKU KENKYUSHO.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
DR WPI; 2003-857283/80.
XX
PT Liver regeneration promoter for treating and preventing hepatic disorder,
PT contains anti-kallikrein antibody as active ingredient.
PS Disclosure; SEQ ID NO 9; 25pp; Japanese.
XX
CC This invention relates to a novel liver regeneration promoter for
CC treating and preventing a hepatic disorder, which contains anti-
CC kallikrein antibody as an active ingredient. The invention may be useful
CC in the development of compositions with hepatotropic, antiinflammatory or
CC virucide activities as a transforming growth factor (TGF)-agonist. The
CC invention may be useful for treating and preventing hepatic disorders
CC resulting from the effect of transforming growth factor-beta, liver
CC tissue fibrosis, liver cirrhosis, hepatitis or liver regeneration
CC insufficiency.
XX
SQ Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1965 TTTCGAGGTATCGATGGCAC 1984
DB 1 TTTCGAGGTATCGATGGCAC 20
RESULT 265
ADF86264/c
ID ADF86264 standard; DNA; 20 BP.
XX
AC ADF86264;
XX
DT 26-FEB-2004 (first entry)
XX
DE Rat TGF-beta 2 PCR primer related to liver regeneration SeqID10.
XX
KW liver regeneration promoter; hepatic disorder; anti-kallikrein antibody;
KW hepatotropic; antiinflammatory; virucide; TGF;
KW transforming growth factor-beta; liver tissue fibrosis; liver cirrhosis;
KW hepatitis; liver regeneration insufficiency; PCR; primer; ss; rat;
KW TGF-beta 2.
XX
OS Rattus sp.
XX
PN JP2003252792-A.
XX
PD 10-SEP-2003.
XX
PF 04-MAR-2002; 2002JP-00057253.
XX
PR 04-MAR-2002; 2002JP-00057253.
XX
PA (RIKA ) RIKAGAKU KENKYUSHO.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
DR WPI; 2003-857283/80.
XX
PT Liver regeneration promoter for treating and preventing hepatic disorder,
PT contains anti-kallikrein antibody as active ingredient.
PS Disclosure; SEQ ID NO 10; 25pp; Japanese.
XX
CC This invention relates to a novel liver regeneration promoter for
CC treating and preventing a hepatic disorder, which contains anti-
CC kallikrein antibody as an active ingredient. The invention may be useful
CC in the development of compositions with hepatotropic, antiinflammatory or
CC virucide activities as a transforming growth factor (TGF)-agonist. The
CC invention may be useful for treating and preventing hepatic disorders
CC resulting from the effect of transforming growth factor-beta, liver
CC tissue fibrosis, liver cirrhosis, hepatitis or liver regeneration
CC insufficiency.
XX
SQ Sequence 20 BP; 6 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2159 GCATAATTGCTGCTTGGCC 2178
DB 20 GCATAATTGCTGCTTGGCC 1
RESULT 266
ABZ86060/c
ID ABZ86060 standard; DNA; 20 BP.
XX
AC ABZ86060;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;

```

antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.
Homo sapiens.
WO200285308-A2.
31-OCT-2002.
23-APR-2002; 2002WO-US013135.
24-APR-2001; 2001US-0286137P.
(SPIG-) EPIGENESIS PHARM INC.
Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahabuddin S;
WPI; 2003-229219/22.
Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.
Claim 15; SEQ ID NO 1302; 872pp; English.
The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisense to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
immunosuppressive, and cytostatic activity. The composition may have a
use in antisense gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of adenosine
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences
Sequence 20 BP; 0 A; 1 C; 5 G; 14 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY 2667 CAGCAACAAACCAACCAAAA 2686
DB 20 CAGCAACAAACCAACCAAAA 1
|||||
RESULT 267
ABZ89592/c
ID ABZ89592 standard; DNA; 20 BP.
XX
AC ABZ89592;
DT
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.
Homo sapiens.
WO200285308-A2.
31-OCT-2002.
23-APR-2002; 2002WO-US013135.
24-APR-2001; 2001US-0286137P.
(EPIG-) EPIGENESIS PHARM INC.
Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahabuddin S;
WPI; 2003-229219/22.
Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.
Disclosure; SEQ ID NO 4834; 872pp; English.
The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisense to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
immunosuppressive, and cytostatic activity. The composition may have a
use in antisense gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of adenosine
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences
Sequence 20 BP; 8 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Qy 2749 TTTTITTAAGGAAAAAATA 2768
||||| |||||||
Db 20 TTTTITTAAGGAAAAAAGA 1
RESULT 268
ABD22290/c
ID ABD22290 standard; DNA; 20 BP.
XX ABD22290;
XX
XX 29-JUL-2004 (first entry)
XX Human stanniocalcin-derived oligo SEQ ID 1302.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung cancer;

KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 XX Homo sapiens.
 OS
 XX W0200285309-A2.
 PN
 XX 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013143.
 XX
 XX 24-APR-2001; 2001US-0286036P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 XX WPI; 2003-093058/08.
 DR
 XX
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 XX Claim 15; SEQ ID NO 1302; 763pp; English.
 PS
 XX
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiasthmatic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 0 A; 1 C; 5 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2667 CAGCAACAAACCAACAAA 2686
 Db 20 CAGCAACAAACCAACAAA 1

RESULT 269
 ABD25822/c
 ID ABD25822 standard; DNA; 20 BP.
 XX
 XX ABD25822;
 AC
 XX 29-JUL-2004 (first entry)
 DT
 XX
 XX AI085559-derived oligonucleotide SEQ ID 4834.
 DE
 XX
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 XX Homo sapiens.
 OS
 XX W0200285309-A2.
 PN
 XX 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013143.
 XX
 XX 24-APR-2001; 2001US-0286036P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 XX WPI; 2003-093058/08.
 DR
 XX
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 XX Claim 15; SEQ ID NO 4834; 763pp; English.
 PS
 XX
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiasthmatic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to
 CC prevent any unwanted effects due to it

[illegible]

DT 22-APR-2004 (first entry)
 XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 71.
 DE
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 KW
 XX Homo sapiens.
 OS
 XX US2004006030-A1.
 XX
 XX 08-JAN-2004.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 XX
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 XX Example 15; SEQ ID NO 71; 135pp; English.
 PS
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3056 TGGATGGCTTAAGGAGTTTG 3075
 Db 20 TGGATGGCTTAAGGAACTTG 1
 RESULT 273
 ADI80187
 ID ADI80187 standard; DNA; 20 BP.
 XX
 AC ADI80187;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 188.

XX
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX
 OS Homo sapiens.
 XX
 XX US2004006030-A1.
 PN
 XX 08-JAN-2004.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX 02-JUL-2002; 2002US-00189267.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 XX
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX
 XX Example 16; SEQ ID NO 188; 135pp; English.
 PS
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2127 TTGGATGCTGCTACTGCTT 2146
 Db 1 TTGGATGGGCTATTGCTT 20
 RESULT 274
 ADI80040/c
 ID ADI80040 standard; DNA; 20 BP.
 XX
 AC ADI80040;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 41.
 DE
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 XX immune; ss; human.
 OS Homo sapiens.
 XX US2004006030-A1.
 PN 08-JAN-2004.
 XX 02-JUL-2002; 2002US-00189267.
 XX 02-JUL-2002; 2002US-00189267.
 PF (ISIS-) ISIS PHARM INC.
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 DR New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 PS Example 15; SEQ ID NO 41; 135pp; English.
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX Sequence 20 BP; 7 A; 4 C; 1 G; 8 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1870 TGGGGTTTAAATAAGTTTA 1889
 Db 20 TGGGATTAAATAAGCTTA 1
 RESULT 275
 AD180185
 ID AD180185 standard; DNA; 20 BP.
 AC AD180185;
 XX 22-APR-2004 (first entry)
 DT Human transforming growth factor-beta 2 target DNA region, SEQ ID No 186.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX

OS Homo sapiens.
 XX US2004006030-A1.
 XX 08-JAN-2004.
 PD 02-JUL-2002; 2002US-00189267.
 PF 02-JUL-2002; 2002US-00189267.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Freier SM, Dobie KW;
 XX WPI; 2004-081742/08.
 DR New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX Example 16; SEQ ID NO 186; 135pp; English.
 XX The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.
 XX Sequence 20 BP; 8 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1870 TGGGGTTTAAATAAGTTTA 1889
 Db 1 TGGGATTAAATAAGCTTA 20
 RESULT 276
 AD180006
 ID AD180006 standard; DNA; 20 BP.
 XX AD180006;
 AC AD180006;
 XX 22-APR-2004 (first entry)
 DT Human transforming growth factor-beta 2 PCR probe.
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; human; probe; ss.
 XX Homo sapiens.
 XX US2004006030-A1.
 PN

XX PD 08-JAN-2004.
 XX XX
 XX PF 02-JUL-2002; 2002US-00189267.
 XX XX
 XX PR 02-JUL-2002; 2002US-00189267.
 XX XX
 XX PA (ISIS-) ISIS PHARM INC.
 XX XX
 XX PI Monia BP, Freier SM, Dobie KW;
 XX XX
 XX DR WPI; 2004-081742/08.
 XX XX
 XX PT New compounds, particularly antisense oligonucleotides targeted to a
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX PS Example 13; SEQ ID NO 7; 135pp; English.
 XX XX
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents a probe used in the exemplification of the invention.
 XX XX
 XX SQ Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2119 AGCGGCTTTGGATGCTGCC 2138
 DB 1 AGCGTCTTTGGATGCGGCC 20
 RESULT 277
 ADI80034/c
 ID ADI80034 standard; DNA; 20 BP.
 XX AC
 XX AC ADI80034;
 XX DT 22-APR-2004 (first entry)
 XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 35.
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX OS Homo sapiens.
 XX PN US2004006030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PR 02-JUL-2002; 2002US-00189267.

PF 02-JUL-2002; 2002US-00189267.
 XX XX
 PR 02-JUL-2002; 2002US-00189267.
 XX XX
 PA (ISIS-) ISIS PHARM INC.
 XX XX
 XX PI Monia BP, Freier SM, Dobie KW;
 XX XX
 XX DR WPI; 2004-081742/08.
 XX XX
 XX PT New compounds, particularly antisense oligonucleotides targeted to a
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX PS Example 15; SEQ ID NO 35; 135pp; English.
 XX XX
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX XX
 XX SQ Sequence 20 BP; 1 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2094 TCACAAACAGTCCAGCGCGC 2113
 DB 20 TCACAAACAGACCAACCGCGC 1
 RESULT 278
 ADI80022/c
 ID ADI80022 standard; DNA; 20 BP.
 XX AC
 XX AC ADI80022;
 XX DT 22-APR-2004 (first entry)
 XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 23.
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX OS Homo sapiens.
 XX PN US2004006030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Freier SM, Dobie KW;
 XX DR WPI; 2004-081742/08.
 XX PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX PS Example 15; SEQ ID NO 23; 135pp; English.
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2349 CCTTCTGTGTCTCCAGGA 2368
 DB 20 CCTTCTGTGTCTCCAGA 1
 RESULT 279
 ADI80043/c
 ID ADI80043 standard; DNA; 20 BP.
 XX AC ADI80043;
 XX DT 22-APR-2004 (first entry)
 XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 44.
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX OS Homo sapiens.
 XX PN US2004006030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PP 02-JUL-2002; 2002US-00189267.
 XX PR 02-JUL-2002; 2002US-00189267.
 XX PA (ISIS-) ISIS PHARM INC.

PI Monia BP, Freier SM, Dobie KW;
 XX DR WPI; 2004-081742/08.
 XX PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
 PT neurodegenerative disorder, or a disease involving hyperactivation of
 PT immune response.
 XX PS Example 15; SEQ ID NO 44; 135pp; English.
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
 CC in length targeted to, and which specifically hybridizes with, a nucleic
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
 CC inhibits the expression of TGF-beta 2. The invention further relates to:
 CC a compound 8-80 nucleobases in length that specifically hybridizes with
 CC at least an 8-nucleobase portion of an active site on a nucleic acid
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
 CC tissues by contacting the cells or tissues with the compound so that
 CC expression of TGF-beta 2 is inhibited; treating an animal having a
 CC disease or condition associated with TGF-beta 2 by administering to the
 CC animal a therapeutic or prophylactic amount of the compound so that
 CC expression of TGF-beta 2 is inhibited; and screening an antisense
 CC compound. The antisense compound has cytostatic, neurotropic,
 CC neuroprotective, and immunosuppressive activities. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
 CC cancer, a neurodegenerative disorder, or a disease or condition involving
 CC hyperactivation of an immune response. This polynucleotide sequence
 CC represents an antisense oligonucleotide of the invention.
 XX SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2127 TTGGATGCTGCTACTGCTT 2146
 DB 20 TTGGATGCGGCTATTGCTT 1
 RESULT 280
 ADI80173
 ID ADI80173 standard; DNA; 20 BP.
 XX AC ADI80173;
 XX DT 22-APR-2004 (first entry)
 XX DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 174.
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
 KW immune; ss; human.
 XX OS Homo sapiens.
 XX PN US2004006030-A1.
 XX PD 08-JAN-2004.
 XX PF 02-JUL-2002; 2002US-00189267.
 XX PP 02-JUL-2002; 2002US-00189267.
 XX PR (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Freier SM, Dobie KW;
 XX DR WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 174; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2349 CCTGCTGTGTGCCAGCA 2368
DB 1 CCTGCTGTGTGCCAGCA 20
RESULT 281
AD180045/c
ID AD180045 standard; DNA; 20 BP.
XX AC AD180045;
XX DT 22-APR-2004 (first entry)
XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 46.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; human.
XX OS Homo sapiens.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 15; SEQ ID NO 46; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2446 CTTGTAATGTCAGCTAAAGT 2465
DB 20 CTTGTAATGTCAGCTAAAT 1
RESULT 282
ADK79195
ID ADK79195 standard; DNA; 20 BP.
XX AC ADK79195;
XX DT 20-MAY-2004 (first entry)
XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #6529.
XX KW Nav1.3; Analgesic; Neurotropic; Neuroprotective; post-herpetic neuralgia;
XX KW diabetic neuropathy; arthritic pain; migraine headache;
XX KW infantile epilepsy; ataxia; ss.
XX OS Synthetic.
XX PN WO2004016754-A2.
XX PD 26-FEB-2004.
XX PF 14-AUG-2003; 2003WO-US025465.
XX PR 14-AUG-2002; 2002US-0403416P.
XX PA (PHAA) PHARMACIA CORP.
XX PI Robertds SL;
XX DR WPI; 2004-203785/19.
XX PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX Claim 4; SEQ ID NO 6529; 417pp; English.
PS

XX The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 13 A; 2 C; 1 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACATCAA 2820
 DB 1 TGAATAAAAAAAAAACATCTA 20

RESULT 283
 ADOS3074/C
 ID ADOS3074 standard; DNA; 20 BP.
 AC
 AC ADOS3074;
 XX
 XX 15-JUL-2004 (first entry)
 XX Farnesoid X receptor gene expression antisense inhibitory oligo #447.
 DE ss; antidiabetic; immunosuppressive; cardiovascular; antilipemic;
 XX antihypertensive; hepatotropic; litholytic; anorectic;
 KW neuroprotective; vasotropic; antisense; gene therapy;
 KW Farnesoid X receptor; diabetes; immunological disorder;
 KW cardiovascular disorder; dyslipidemia; atherosclerosis;
 KW high density lipoprotein; low density lipoprotein; hypercholesterolemia;
 KW gallstones; hypertriglyceridemia; obesity; neurological disorder;
 KW ischemia; reperfusion; diagnostics; prophylaxis.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2004030750-A1.
 PN
 XX
 XX 15-APR-2004.
 PD
 XX
 XX 25-SEP-2003; 2003WO-US030353.
 PF
 XX
 XX 25-SEP-2002; 2002US-0413588P.
 PR
 XX
 XX (PHAA) PHARMACIA CORP.
 PA
 XX
 XX Kane CD;
 PI
 XX
 XX WPI; 2004-347928/32.
 DR
 XX
 XX New antisense oligonucleotides useful for modulating expression of
 PT Farnesoid X Receptor (FXR) or for treating diseases associated with FXR,
 PT e.g. diabetes, immunological disorders, cardiovascular disorders,
 PT gallstones or obesity.
 PT
 XX
 XX Claim 4; SEQ ID NO 447; 150pp; English.
 PS
 XX
 XX The invention relates to an antisense compound 8-30 nucleobases in length
 CC targeted to a nucleic acid molecule encoding Farnesoid X receptor (FXR),
 CC where the antisense compound specifically hybridizes with and inhibits
 CC the expression of FXR. The composition and methods are useful for

CC inhibiting the expression of FXR (Farnesoid X receptor) in cells or
 CC tissues, or for treating diseases or conditions associated with FXR, such
 CC as diabetes, immunological disorders, cardiovascular disorders, e.g.
 CC dyslipidemia and its symptoms, atherosclerosis, low HDL (high density
 CC lipoprotein), elevated LDL (low density lipoprotein) or
 CC hypercholesterolemia, gallstones, hypertriglyceridemia, obesity,
 CC neurological disorders, or ischemia/reperfusion injury. In addition, the
 CC composition is used for diagnostics, prophylaxis, or as research reagents
 CC or kits. This sequence corresponds to an antisense oligonucleotide of the
 CC invention.

XX Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3346 TCAGACTTTTGACCGTGAAG 3365
 DB 20 TCAGACTTTTGACCATGAAG 1

RESULT 284
 AAQ73754/C
 ID AAQ73754 standard; DNA; 21 BP.
 XX
 XX AAQ73754;
 AC
 AC
 XX 10-JUL-1995 (first entry)
 DT
 XX Rice starch branching enzyme promoter 3'-primer.
 DE
 XX Starch branching enzyme promoter; rice; starch content; PCR primer; ss.
 KW
 KW
 XX Synthetic.
 OS
 XX JP06261767-A.
 PN
 XX 20-SEP-1994.
 PD
 XX 22-OCT-1993; 93JP-00265171.
 PF
 XX 29-OCT-1992; 92JP-00291719.
 PR
 XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 PA
 XX WPI; 1994-337418/42.
 DR
 XX
 XX New gene of branching enzyme of rice starch - useful for increasing
 PT starch yield of grain.
 PT
 XX
 XX Example 2; Page 13; 13pp; Japanese.
 PS
 XX The rice starch branching enzyme gene promoter was amplified using a 5'-
 CC primer (AAQ73753) and a 3'-primer (AAQ73754) corresponding to nucleotides
 CC 4-23 and 995-1115, respectively, of the promoter sequence. The promoter
 CC can be operatively linked to the branching enzyme gene or to heterologous
 CC genes for expression in plant seeds

XX Sequence 21 BP; 0 A; 3 C; 12 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 629 ACGCGCGCACGCGCACAC 648
 DB 21 ACGCGCGCACACACACAC 2

RESULT 285
 AAQ75791/C
 ID AAQ75791 standard; DNA; 21 BP.

XX AC AAQ75791;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 9; 11pp; Japanese.
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 XX CC and using the aggregate of mRNAs as the template for each reverse
 XX CC transcription primer; (b) digesting each of the prepared aggregates of
 XX CC the double-stranded cDNAs with restriction enzyme and; (c)
 XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 XX CC method can be used to analyse gene expression rapidly and easily
 XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 925 CAGGAGAAAAAACAACAAA 944
 Db 21 CAGGAGAAAAAACAACAAA 2
 RESULT 286
 ADD29304/c
 ID ADD29304 standard; DNA; 24 BP.
 XX AC ADD29304;
 XX DT 15-JAN-2004 (first entry)
 XX DE Molecular and biological process inhibiting oligonucleotide seq id 67.
 XX KW molecular process inhibition; monomeric unit;
 XX KW oligonucleotide interaction; polynucleotide interaction;
 XX KW enzyme interaction; local interaction; ss.
 XX OS Synthetic.
 XX PN US6548251-B1.
 XX PD 15-APR-2003.
 XX PF 05-SEP-2000; 2000US-00655804.
 XX PR 05-SEP-2000; 2000US-00655804.

PA (FIDE-) FIDELITY SYSTEMS INC.
 XX Kozyavkin SA, Malykh AG, Polouchine NN, Slesarev AI;
 XX WPI; 2003-786284/74.
 XX DR Inhibiting nucleic acid hybridization and/or extension in a sample
 XX PT comprises administering to the sample a modified oligonucleotide or
 XX PT polynucleotide that contains at least one monomeric unit.
 XX PS Disclosure; SEQ ID NO 67; 38pp; English.
 XX CC The invention describes a method of inhibiting a molecular process
 XX CC involving the interaction between nucleic acids in a sample capable of
 XX CC undergoing the molecular process. The method comprises administering to
 XX CC the sample an oligonucleotide or polynucleotide that contains at least
 XX CC one monomeric unit having a specific formula. The method is useful in
 XX CC inhibiting undesired molecular interaction between oligonucleotides and
 XX CC their complexes with polynucleotides and enzymes, including local
 XX CC interactions between their chemical units (nucleotides or amino acids).
 XX CC This sequence represents an oligonucleotide used to inhibit undesired
 XX CC molecular interaction between oligonucleotides and their complexes with
 XX CC polynucleotides and enzymes.
 XX SQ Sequence 24 BP; 11 A; 3 C; 0 G; 10 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.6; DB 1; Length 24;
 Best Local Similarity 82.6%; Pred. No. 2.9e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2732 AAAAGAAAACATCTTTTTTTTTT 2754
 Db 24 AAAAGAAAACATCTTTTTTTTTT 2
 RESULT 287
 AAQ78427/c
 ID AAQ78427 standard; DNA; 18 BP.
 XX AC AAQ78427;
 XX DT 25-MAR-2003 (revised)
 XX DT 27-JUN-1995 (first entry)
 XX DE TGF-beta gene phosphorothioate antisense oligonucleotide.
 XX KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 XX KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 XX KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 XX KW immunosuppression; oligonucleotide; ss.
 XX OS Synthetic.
 XX PN WO9425588-A2.
 XX PD 10-NOV-1994.
 XX PF 29-APR-1994; 94WO-EP001362.
 XX PR 30-APR-1993; 93EP-00107089.
 XX PR 13-MAY-1993; 93EP-00107849.
 XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 XX PI Bogdahn U;
 XX DR WPI; 1994-358266/44.
 XX PT New transforming growth factor beta anti-sense oligo-nucleotide(s) - for
 XX PT treating immunosuppression, tumours, etc.
 XX PS Claim 6; Page 46; 74pp; English.

XX The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 18 BP; 6 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1589 ACCCTACTTCAGAAATCGT 1606
 |||||
 DB 18 ACCCTACTTCAGAAATGTT 1
 RESULT 288
 AAQ78484/C
 ID AAQ78484 standard; DNA; 18 BP.
 XX
 AC AAQ78484;
 XX
 XX Transforming growth factor beta; TGF-beta; antisense; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX
 OS Synthetic.
 XX
 XX WO9425588-A2.
 PN
 PD 10-NOV-1994.
 XX
 XX 29-APR-1994; 94WO-EP001362.
 PF
 XX
 XX 30-APR-1993; 93EP-00107089.
 PR
 XX 13-MAY-1993; 93EP-00107849.
 PR
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 PI Bogdahn U;
 XX
 XX WPI; 1994-358266/44.
 DR
 XX
 XX New transforming growth factor beta anti-sense oligonucleotide(s) - for
 PT treating immunosuppression, tumours, etc.
 PT
 XX
 XX Claim 6; Page 62; 74pp; English.
 PS
 XX The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric

CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2446 CTTGTAAATGCAGCTAAA 2463
 |||||
 DB 18 CTTGCAATGCAGCTAAA 1
 RESULT 289
 AAZ65452/C
 ID AAZ65452 standard; DNA; 18 BP.
 XX
 AC AAZ65452;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-12.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 XX WO9963975-A2.
 PN
 XX 16-DEC-1999.
 PD
 XX 10-JUN-1999; 99WO-EP004013.
 PF
 XX 10-JUN-1998; 98EP-00110709.
 PR
 XX 25-JUL-1998; 98EP-00113974.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI WPI; 2000-097470/08.
 XX
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 PT
 XX
 XX Claim 5; Fig 1; 30pp; English.
 PS
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-

CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 18 BP; 6 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1589 ACCCTACTTCAGATCGT 1606
 |||||
 Db 18 ACCCTACTTCAGATTCGT 1

RESULT 290
 AAZ65510/C
 ID AAZ65510 standard; DNA; 18 BP.
 XX
 AC AAZ65510;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta-123-2262.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 PN WO9963975-A2.
 XX
 PD 16-DEC-1999.
 XX
 PF 10-JUN-1999; 99WO-EP004013.
 XX
 PR 10-JUN-1998; 98EP-00110709.
 PR 25-JUL-1998; 98EP-00113974.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX
 DR WPI; 2000-097470/08.
 XX
 PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 XX
 PS Claim 10; Fig 1; 30pp; English.
 XX
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC

CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 18 BP; 5 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2237 GTACATGCTAACTTCGT 2254
 |||||
 Db 18 GTACATGCCAACTTCGT 1

RESULT 291
 AAZ65466/C
 ID AAZ65466 standard; DNA; 18 BP.
 XX
 AC AAZ65466;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-26.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 PN WO9963975-A2.
 XX
 PD 16-DEC-1999.
 XX
 PF 10-JUN-1999; 99WO-EP004013.
 XX
 PR 10-JUN-1998; 98EP-00110709.
 PR 25-JUL-1998; 98EP-00113974.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX
 DR WPI; 2000-097470/08.
 XX
 PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 XX
 PS Claim 5; Fig 1; 30pp; English.
 XX
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX

SQ Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2446 CTTGTAATGCAGCTAAA 2463
 ||||| ||||| ||||| |||||
 Db 18 CTTGCAATGCAGCTAAA 1

RESULT 292
 ABA97624/C
 ID ABA97624 standard; DNA; 18 BP.
 XX AC ABA97624;
 XX DT 11-APR-2002 (first entry)
 XX DE Probe c.
 XX ss; fluorochrome; nucleic acid probe; fluorescence.
 XX Unidentified.
 XX JP2001286300-A.
 XX PD 16-OCT-2001.
 XX PF 20-APR-2000; 2000JP-00120097.
 XX PR 20-APR-1999; 99JP-00111601.
 XX PR 24-AUG-1999; 99JP-00236666.
 XX PR 30-AUG-1999; 99JP-00242693.
 XX PR 01-FEB-2000; 2000JP-00028896.
 XX PA (BIOI-) BIOINDUSTRY KYOKAI SH.
 XX PA (KANK-) KANKYO ENG KK.
 XX PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIUTSU SOGO KEN.
 XX DR WPI; 2002-134193/18.
 XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
 the obtained data.
 XX Example 5; Page 17; 34pp; Japanese.
 XX This invention relates to a method for measuring nucleic acids using a
 nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
 decreases the fluorescence of the fluorochrome when hybridised with a
 target nucleic acid, the decrease in the fluorescence is measured. The
 method can be used for measuring a target nucleic acid

SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1151 GTTCTCTTTTATATATA 1168
 ||||| ||||| ||||| |||||
 Db 18 GTTTTCTTTTATATATA 1

RESULT 293
 ABL95897/C
 ID ABL95897 standard; DNA; 18 BP.
 XX AC ABL95897;
 XX DT 19-JUN-2002 (first entry)
 XX DE Probe c for assaying nucleic acids.

XX Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX Unidentified.
 XX WO200208414-A1.
 XX 31-JAN-2002.
 XX 27-JUN-2001; 2001WO-1B001147.
 XX 27-JUN-2000; 2000JP-00193133.
 XX 03-AUG-2000; 2000JP-00236115.
 XX 26-SEP-2000; 2000JP-00292483.
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX (KANK-) KANKYO ENG CO LTD.
 XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;
 XX WPI; 2002-195876/25.
 XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 their polymorphism and mutation, particularly useful in science and
 medicine for e.g. analytical applications, disease diagnosis and
 microbial identification.
 XX Example 12; Page 60; 152pp; Japanese.
 XX The present invention relates to nucleic acid probes, which are useful
 for assaying nucleic acids by hybridising with a target nucleic acid, in
 which a single-stranded oligonucleotide is labelled with a fluorescent
 substance and a quencher in a manner that the fluorescence intensity of
 the hybridisation reaction system is increased after completion of the
 hybridisation but no stem loop structure is formed. The probes are useful
 for assaying nucleic acids and their polymorphism and mutation,
 particularly useful for e.g. analytical applications, disease diagnosis
 and microbial identification. The present sequence was used to illustrate
 the invention

SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1151 GTTCTCTTTTATATATA 1168
 ||||| ||||| ||||| |||||
 Db 18 GTTTTCTTTTATATATA 1

RESULT 294
 AAA85942/C
 ID AAA85942 standard; DNA; 19 BP.
 XX AC AAA85942;
 XX DT 04-DEC-2000 (first entry)
 XX DE Cdc 25 hs ribozyme binding site #50.
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; reestenosis; ss.
 XX Mammalia.
 XX WO200032765-A2.
 XX 08-JUN-2000.
 XX 06-DEC-1999; 99WO-US028772.
 XX

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PR 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 100; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 924 CCAGGAGAGAAAAAACAAC 941
DB 18 CCAGGAGAGAAAAAACAAC 1
RESULT 295
ID AAA85941 standard; DNA; 19 BP.
XX AAA85941;
XX
XX 04-DEC-2000 (first entry)
XX
XX Cdc 25 hs ribozyme binding site #49.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 100; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 924 CCAGGAGAGAAAAAACAAC 941
DB 19 CCAGGAGAGAAAAAACAAC 2
RESULT 296
ID AAH61103 standard; DNA; 19 BP.
XX AAH61103;
XX
XX 10-SEP-2001 (first entry)
XX
XX Cdc25 hs ribozyme binding site SEQ ID NO:3527.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX recognition site; target; ribozyme binding site; eye disease; vulnery;
XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
XX antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
XX atopic dermatitis; actinic keratosis; squamous cell carcinoma;
XX basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
XX sickle cell retinopathy; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200130362-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
XX (IMMU-) IMMUSOL INC.
XX
XX Robbins JM, Tritz R;
XX WPI; 2001-300427/31.
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
XX that cleave RNA encoding cytokines involved in inflammation, matrix
XX metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 328; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
XX skin or eye disease and scarring. The method involves administering a
XX ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX dependent kinase, growth factor or a reductase, or administering a
XX nucleic acid molecule (II) comprising a promoter operably linked to a
XX nucleic acid segment encoding (I). (I) can have antipsoriatic,
XX dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
XX ophthalmological, vulnery, keratolytic and virucide activities, and
XX cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX in gene therapy. (I) and (II) are useful for treating proliferative skin
XX diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX also be used for treating proliferative eye diseases such as diabetic
```


CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 924 CCAGGAGAAAAAAAC 941
|||||
Db 19 CCAGGAGAAAAAAAC 2
RESULT 297
AAH61104/C
ID AAH61104 standard; DNA; 19 BP.
XX
AC AAH61104;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdc25 hs ribozyme binding site SEQ ID NO:3528.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; virucide;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiscaling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 328; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscaling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 924 CCAGGAGAAAAAAAC 941
|||||
Db 18 CCAGGAGAAAAAAAC 1
RESULT 298
ADQ60911
ID ADQ60911 standard; RNA; 19 BP.
XX
AC ADQ60911;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-BMX siRNA related DNA sequence SEQ ID NO:613.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.
XX
OS Synthetic.
XX
PN WO2004045543-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.
PR 10-SEP-2003; 2003US-0502050P.
XX
PA (DHAR-) DHARMA CON INC.
XX
PI Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
DR WPI; 2004-420527/39.
XX
PS Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
PS Example 12; SEQ ID NO 613; 199pp; English.
XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the
CC functionality of sequences of 19-25 nucleotides in length that are
CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA molecule
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC sequence consisting of GGGAGUAGUGAUGAUGA; GAAGUACUCCUUGUAG;
CC GUACGACACCGGAGUA; AGUAGUGAUGAUGAUGA; UGAAGACUCUGUCAGUUU;
CC GUACGACACCGGAGUA; UGCGCCUCUUGUAGUUU; GAGUAGUGAUGAUGA;
CC GAGUAGUGAUGAUGAUGA; and GAAGUACUCCUUGUAGUUU. The siRNA molecule
CC comprises a sense strand and an anti-sense strand. The siRNA molecule
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 bases

CC pairs. The kit comprises at least two siRNA, comprising a first optimised
CC siRNA and a second optimised siRNA. The method is useful in selecting
CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention. The sequence is shown in
CC the specification as DNA, but described as siRNA.

XX SQ Sequence 19 BP; 8 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 938 AAACAAACCTTCTCTACT 955
Db 1 AAACAAACCTTCTCTACT 18

RESULT 299

ADS90660
ID ADS90660 standard; DNA; 19 BP.

XX AC ADS90660;

XX DT 18-NOV-2004 (first entry)

XX DE Oligonucleotide of the invention SEQ ID NO:1676.

XX KW ss; cell proliferative disorder; breast; methylation; cytostatic;
XX KW gene therapy; single nucleotide polymorphism; SNP.

XX OS Unidentified.

XX PN WO2004035803-A2.

XX PD 29-APR-2004.

XX PF 01-OCT-2003; 2003WO-EP010881.

XX PR 01-OCT-2002; 2002DE-01045779.

XX PR 07-JAN-2003; 2003DE-0100096.

XX PR 17-APR-2003; 2003DE-01017955.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
XX PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX WPI; 2004-348469/32.

XX PT Predicting responsiveness of a subject with breast cell proliferative
XX PT disorder, useful for treating or differentiating breast cell
XX PT proliferative disorders comprises analyzing methylation pattern of a
XX PT genomic DNA from the subject.

XX PS Disclosure; SEQ ID NO 1676; 104pp; English.

XX CC The invention relates to a novel method for predicting the responsiveness
XX CC of a subject with a cell proliferative disorder of the breast tissues to
XX CC a therapy comprising analysing the methylation pattern of a target
XX CC nucleic acid by contacting at least one of the target nucleic acids in a
XX CC biological sample obtained from the subject prior to or during treatment.
XX CC The method of the invention has cytostatic activity, and may have a use
XX CC in gene therapy. The set of oligonucleotides comprising at least two of
XX CC the oligomers are useful for detecting the cytosine methylation state
XX CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
XX CC methods, nucleic acid, oligonucleotide, and kit are useful for the
XX CC treatment, characterisation, classification and/or differentiation, of
XX CC breast cell proliferative disorders. The method is also useful for
XX CC predicting the responsiveness of a subject with a cell proliferative
XX CC disorder of the breast tissues to a therapy. The present sequence is used
XX CC in the exemplification of the invention.

XX SQ Sequence 19 BP; 5 A; 0 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2745 TTTTTCCTTTTAAAGGAAA 2762
Db 1 TTTTTCCTTTTAAAGGAAA 18

RESULT 300

AAX32003
ID AAX32003 standard; DNA; 20 BP.

XX AC AAX32003;

XX DT 14-JUN-1999 (first entry)

XX DE MSH2 gene specific primer.

XX KW Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
XX KW CPT2; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
XX KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
XX KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
XX KW BAP1 gene; PCR primer; ss.

XX OS Synthetic.

XX PN WO9906598-A2.

XX PD 11-FEB-1999.

XX PF 04-AUG-1998; 98WO-US016574.

XX PR 04-AUG-1997; 97US-00905772.

XX PR 22-MAY-1998; 98US-00084471.

XX PA (ONCO-) ONCORMED INC.

XX PI Murphy PD;

XX DR WPI; 1999-153820/13.

XX PT Determining common functional alleles in a population - useful in the
XX PT diagnosis of disease associated with allelic heterogeneity.

XX PS Example 1; Page 24; 78pp; English.

XX CC The invention relates to methods of determining a functional allele
XX CC profile of a gene in a population. Functional allele profiles comprise
XX CC the commonly occurring alleles in a population, and the relative
XX CC frequencies at which such alleles of a given gene occur. The methods are
XX CC used to identify and determine the frequency of the functional alleles of
XX CC genes which display extensive allelic heterogeneity, particularly those
XX CC implicated in disease or conditions, such as the BRCA1 gene associated
XX CC with breast cancer, CPT2 associated with cystic fibrosis, dystrophin
XX CC associated with Duchenne muscular dystrophy and Becker muscular
XX CC dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
XX CC also be employed for diseases where allelic and genetic heterogeneity
XX CC exist, such as breast cancer, neurofibromatosis, and hereditary non-
XX CC polyposis colorectal cancer. Identification of functional alleles is
XX CC necessary for identification of mutations which may be implicated in the
XX CC disease. Sequences AAX32001-172 represent primers for determining the
XX CC functional allele profiles of various genes. The primers are specific for
XX CC genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene
XX CC

XX SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2743 TCTTTTTCCTTTTAAAGGA 2760


```
DT 11-MAR-2004 (first entry)
DE Human talin phosphorothioate antisense oligonucleotide, SEQ ID NO:10.
KW Human; talin; cellular adhesion; muscle strength; cardiac function;
KW cardiomyocyte; platelet; prostate; androgen downregulation;
KW prostate cancer; talin-related disorder;
KW cellular adhesion-related disorder; expression inhibition;
KW antisense therapy; phosphorothioate; antisense oligonucleotide; ss.
XX Homo sapiens.
OS
FH
FT Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 5 nucleotides in length. Also all
FT cytosine nucleotides are 5-methylcytosines"
XX
XX WO200268446-A1.
XX
XX 06-SEP-2002.
XX
XX 30-OCT-2001; 2001WO-US048435.
XX
XX 22-FEB-2001; 2001US-00791942.
XX
XX (ISIS-) ISIS PHARM INC.
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
XX Bennett CF, Rothlein R, Kishimoto TK, Cowsett LM;
XX WPI; 2002-691651/74.
XX
XX New antisense oligonucleotides targeted to nucleic acid molecules
XX encoding human Talin, useful for inhibiting the expression of human Talin
XX and for treating a human having a disease or condition associated with
XX Talin.
XX
XX Example 15; SEQ ID NO 10; 114pp; English.
XX
XX Sequences ADG90460-ADG90539 represent phosphorothioate targeted to the
XX human talin gene, which inhibit its expression. The antisense were
XX designed to target different regions of human talin RNA, and were
XX analysed for their effect on talin expression by quantitative real-time
XX PCR. Talin is a cytoplasmic protein which links cytoskeletal proteins
XX such as actin, myosin and vinculin to integrins, thereby linking the
XX extracellular matrix to other cells. It is thought to be involved in the
XX regulation of cellular adhesion and cell morphology. Talin is highly
XX expressed in platelets, and may play a role in platelet adhesion as its
XX subcellular distribution differs between resting non-adhesive platelets
XX and activated adhesive platelets. It could also play a major role in
XX determining muscle strength and cardiac function as it has been found to
XX participate in the transmission of contractile force to the extracellular
XX matrix in cardiomyocytes, and exhibits mechanical loading-dependent
XX expression at myotendinous junctions. The expression of talin is
XX downregulated by androgens in prostate tissues, a phenomenon known to
XX contribute to the development of prostate cancer. The oligonucleotides of
XX the invention are useful for diagnosis, prevention and treatment of talin
XX -related disorders, such as those related to cellular adhesion. The
XX present sequence represents a human c-Ha-ras phosphorothioate antisense
XX oligonucleotide used as a positive control in determining optimal
XX oligonucleotide concentration for a particular cell line.
XX
XX Sequence 20 BP; 2 A; 5 C; 3 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 16.4; DB 1; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 3393 TCCTTGTCTTGGTATAT 3410
```

```
Db
||||| ||||| ||||| |||||
2 TCCTTGTCTTGGTATAT 19

RESULT 304
ADA45244
ID ADA45244 standard; DNA; 20 BP.
XX
XX ADA45244;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MSH2 gene PCR primer #3.
DE
XX
XX Functional allele profile; genetic inheritance; haplotype; population;
XX disease; pharmacogenetic application; selective pressure; human; MSH2;
XX MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX US2003096236-A1.
XX
XX 22-MAY-2003.
XX
XX 08-AUG-2001; 2001US-00923327.
XX
XX 12-FEB-1996; 96US-00598591.
XX 12-FEB-1997; 97US-00798691.
XX 04-AUG-1997; 97US-00905772.
XX 22-MAY-1998; 98US-00084471.
XX 04-AUG-1998; 98US-00129134.
XX 14-MAR-2000; 2000US-00524794.
XX
XX (ONCO-) ONCORMED INC.
XX
XX Murphy PD;
XX
XX WPI; 2003-576875/54.
XX
XX Determining a functional allele profile of a gene in a population by
XX identifying the nucleotide sequence of a gene of genomic DNA from each of
XX the individuals with a family history of functional alleles of the gene
XX of interest.
XX
XX Example 1; Page 9; 28pp; English.
XX
XX The present invention relates to a method for determining a functional
XX allele profile of a gene in a population. The method comprises
XX identifying the nucleotide sequence of a gene of interest out of genomic
XX DNA from each of a population of individuals identified as having a
XX family history which indicates inheritance of functional alleles of the
XX gene of interest, and rank ordering the frequency of occurrence of each
XX haplotype, where the identity of the alleles containing each haplotype
XX and the determination of their relative frequencies constitutes the
XX functional allele profile of the gene of interest in the population. The
XX method is useful for determining functional allele profiles which are
XX useful in the treatment and diagnosis of diseases, for genetic and
XX pharmacogenetic applications, and for evaluating the degree to which the
XX gene(s) are under selective pressure. The present sequence represents a
XX PCR primer used in the method of the invention.
XX
XX Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 16.4; DB 1; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 2743 TCCTTTTCTTTTAAAGGA 2760
DB 1 TTTTCTTTTCTTTTAAAGGA 18

RESULT 305
```

ABZ86070/c	ABZ89593/c
ID ABZ86070 standard; DNA; 20 BP.	ID ABZ89593 standard; DNA; 20 BP.
XX AC ABZ86070;	XX AC ABZ89593;
XX DT 17-OCT-2003 (first entry)	XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.	XX DE Human oligonucleotide sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;	XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;	XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;	XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;	XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;	XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.	XX KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.	XX OS Homo sapiens.
XX PN WO200285308-A2.	XX PN WO200285308-A2.
XX PD 31-OCT-2002.	XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.	XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.	XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.	XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PY Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	XX PY Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;	XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.	XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired	XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its	XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.	XX PT ubiquinone.
XX PS Claim 15; SEQ ID NO 1312; 872pp; English.	XX PS Disclosure; SEQ ID NO 4835; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a	XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the	XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,	XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or	XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an	XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention	XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,	XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a	XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or	XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also	XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an	XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels	XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine	XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or	XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,	XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.	XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed	XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO	XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences	XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;	XX SQ Sequence 20 BP; 12 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 20;	Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;	Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 426 GCAGCAGCGCGCTGCA 443	QY 2745 TTTTITTTTTTAAAGAAA 2762
DB 18 GCAGCAGCGCGCGAGCA 1	DB 18 TTTTITTTTTTAAAGAAA 1
RESULT 306	RESULT 307

ABZ89178
 ID ABZ89178 standard; DNA; 20 BP.
 AC ABZ89178;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4420; 872bp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytosstatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 13 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. NO. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588
 Db 2 TGTTTAAAAA 19

RESULT 308

ABZ97995/c
 ID ABZ97995 standard; DNA; 20 BP.
 AC ABZ97995;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human RANTES oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 13237; 872bp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytosstatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 0 A; 1 C; 6 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. NO. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2670 CAACACACACACAAAA 2687
 Db 20 CAACACACACACAAAA 3

RESULT 309

ABD25408
ID ABD25408 standard; DNA; 20 BP.
XX
AC ABD25408;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI122807-derived oligonucleotide SEQ ID 4420.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytotatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4420; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytotatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX

SQ Sequence 20 BP; 13 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2571 TGTTTAAAAA 2588
Db 2 TGTTTAAAAA 19
RESULT 310
ABD31026/c
ID ABD31026 standard; DNA; 20 BP.
XX
AC ABD31026;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human RANTES-derived oligonucleotide SEQ ID 13237.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytotatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 13237; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytotatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 0 A; 1 C; 6 G; 13 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2670 CAACAACACCAACAAAA 2687
 Db 20 CAACAACACCAACAAAA 3
 RESULT 311
 ABD22300/c
 ID ABD22300 standard; DNA; 20 BP.
 XX
 AC ABD22300;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human stanniocalcin-derived oligo SEQ ID 1312.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200285309-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013143.
 XX
 PR 24-APR-2001; 2001US-0286036P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-093058/08.
 XX
 PT Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 PS Claim 15; SEQ ID NO 1312; 763pp; English.
 XX
 CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 426 GCAGCAGCGCGCGTCCA 443
 Db 18 GCAGCAGCGCGCGCAGCA 1
 RESULT 312
 ABD25823/c
 ID ABD25823 standard; DNA; 20 BP.
 XX
 AC ABD25823;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE AI085559-derived oligonucleotide SEQ ID 4835.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200285309-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013143.
 XX
 PR 24-APR-2001; 2001US-0286036P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-093058/08.
 XX
 PT Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to

DR WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX

PS Example 15; SEQ ID NO 27; 135pp; English.

XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents an antisense oligonucleotide of the invention.

XX

SQ Sequence 20 BP; 1 A; 5 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1683 AACCCCAAGCCAGATG 1700

Db 19 AACCCCAAGCCAGATG 2

RESULT 315

ADJ59860/c

ID ADJ59860 standard; DNA; 20 BP.

XX

AC ADJ59860;

XX

DT 06-MAY-2004 (first entry)

XX

DE Oligonucleotide associated to RANTES #109.

XX

XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;

KW airway inflammation; allergy; asthma; impeded respiration;

KW cystic fibrosis; acute respiratory distress syndrome;

KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;

KW ss.

XX

OS Homo sapiens.

XX

PN WO2004011613-A2.

XX

PD 05-FEB-2004.

XX

XX 25-JUL-2003; 2003WO-US023509.

XX

PF 29-JUL-2002; 2002US-0399076P.

XX

PR (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;

PI Shahabuddin S, Lu H, Cong H;

XX

PS WPI; 2004-203534/19.

DR

XX

PT Novel single or multiple target oligonucleotide anti-sense to e.g.

PT initiation codons and introns of respiratory disease-relevant genes e.g.,

PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory

PT disease e.g., asthma.

XX

PS Claim 2; SEQ ID NO 716; 85pp; English.

XX

CC The present invention relates to an oligonucleotide anti-sense to e.g.,

CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-

CC end of nucleic acid target comprising gene(s) chosen from e.g.

CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the

CC oligonucleotide and optionally surfactant operatively linked to the

CC oligonucleotide. The method is useful for preventing or treating a

CC respiratory or lung disease, which involves administering to the airways

CC of a subject an effective amount of an inhibitor. The oligonucleotide is

CC useful for production of a medicament for the prevention and/or treatment

CC of a respiratory or lung disease. The respiratory or lung disease is

CC chosen from airway inflammation, allergy(ies), asthma, impeded

CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases

CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome

CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway

CC obstruction. The present sequence represents an oligonucleotide of the

CC invention.

XX

SQ Sequence 20 BP; 0 A; 1 C; 6 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2670 CAACCAACCAACCAACCA 2687

Db 20 CAACCAACCAACCAACCA 3

RESULT 316

ADK81379

ID ADK81379 standard; DNA; 20 BP.

XX

AC ADK81379;

XX

DT 20-MAY-2004 (first entry)

XX

DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8713.

XX

KW Nav1.3; Analgesic; Neurotropic; Neuroprotective; post-herpetic neuralgia;

KW diabetic neuropathy; arthritic pain; migraine headache;

KW infantile epilepsy; ataxia; ss.

XX

OS Synthetic.

XX

PN WO2004016754-A2.

XX

PD 26-FEB-2004.

XX

XX 14-AUG-2003; 2003WO-US025465.

XX

PR 14-AUG-2002; 2002US-0403416P.

XX

PA (PHAA) PHARMACIA CORP.

XX

PI Roberts SL;

XX

DR WPI; 2004-203785/19.

XX

XX New antisense compound targeted to a nucleic acid molecule encoding

PT Nav1.3, useful for useful for treating a disease or condition associated

PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure

PT disorder, or ataxia.

XX

PS Claim 4; SEQ ID NO 8713; 417pp; English.

XX

CC The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 CC different regions of the human Nav1.3 RNA.
 XX
 SQ Sequence 20 BP; 12 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2801 TGAATAAAAAAAACATC 2818
 DB 2 TGAATAAAAAAAACATC 19
 RESULT 317
 ADK80967
 ID ADK80967 standard; DNA; 20 BP.
 AC ADK80967;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8301.
 XX
 KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
 KW diabetic neuropathy; arthritic pain; migraine headache;
 KW infantile epilepsy; ataxia; ss.
 XX
 OS Synthetic.
 XX
 FN WO2004016754-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 14-AUG-2003; 2003WO-US025465.
 XX
 PR 14-AUG-2002; 2002US-0403416P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Robert's SL;
 XX
 DR WPI; 2004-203785/19.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT Nav1.3, useful for treating a disease or condition associated
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
 PT disorder, or ataxia.
 XX
 PS Claim 4; SEQ ID NO 8301; 417pp; English.
 XX
 CC The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present

CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 CC different regions of the human Nav1.3 RNA.
 XX
 SQ Sequence 20 BP; 12 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2801 TGAATAAAAAAAACATC 2818
 DB 3 TGAATAAAAAAAACATC 20
 RESULT 318
 ADL58169/C
 ID ADL58169 standard; DNA; 20 BP.
 XX
 AC ADL58169;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human ESM-1 antisense oligonucleotide seqid 418.
 XX
 KW cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
 KW gene therapy; endothelial specific molecule-1; ESM-1;
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;
 KW neurological disorder; antisense technology; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone. All cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 PN WO2004021978-A2.
 XX
 PD 18-MAR-2004.
 XX
 PF 19-AUG-2003; 2003WO-US025833.
 XX
 PR 19-AUG-2002; 2002US-0404495P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Weinstein EJ, Griggs DW;
 XX
 DR WPI; 2004-248358/23.
 XX
 PT New antisense compound, having a sequence targeted to a nucleic acid
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
 PT composition for treating e.g., diabetes, cancer or cardiovascular
 PT disorder.
 XX
 PS Claim 3; SEQ ID NO 418; 555pp; English.
 XX
 CC The invention describes a new antisense compound, having a sequence
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial
 CC specific molecule-1 (ESM-1), that specifically hybridises with the

CC nucleic acid ESM-1 and inhibits its expression. Also described are: a
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and
 CC treating an animal having a disease or condition associated with ESM-1.
 CC The compound is useful for preparing a composition for treating diabetes,
 CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
 CC cardiovascular or neurological disorder. This sequence represents an
 CC antisense oligonucleotide that can be used to modulate expression of
 CC endothelial specific molecule-1 (ESM-1).
 XX
 SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 362 TGGCGCGCTGGAGCAAGA 379
 Db 18 TGGCGCGCTGGAGCAATA 1
 RESULT 319
 ADL58390/c
 ID ADL58390 standard; DNA; 20 BP.
 XX AC ADL58390;
 XX AC
 DT 03-JUN-2004 (first entry)
 DE Human ESM-1 antisense oligonucleotide seqid 639.
 XX
 KW cytostatic; antidiabetic; immunomodulator; cardiact; neuroprotective;
 KW gene therapy; endothelial specific molecule-1; ESM-1;
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;
 KW neurological disorder; antisense technology; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone. All cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 PN WC02004021978-A2.
 XX
 PD 18-MAR-2004.
 XX
 PF 19-AUG-2003; 2003WO-US025833.
 XX
 PR 19-AUG-2002; 2002US-0404495P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Weinstein EJ, Griggs DW;
 XX
 DR WPI; 2004-248358/23.
 XX
 PT New antisense compound, having a sequence targeted to a nucleic acid
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
 PT composition for treating e.g., diabetes, cancer or cardiovascular
 PT disorder.
 XX
 PS Claim 3; SEQ ID NO 639; 555pp; English.

XX
 CC The invention describes a new antisense compound, having a sequence
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial
 CC specific molecule-1 (ESM-1), that specifically hybridises with the
 CC nucleic acid ESM-1 and inhibits its expression. Also described are: a
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and
 CC treating an animal having a disease or condition associated with ESM-1.
 CC The compound is useful for preparing a composition for treating diabetes,
 CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
 CC cardiovascular or neurological disorder. This sequence represents an
 CC antisense oligonucleotide that can be used to modulate expression of
 CC endothelial specific molecule-1 (ESM-1).
 XX
 SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 363 GGCGCGCTGGAGCAAGAA 380
 Db 20 GGCGCGCTGGAGCAATAA 3
 RESULT 320
 ADO45350/c
 ID ADO45350 standard; DNA; 20 BP.
 XX AC ADO45350;
 XX AC
 DT 15-JUL-2004 (first entry)
 DE Human oligonucleotide #716.
 XX
 KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease;
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX Homo sapiens.
 OS
 XX
 PN US2004049022-A1.
 XX
 PD 11-MAR-2004.
 XX
 PF 25-JUL-2003; 2003US-00627930.
 XX
 PR 23-APR-2002; 2002WO-US013135.
 PR 23-APR-2002; 2002WO-US013143.
 XX
 PA (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.
 PA (TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX
 PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 DR WPI; 2004-293804/27.
 XX
 PT Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.

XX
PS Claim 2; SEQ ID NO 716; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 0 A; 1 C; 6 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2670 CAACACACACACACAAAA 2687
DB 20 CAACACACACACACAAAA 3

RESULT 321
ADP85665
ID ADP85665 standard; DNA; 20 BP.
XX
AC ADP85665;
DT 26-AUG-2004 (first entry)
XX
DE Human Talin antisense oligonucleotide, ISIS #109109.
XX
KW Antisense; Talin; muscular disorder; haematologic disorder;
KW cardiac disorder; hyperproliferative disorder; cancer; human;
KW phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone where all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN US2004110705-A1.
XX

PD 10-JUN-2004.
XX
PF 11-SEP-2003; 2003US-00415463.
XX
PR 30-OCT-2000; 2000US-00702251.
XX
PR 30-OCT-2001; 2001WO-US047585.
XX
PA (BENN/) BENNETT C F.
PA (COWS/) COWSERT L M.
XX
PI Bennett CF, Cowsert LM;
XX WPI; 2004-440384/41.
DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding talin, useful for treating muscular, cardiac,
XX hematologic, or hyperproliferative disorders.
PT
XX Example 15; SEQ ID NO 10; 48pp; English.
PS
XX The invention relates to novel antisense compounds targeted to a nucleic
XX acid molecule encoding human Talin to and inhibit its expression. The
XX invention is useful for treating a disease or condition associated with
XX talin such as a disease or condition e.g. muscular, haematologic, cardiac
XX or hyperproliferative disorder such as cancer. The present sequence is an
XX antisense oligonucleotide targeted to human Talin DNA.
XX
SQ Sequence 20 BP; 2 A; 5 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3393 TCCTTGTCTGTGTATAT 3410
DB 2 TCCTTGTCTGTGTATAT 19

RESULT 322
ADP69475/C
ID ADP69475 standard; DNA; 20 BP.
XX
AC ADP69475;
DT 09-SEP-2004 (first entry)
XX
DE Human mitoneET-specific antisense oligonucleotide #369.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolidinediones; mitoneET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss.
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX Colca JR;
XX WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoneET, useful for modulating
PT mitoneET expression or for treating diseases associated with mitoneET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.

XX Claim 4; SEQ ID NO 369; 226pp; English.

PS The invention comprises antisense oligonucleotides that are targeted to

CC the nucleic acids encoding a family of human proteins from mitochondrial

CC membranes, which bind insulin sensitising, antidiabetic

CC thiazolidinediones (referred to as: mitONEET). The antisense

CC oligonucleotides of the invention are useful for modulating mitONEET

CC expression and for treating diseases or conditions associated with

CC mitONEET, such as: diabetes, immunological disorders, cardiovascular

CC disorders including hypertension, neurological disorders, and

CC ischaemia/reperfusion injuries. The present DNA sequence represents a

CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The

CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a

CC phosphorothioate backbone.

XX Sequence 20 BP; 5 A; 1 C; 1 G; 13 T; 0 U; 0 Other;

Seq Query Match 0.4%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588

Db 19 TGTTTAAACAAAAA 2

RESULT 323

ADP69581/c

ID ADP69581 standard; DNA; 20 BP.

XX ADP69581;

AC ADP69581;

XX 09-SEP-2004 (first entry)

DT Human mitONEET-specific antisense oligonucleotide #475.

DE human; antisense oligonucleotide; mitochondrial membrane;

XX insulin sensitising antidiabetic thiazolidinediones; mitONEET; diabetes;

KW immunological disorder; cardiovascular disorder; including hypertension;

KW neurological disorders; ischaemia; reperfusion; ss;

KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.

XX Homo sapiens.

OS

XX WO2004053060-A2.

PN 24-JUN-2004.

XX

XX 25-NOV-2003; 2003WO-US037621.

PF

XX 06-DEC-2002; 2002US-0431529P.

PR

XX (PHAA) PHARMACIA CORP.

PA

XX Colca JR;

PI

XX WPI; 2004-468836/44.

DR

XX New antisense oligonucleotides encoding mitONEET, useful for modulating

PT mitONEET expression or for treating diseases associated with mitONEET,

PT e.g. diabetes, immunological disorders or cardiovascular disorders.

XX

PS Claim 4; SEQ ID NO 475; 226pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to

CC the nucleic acids encoding a family of human proteins from mitochondrial

CC membranes, which bind insulin sensitising, antidiabetic

CC thiazolidinediones (referred to as: mitONEET). The antisense

CC oligonucleotides of the invention are useful for modulating mitONEET

CC expression and for treating diseases or conditions associated with

CC mitONEET, such as: diabetes, immunological disorders, cardiovascular

CC disorders including hypertension, neurological disorders, and

XX

CC ischaemia/reperfusion injuries. The present DNA sequence represents a

CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The

CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a

CC phosphorothioate backbone.

XX Sequence 20 BP; 6 A; 1 C; 1 G; 12 T; 0 U; 0 Other;

Seq Query Match 0.4%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588

Db 18 TGTTTAAACAAAAA 1

RESULT 324

ADP69398/c

ID ADP69398 standard; DNA; 20 BP.

XX ADP69398;

AC ADP69398;

XX 09-SEP-2004 (first entry)

DT Human mitONEET-specific antisense oligonucleotide #292.

DE human; antisense oligonucleotide; mitochondrial membrane;

XX insulin sensitising antidiabetic thiazolidinediones; mitONEET; diabetes;

KW immunological disorder; cardiovascular disorder; including hypertension;

KW neurological disorders; ischaemia; reperfusion; ss;

KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.

XX Homo sapiens.

OS

XX WO2004053060-A2.

PN 24-JUN-2004.

XX

XX 25-NOV-2003; 2003WO-US037621.

PF

XX 06-DEC-2002; 2002US-0431529P.

PR

XX (PHAA) PHARMACIA CORP.

PA

XX Colca JR;

PI

XX WPI; 2004-468836/44.

DR

XX New antisense oligonucleotides encoding mitONEET, useful for modulating

PT mitONEET expression or for treating diseases associated with mitONEET,

PT e.g. diabetes, immunological disorders or cardiovascular disorders.

XX

PS Claim 4; SEQ ID NO 292; 226pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to

CC the nucleic acids encoding a family of human proteins from mitochondrial

CC membranes, which bind insulin sensitising, antidiabetic

CC thiazolidinediones (referred to as: mitONEET). The antisense

CC oligonucleotides of the invention are useful for modulating mitONEET

CC expression and for treating diseases or conditions associated with

CC mitONEET, such as: diabetes, immunological disorders, cardiovascular

CC disorders including hypertension, neurological disorders, and

CC ischaemia/reperfusion injuries. The present DNA sequence represents a

CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The

CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a

CC phosphorothioate backbone.

XX

Seq Query Match 0.4%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTATAAAAAAAAAA 2588
 ID AAQ78464/c
 Db 20 TGTATAAAAAAAAAA 3

RESULT 325

AAQ78464/c
 ID AAQ78464 standard; DNA; 16 BP.

XX AC AAQ78464;

XX 25-MAR-2003 (revised)

DT 27-JUN-1995 (first entry)

XX TGF-beta gene phosphorothioate antisense oligonucleotide.

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.

XX OS Synthetic.

XX PN WO9425588-A2.

XX 10-NOV-1994.

XX 29-APR-1994; 94WO-EP001362.

XX 30-APR-1993; 93EP-00107089.

PR 13-MAY-1993; 93EP-00107849.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 PI Bogdahn U;

XX WPI; 1994-358266/44.

XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
 PT treating immunosuppression, tumours, etc.

XX Claim 6; Page 56; 74pp; English.

XX The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.4%; Score 16; DB 1; Length 16;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTCG 2168

Db 16 TGTGCAGGATAATTCG 1

RESULT 326

AAQ78456/c

ID AAQ78456 standard; DNA; 16 BP.

XX

AC AAQ78456;

XX 25-MAR-2003 (revised)

DT 27-JUN-1995 (first entry)

XX TGF-beta gene phosphorothioate antisense oligonucleotide.

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.

XX OS Synthetic.

XX PN WO9425588-A2.

XX 10-NOV-1994.

XX 29-APR-1994; 94WO-EP001362.

XX 30-APR-1993; 93EP-00107089.

PR 13-MAY-1993; 93EP-00107849.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 PI Bogdahn U;

XX WPI; 1994-358266/44.

XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
 PT treating immunosuppression, tumours, etc.

XX Claim 6; Page 54; 74pp; English.

XX The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 16 BP; 2 A; 3 C; 3 G; 8 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.4%; Score 16; DB 1; Length 16;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAAA 2035

Db 16 AGTCCACTAGGAAAAA 1

RESULT 327

AAV63225/c

ID AAV63225 standard; DNA; 16 BP.

XX AAV63225;

XX 14-JAN-1999 (first entry)

XX Phosphorothioate oligonucleotide directed against TGF-beta2.

RESULT 328

AAQ78456/c

ID AAQ78456 standard; DNA; 16 BP.

XX

XX Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
 KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
 KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;

KW preclempsia; pregnancy; choriocarcinoma; phosphorothioate; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9840747-A1.
 PN 17-SEP-1998.
 PD 05-MAR-1998; 98WO-CA000180.
 PF 07-MAR-1997; 97US-0039919P.
 XX (MOUN) MOUNT SINAI HOSPITAL CORP.
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 XX Caniggia I, Post M, Lye S;
 PI WPI; 1998-520837/44.
 XX Regulation of trophoblast invasion - by, e.g. transforming growth factor-
 DR beta3 inhibitor, useful for detecting or treating preeclampsia in
 PT pregnant women.
 PT Example 4; Page 22; 59pp; English.
 XX AAV63225-26 represent phosphorothioate oligonucleotides directed against
 CC nucleic acid encoding human transforming growth factor-beta 2 (TGF-
 CC beta2). The specification describes a composition for regulating
 CC trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta
 CC family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha)
 CC or oxygen tension. The composition is used in methods of diagnosing,
 CC monitoring, preventing or treating conditions requiring regulation of
 CC trophoblast invasion, especially preeclampsia in pregnant women or
 CC choriocarcinomas
 XX
 SQ Sequence 16 BP; 5 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1217 CATGCACACTACTGTGTG 1232
 Db 16 CATGCACACTACTGTGTG 1
 RESULT 328
 AAV63226
 ID AAV63226 standard; DNA; 16 BP.
 XX AAV63226;
 AC
 XX 14-JAN-1999 (first entry)
 DT
 XX Phosphorothioate oligonucleotide directed against TGF-beta2.
 DE
 XX Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
 KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
 KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
 KW preeclampsia; pregnancy; choriocarcinoma; phosphorothioate; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9840747-A1.
 PN 17-SEP-1998.
 PD 05-MAR-1998; 98WO-CA000180.
 PF 07-MAR-1997; 97US-0039919P.
 XX

PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 XX Caniggia I, Post M, Lye S;
 PI WPI; 1998-520837/44.
 XX Regulation of trophoblast invasion - by, e.g. transforming growth factor-
 DR beta3 inhibitor, useful for detecting or treating preeclampsia in
 PT pregnant women.
 PT Example 4; Page 22; 59pp; English.
 XX AAV63225-26 represent phosphorothioate oligonucleotides directed against
 CC nucleic acid encoding human transforming growth factor-beta 2 (TGF-
 CC beta2). The specification describes a composition for regulating
 CC trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta
 CC family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha)
 CC or oxygen tension. The composition is used in methods of diagnosing,
 CC monitoring, preventing or treating conditions requiring regulation of
 CC trophoblast invasion, especially preeclampsia in pregnant women or
 CC choriocarcinomas
 XX
 SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1217 CATGCACACTACTGTGTG 1232
 Db 1 CATGCACACTACTGTGTG 16
 RESULT 329
 AAV48957/c
 ID AAV48957 standard; DNA; 16 BP.
 XX AAV48957;
 AC
 XX 15-OCT-1998 (first entry)
 DT
 XX TGF-beta2 antisense oligonucleotide TGF-beta2-28.
 DE
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 KW Synthetic.
 OS Homo sapiens.
 XX EP856579-A1.
 PN 05-AUG-1998.
 PD
 XX 31-JAN-1997; 97EP-00101531.
 PF
 XX 31-JAN-1997; 97EP-00101531.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA Schlingensiepen K, Brysch W;
 PI WPI; 1998-400910/35.
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX Claim 10; Fig 8a; 286pp; English.
 PS
 XX AAV48930-49007 represent antisense oligonucleotides directed against

CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV49930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV49968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2156 GCAGGATAATTGCTGC 2171
 Db 16 GCAGGATAATTGCTGC 1
 |||||

RESULT 330
 AA265460/c
 ID AA265460 standard; DNA; 16 BP.
 XX
 AC AA265460;

XX 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-20.
 XX

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX Unidentified.
 XX WO9963975-A2.
 XX 16-DEC-1999.
 XX 10-JUN-1999; 99WO-EP004013.
 XX 10-JUN-1998; 98EP-00110709.
 PR 25-JUL-1998; 98EP-00113974.
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI WPI; 2000-097470/08.
 DR
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX Claim 5; Fig 1; 30pp; English.
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which

CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2153 TGTGCAGGATAATTGC 2168
 Db 16 TGTGCAGGATAATTGC 1
 |||||

RESULT 331
 AA265458/c
 ID AA265458 standard; DNA; 16 BP.
 XX
 AC AA265458;

XX 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-18.
 XX

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX Unidentified.
 XX WO9963975-A2.
 XX 16-DEC-1999.
 XX 10-JUN-1999; 99WO-EP004013.
 XX 10-JUN-1998; 98EP-00110709.
 PR 25-JUL-1998; 98EP-00113974.
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI WPI; 2000-097470/08.
 DR

XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX Claim 5; Fig 1; 30pp; English.
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor

CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 16 BP; 2 A; 3 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2020 AGTCACCTAGGAAAA 2035
 Db 16 AGTCACCTAGGAAAA 1

RESULT 332
 AAZ65461/C
 ID AAZ65461 standard; DNA; 16 BP.
 AC AAZ65461;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-21.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 PN WO9963975-A2.
 XX
 PD 16-DEC-1999.
 XX
 PF 10-JUN-1999; 99WO-EP004013.
 XX
 PR 10-JUN-1998; 98EP-00110709.
 XX
 PR 25-JUL-1998; 98EP-00113974.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX
 DR WPI; 2000-097470/08.
 XX
 PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 XX
 PS Claim 5; Fig 1; 30pp; English.
 XX
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes

CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2156 GCAGGATAATTCGTGC 2171
 Db 16 GCAGGATAATTCGTGC 1

RESULT 333
 AAZ00479
 ID AAZ00479 standard; DNA; 17 BP.
 AC AAZ00479;
 XX
 DT 06-OCT-1999 (first entry)
 XX
 DE Human thioredoxin DNA binding antisense oligonucleotide 2602.
 XX
 KW Thioredoxin; thioredoxin reductase; human; antisense; primer; metastasis;
 KW cytosolic; tumour growth inhibitor; detection; nuclease resistant;
 KW phosphorothioate linkage; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9938963-A1.
 XX
 PD 05-AUG-1999.
 XX
 PF 29-JAN-1999; 99WO-CA000077.
 XX
 PR 30-JAN-1998; 98US-0073196P.
 XX
 PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 PI Wright JA, Young AH, Lee YS;
 XX
 DR WPI; 1999-469328/39.
 XX
 PT Antisense oligonucleotides against thioredoxin and thioredoxin reductase
 PT genes, useful for inhibiting tumor growth and metastasis.
 XX
 PS Claim 1; Page 18; 88pp; English.
 XX
 CC This invention describes novel antisense oligonucleotides against
 CC thioredoxin and thioredoxin reductase gene which have cytostatic activity
 CC and are useful for inhibiting tumour growth and metastasis in mammals.
 CC They may also be used as hybridization probes to detect the presence of
 CC the thioredoxin and thioredoxin reductase mRNAs in mammalian cells. They
 CC may also be used as molecular weight markers. The antisense
 CC oligonucleotides are nuclease resistant due to the presence of
 CC phosphorothioate internucleotide linkages. AAZ00478-Z00503 represent
 CC oligonucleotide primers capable of binding to human thioredoxin mRNA
 XX
 SQ Sequence 17 BP; 7 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match		0.4%;	Score 16;	DB 1;	Length 17;		
Best Local Similarity		100.0%;	Pred. No. 1.5e+02;				
Matches 16;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	2209 GATGGAATGGATCCA 2224						
Db	1 GATGGAATGGATCCA 16						
RESULT 334							
ID	AAZ65500/c						
XX	AAZ65500 standard; DNA; 17 BP.						
AC	AAZ65500;						
DT	30-MAR-2000 (first entry)						
XX	Immunosuppressant inhibitor oligonucleotide TGF-beta2-98-3.						
DE	Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;						
KW	vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;						
KW	prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;						
KW	monocyte chemoattractic protein-1; MCP-1; ulcerative colitis; diabetes;						
KW	glomerulonephritis; acute respiratory distress syndrome; ss;						
KW	atherosclerosis.						
XX	Unidentified.						
OS	WO9963975-A2.						
XX	16-DEC-1999.						
PD	10-JUN-1999; 99WO-EP004013.						
XX	10-JUN-1998; 98EP-00110709.						
PR	25-JUL-1998; 98EP-00113974.						
XX	(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.						
PA	Schlingensiepen K, Schlingensiepen R, Brysch W;						
XX	WPI; 2000-097470/08.						
DR	Composition containing immune stimulant and inhibitor of agent that						
PT	adversely affects the immune response, for treating cancers and						
PT	infections.						
XX	Claim 10; Fig 1; 30pp; English.						
PS	This sequence is an immunosuppressant inhibitor oligonucleotide, which is						
XX	used in the invention. The invention relates to a composition which						
CC	contains at least one inhibitor (less than 100 kD) of a substance (e.g.						
CC	transforming growth factor TGF-beta, vascular endothelial growth factor						
CC	VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)						
CC	that adversely affects the immune response. The composition also includes						
CC	at least one stimulant that positively affects the immune response. This						
CC	oligonucleotide is an example of an inhibitor that is used in the						
CC	composition. The composition is used as an immunostimulant for the						
CC	treatment of neoplasms and infections, particularly hyperproliferation;						
CC	leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,						
CC	colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,						
CC	breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,						
CC	malignant melanoma, brain tumours and sarcomas. The oligonucleotides,						
CC	most of which are directed against TGFbeta or VEGF, are inhibitors of						
CC	monocyte chemoattractic protein-1 (MCP-1) and are useful as anti-						
CC	inflammatories for treating e.g. asthma, Crohn's disease, ulcerative						
CC	colitis, diabetes, glomerulonephritis, acute respiratory distress						
CC	syndrome and the formation of atherosclerotic plaque						
XX	Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;						
Query Match							
Best Local Similarity 0.4%; Score 16; DB 1; Length 17;							
Matches 16; Conservative 100.0%; Pred. No. 1.5e+02;							
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	424 AGGCAGCAGCGCGC 439						
Db	1 AGGCAGCAGCGCGC 16						
RESULT 336							
ID	ADL49410/c						
XX	ADL49410 standard; RNA; 17 BP.						
Query Match							
Best Local Similarity 0.4%; Score 16; DB 1; Length 17;							
Matches 16; Conservative 100.0%; Pred. No. 1.5e+02;							
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	1806 GAATGGCTCTCCTTCG 1821						
Db	16 GAATGGCTCTCCTTCG 1						
RESULT 335							
ID	ABZ59896						
XX	ABZ59896 standard; RNA; 17 BP.						
AC	ABZ59896;						
DT	21-MAR-2003 (first entry)						
XX	Human K-Ras DNzyme substrate #8.						
DE	Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;						
KW	enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;						
KW	anti-rheumatic; cancer; AIDS; ss.						
XX	Homo sapiens.						
XX	WO200297114-A2.						
PN	05-DEC-2002.						
XX	29-MAY-2002; 2002WO-US016840.						
XX	29-MAY-2001; 2001US-0294140P.						
PR	06-JUN-2001; 2001US-0296249P.						
PR	10-SEP-2001; 2001US-0318471P.						
XX	(RIBO-) RIBOZYME PHARM INC.						
PA	Mcswiggan J;						
PI	WPI; 2003-140484/13.						
XX	Novel short interfering RNA and enzymatic nucleic acid useful for						
PT	treating cancer. modulates the expression of a nucleic acid encoding						
PT	HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.						
XX	Claim 58; Page 85; 185pp; English.						
PS	The invention relates to a novel short interfering RNA (siRNA) nucleic						
XX	acid molecule or an enzymatic nucleic acid molecule, that modulates						
CC	expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,						
CC	human immunodeficiency virus (HIV) or a component of HIV. The nucleic						
CC	acid molecule of the invention has cytostatic, anti-HIV, and anti-						
CC	rheumatic activity. The nucleic acid molecules are useful for reducing						
CC	HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are						
CC	also useful for treating breast, ovarian, colorectal, lung, prostate,						
CC	bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences						
CC	shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 -						
CC	ABZ66530 - ABZ66585 represent substrate/target sequences for the human						
CC	ribozymes of the invention						
XX	Sequence 17 BP; 3 A; 5 C; 9 G; 0 T; 0 U; 0 Other;						
SQ	Query Match						
	Best Local Similarity 0.4%; Score 16; DB 1; Length 17;						
	Matches 16; Conservative 100.0%; Pred. No. 1.5e+02;						
	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	424 AGGCAGCAGCGCGC 439						
Db	1 AGGCAGCAGCGCGC 16						
RESULT 336							
ID	ADL49410/c						
XX	ADL49410 standard; RNA; 17 BP.						

```

AC ADL49410;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Human PKR substrate sequence #524.
XX
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
XX
OS Unidentified.
XX
XX
FN WO200281628-A2.
XX
XX
PD 17-OCT-2002.
XX
XX
PF 03-APR-2002; 2002WO-US010512.
XX
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX
XX
DR WPI; 2003-058513/05.
XX
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX
PS Claim 59; SEQ ID NO 2943; 317pp; English.
XX
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 0 C; 0 G; 0 T; 14 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
DB 17 TTTAAAAA 2
RESULT 337
ADL49411/c
ID ADL49411 standard; RNA; 17 BP.
XX

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AC ADL49411;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Human PKR substrate sequence #525.
XX
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
XX
OS Unidentified.
XX
XX
FN WO200281628-A2.
XX
XX
PD 17-OCT-2002.
XX
XX
PF 03-APR-2002; 2002WO-US010512.
XX
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX
XX
DR WPI; 2003-058513/05.
XX
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX
PS Claim 59; SEQ ID NO 2944; 317pp; English.
XX
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
DB 16 TTTAAAAA 1
RESULT 338
AAQ38707/c
ID AAQ38707 standard; RNA; 18 BP.
XX

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AC AAQ38707;
XX
XX 25-MAR-2003 (revised)
DT 15-JUL-1993 (first entry)
XX
XX First chimeric primer for adding poly A tails.
DE
XX
XX oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;
KW treatment; diagnosis; testing; assay; Candida; papillomavirus;
KW cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;
KW liver disease; human immunodeficiency virus; herpes simplex virus; HSV;
KW human immunodeficiency virus; HIV; AIDS; influenza virus;
KW genetic disease; genetic abnormalities.
XX
XX Synthetic.
OS
XX
XX WO9305182-A1.
PN
XX
XX 18-MAR-1993.
PD
XX
XX 04-SEP-1992; 92WO-US007489.
PF
XX
XX 05-SEP-1991; 91US-00755485.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bruce TW;
PI
XX
XX WPI; 1993-101001/12.
DR
XX
XX Determn. of oligonucleotide(s) with specific activity for a bio:molecule
PT - for use in therapeutics, diagnostics and research reagents.
PT
XX
XX Disclosure; Page 27; 61pp; English.
PS
XX
XX This sequence was used as a PCR primer in order to add a polyA tail to
CC the 3' end of the highest specific activity selected oligonucleotide in
CC order to form a first strand. The primer is comprised of a 5' known
CC sequence and a 3' polynucleotide portion corresp. to the polynucleotide
CC tail of the first strand. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2803 AAAAAAAAAAACATC 2818
DB 17 AAAAAAAAAAACATC 2
RESULT 339
AAT96107/c
ID AAT96107 standard; DNA; 18 BP.
XX
XX AAT96107;
AC
XX
XX 31-MAR-1998 (first entry)
DT
XX
XX First chimeric primer.
DE
XX
XX Determination; oligonucleotide; specific activity; therapy;
KW target biomolecule; randomised oligonucleotide; diagnosis; research; PCR;
KW chimeric; primer; ss.
XX
XX Synthetic.
OS
XX
XX US5686242-A.
PN
XX
XX 11-NOV-1997.
PD
XX
XX 27-OCT-1994; 94US-00330000.
PF

```

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XX
XX 05-SEP-1991; 91US-00755485.
PR 04-SEP-1992; 92WO-US007489.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Lima WF, Bruce TW;
PI
XX
XX WPI; 1997-558135/51.
DR
XX
XX Determination of oligo-nucleotide with specific activity for target bio-
PT molecule - using set of randomised oligo-nucleotide(s).
PT
XX
XX Disclosure; Col 27-28; 22pp; English.
PS
XX
XX The present sequence was used in the development of a method of
CC determining an oligonucleotide having specific activity for a target
CC biomolecule. The method comprises assaying a set of randomised
CC oligonucleotides for activity against a target biomolecule, separating
CC active from inactive oligonucleotides and recovering, amplifying and
CC determining the nucleic acid sequence of the active oligonucleotides. The
CC oligonucleotides can be used for therapeutic, diagnostic and research
CC purposes
XX
XX Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2803 AAAAAAAAAAACATC 2818
DB 17 AAAAAAAAAAACATC 2
RESULT 340
AAZ88678/c
ID AAZ88678 standard; DNA; 18 BP.
XX
XX AAZ88678;
AC
XX
XX 11-MAY-2000 (first entry)
DT
XX
XX Chimeric primer #1.
DE
XX
XX Primer; detection; diagnosis; ss.
KW
XX
XX Unidentified.
OS
XX
XX US6022691-A.
PN
XX
XX 08-FEB-2000.
PD
XX
XX 07-NOV-1997; 97US-00965908.
PF
XX
XX 05-SEP-1991; 91US-00755485.
PR 04-SEP-1992; 92WO-US007489.
XX
XX 27-OCT-1994; 94US-00330000.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Lima WF, Bruce TW;
PI
XX
XX WPI; 2000-170669/15.
DR
XX
XX Assay for a chemical or drug in a sample comprises detecting binding of
PT an oligonucleotide selected from a set of randomized oligonucleotides.
PT
XX
XX Disclosure; Col 27-28; 20pp; English.
PS
XX
XX This invention describes a novel method (I) for specifically detecting a
CC chemical or drug in a sample comprises contacting the sample with an
CC oligonucleotide having specific activity for a target biomolecule and
CC

```

CC detecting the presence or absence of binding where the presence of
 CC binding indicates the presence of the chemical or drug in the sample. The
 CC oligonucleotide is identified by: (a) assaying a prepared set of
 CC randomized oligonucleotides for activity against a target biomolecule;
 CC (b) separating active from inactive oligonucleotides; (c) recovering the
 CC active oligonucleotides; and (d) characterizing the recovered
 CC oligonucleotides by microanalytical structure determination. The method
 CC can be used for diagnostic or research purposes
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2803 AAAAAAAAAAACATC 2818
 Db 17 AAAAAAAAAAACATC 2

RESULT 341
 ADL95318/C
 ID ADL95318 standard; DNA; 18 BP.
 XX
 AC ADL95318;
 DT 01-JUL-2004 (first entry)
 XX
 DE Anti-proliferative oligonucleotide #9.

ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;
 cancer; malignant tumour.

OS Synthetic.

Key Location/Qualifiers
 modified_base 8
 /*tag= a
 /mod_base= OTHER
 /note= "Optionally 32-P labelled"

XX US2004067197-A1.
 XX 08-APR-2004.
 XX 02-FEB-2001; 2001US-00775479.
 XX 26-NOV-1997; 97WO-CA000892.
 XX 24-MAY-1999; 99US-00318106.
 XX (LECL/) LECLERC G.
 XX (MART/) MARTEL R.
 XX Leclerc G, Martel R;
 XX WPI; 2004-314974/29.
 XX
 XX New anti-proliferative substance comprising a radiolabeled DNA carrier,
 XX useful for preventing or treating uncontrolled cellular proliferation
 XX e.g. restenosis, cancer or malignant tumors.
 XX
 XX Claim 13; SEQ ID NO 9; 28pp; English.

CC The invention relates to an anti-proliferative substance for preventing
 CC uncontrolled cellular proliferation comprising a radiolabelled DNA
 CC carrier, where a radioisotope is located internally within the DNA
 CC sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier
 CC penetrates the cell membrane and is retained intracellularly for a time
 CC sufficient for the radio-isotope to effect a dose therapy. The carrier in
 CC the anti-proliferative substance is an oligonucleotide, which is linear
 CC or a plasmid, which is circular. The plasmid is of viral or bacterial
 CC origin. The oligonucleotide is a double- or a single-stranded DNA
 CC sequence, which is conjugated with an antibody for cell-specific

CC delivery. The oligonucleotide is also conjugated to a stent surface,
 CC cholesterol, oleic acid, linoleic acid, IgGalpha, antibody, IgGbeta,
 CC cytokines or growth factors. The anti-proliferative substance is useful
 CC for preventing or treating uncontrolled cellular proliferation. The
 CC uncontrolled cell proliferation is a restenosis following angioplasty, or
 CC cancer or a malignant tumour. The present sequence represents an
 CC oligonucleotide carrier used in the invention.

SQ Sequence 18 BP; 3 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAAAAAAAAAA 2588
 Db 18 TTTAAAAAAAAAAAAA 3

RESULT 342
 AAZ11781
 ID AAZ11781 standard; DNA; 19 BP.
 XX

AC AAZ11781;

DT 23-NOV-1999 (first entry)

XX Oligonucleotide primer JB659.

internal transcribed spacer; ITS; ribosomal RNA; fungal pathogen; PCR;
 primer; detection; plant disease; crop protection; ss.

OS Synthetic.

OS Pyrenophora tritici-repentis.

XX WO9942609-A1.

XX 26-AUG-1999.

XX 18-FEB-1999; 99WO-EP001058.

XX 20-FEB-1998; 98US-00026601.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Beck JU;

XX WPI; 1999-527487/44.

XX New internal transcribed spacer DNA from fungal pathogens, used as
 XX sources of primers and probes for pathogen detection.

XX Claim 13; Page 18; 40pp; English.

CC This primer can be used in the amplification-based detection of a fungal
 CC internal transcribed spacer (ITS) DNA sequence. This sequence was derived
 CC from the ITS sequences, specifically from the regions of the ITS which
 CC exhibit the greatest difference among the fungal pathotypes. This allows
 CC the identification of specific pathogens and provides a method for
 CC detecting them

SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGACGC 3205
 Db 1 GAAGCTTCATGACGC 16

RESULT 343
ADF31846
ID ADF31846 standard; RNA; 19 BP.
XX
AC ADF31846;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IGF-1R siNA lower strand, SEQ ID NO:511.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW proliferative disease; restenosis; polycystic kidney disease;
KW inflammatory disease; allergic disease; autoimmune disease;
KW transplant rejection; cytostatic; vasotropic; nephrotropic;
KW antiinflammatory; antiallergic; immunosuppressive; human;
KW insulin-like growth factor 1 receptor; IGF-1R; ss.
XX
OS Homo sapiens.
XX
XX
PN WO2003070911-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005044.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B;
XX
XX WPI; 2003-721691/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the insulin-like growth
PT factor-1 receptor gene.
XX
PS Example 3; SEQ ID NO 511; 147pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human insulin-like growth factor 1
CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA), double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the IGF-1R gene in cells, tissue explants or organisms
CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC treatment of a variety of conditions. They may be used for treating
CC cancer and other proliferative diseases (e.g., restenosis and polycystic
CC kidney disease), inflammatory and/or allergic diseases, autoimmune
CC diseases and transplant rejection. The siNAs are also useful for drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
CC represents the lower strand of a human IGF-1R-targeted double-stranded
CC siNA.

XX
SQ Sequence 19 BP; 1 A; 15 C; 1 G; 0 T; 2 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 972 TCCTCCCCCACCCTCCG 987
:|||||||
Db 4 UCCCCCCCCACCCCGC 19

RESULT 344
ADF31569/C
ID ADF31569 standard; RNA; 19 BP.
XX
AC ADF31569;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IGF-1R transcript target sequence/siNA upper strand, SEQ ID NO:234.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW proliferative disease; restenosis; polycystic kidney disease;
KW inflammatory disease; allergic disease; autoimmune disease;
KW transplant rejection; cytostatic; vasotropic; nephrotropic;
KW antiinflammatory; antiallergic; immunosuppressive; human;
KW insulin-like growth factor 1 receptor; IGF-1R; target sequence; ss.
XX
OS Homo sapiens.
XX
XX
PN WO2003070911-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005044.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B;
XX
XX WPI; 2003-721691/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the insulin-like growth
PT factor-1 receptor gene.
XX
PS Example 3; SEQ ID NO 234; 147pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human insulin-like growth factor 1
CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA), double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes

of siNA; and vectors that express siNA. The siNAs are used to modulate expression of the IGF-1R gene in cells, tissue explants or organisms (e.g., by ex vivo gene therapy), or in grafts and transplants for the treatment of a variety of conditions. They may be used for treating cancer and other proliferative diseases (e.g., restenosis and polycystic kidney disease), inflammatory and/or allergic diseases, autoimmune diseases and transplant rejection. The siNAs are also useful for drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying gene function, and gene mapping (e.g., of single nucleotide polymorphisms). The present sequence represents the upper strand of a human IGF-1R-targeted double-stranded siNA, which is identical to the IGF-1R transcript target sequence.

Sequence 19 BP; 2 A; 1 C; 15 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 TCCCCCCCCCACCAGC 987
Db 16 TCCCCCCCCCACCAGC 1

RESULT 345
ABD24924
ID ABD24924 standard; DNA; 19 BP.

AC ABD24924;

XX 29-JUL-2004 (first entry)

XX A1095492-derived oligonucleotide SEQ ID 3936.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200283309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

PS Claim 15; SEQ ID NO 3936; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX Sequence 19 BP; 16 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2588
Db 1 TTTAAAAA 16

RESULT 346
AAQ75580/c
ID AAQ75580 standard; DNA; 20 BP.

XX AAQ75580;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in sepearate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2573 TTTAAAAA 2588
 DB 20 TTTAAAAA 5

RESULT 347
 AAC63692
 ID AAC63692 standard; DNA; 20 BP.
 XX
 AC AAC63692;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE Rat P2X₇/P2Z PCR primer #4.
 XX
 KW Rat; P2X₇; neuroprotective; nootropic; antiinflammatory; antirheumatic;
 KW antithritic; antibacterial; antiviral; antiallergic; cyostatic;
 KW cardiant; cerebroprotective; immunosuppressive; P2Z; purinergic receptor;
 KW nervous system disorder; chronic inflammation; Alzheimer's disease;
 KW rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection;
 KW haematopoietic system disorder; immune response; autoimmune disorder;
 KW allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;
 KW tuberculosis; PCR primer; ss.
 XX
 OS Rattus sp.
 XX
 PN US6133434-A.
 XX
 PD 17-OCT-2000.
 XX
 PF 28-APR-1997; 97US-00842079.
 XX
 PR 28-APR-1997; 97US-00842079.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Buell GN, Kawashima E, Surprenant A;
 XX
 XX WPI; 2001-006153/01.
 DR
 PT Mammalian purinergic receptor (P2X₇) useful for screening for modulators
 PT which are useful for treating arthritic, respiratory disorders and
 PT neurodegenerative disorders, and to generate receptors specific
 PT antibodies.
 PS
 SS Example 1; Col 8; 40pp; English.
 XX
 CC The present invention relates to rat and human purinergic receptor
 CC P2X₇/P2Z (AAC63692-C63694). The P2X₇ coding sequences can be used to
 CC treat disorders of the nervous system, particularly diseases with a
 CC component of chronic inflammation, such as Alzheimer's disease, diseases
 CC involving acute or chronic inflammation such as rheumatoid arthritis,
 CC amyloidosis, bacterial, viral and other microbial infections, disorders
 CC of the haematopoietic system and immune response such as autoimmune
 CC disorders, allergies and lymphoproliferative disorders, diseases
 CC involving apoptotic cell death, such as cardiac and cerebral ischaemia
 CC and microbial infections, particularly tuberculosis. The present sequence
 CC is a PCR primer used to isolate the rat P2X₇ coding sequence
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2573 TTTAAAAA 2588
 DB 20 TTTAAAAA 5

RESULT 348
 AAC82917/c
 ID AAC82917 standard; DNA; 20 BP.
 XX
 AC AAC82917;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human S-9 derived oligonucleotide #1.
 XX
 KW Recognition system; screening; identification; pharmaceutical; toxin;
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19923966-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 25-MAY-1999; 99DE-01023966.
 XX
 PR 25-MAY-1999; 99DE-01023966.
 XX
 PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
 XX
 PI Boetenkamp D, Hoppe H, Burgstaller P;
 XX
 DR WPI; 2001-050938/07.
 XX
 PT Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure.
 XX
 PS Example; Fig 1; 9pp; German.
 XX
 CC This invention describes a novel recognition system comprising at least 1
 CC recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides
 XX
 SQ Sequence 20 BP; 3 A; 2 C; 2 G; 13 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2573 TTTAAAAA 2588
 DB 16 TTTAAAAA 1

RESULT 349
 AAC82918/c
 ID AAC82918 standard; DNA; 20 BP.
 XX
 AC AAC82918;
 XX
 DT 21-MAR-2001 (first entry)
 XX

DE Human S-9 derived oligonucleotide #2.
XX Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX Homo sapiens.
XX OS
XX DE19923966-A1.
XX PN
XX 30-NOV-2000.
XX PD
XX XX
XX 25-MAY-1999; 99DE-01023966.
XX PF
XX 25-MAY-1999; 99DE-01023966.
XX PR
XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX PA
XX Boekenkamp D, Hoppe H, Burgstaller P;
XX WPI; 2001-050938/07.
XX DR
XX Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
XX Example; Fig 1; 8pp; German.
XX PS
XX This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
XX Sequence 20 BP; 3 A; 1 C; 2 G; 14 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
|||||
RESULT 350
AAC82919/c
ID AAC82919 standard; DNA; 20 BP.
XX
XX AAC82919;
XX AC
XX 21-MAR-2001 (first entry)
XX DT
XX Human S-9 derived oligonucleotide #3.
XX DE
XX Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
XX Homo sapiens.
XX OS
XX DE19923966-A1.
XX PN
XX 30-NOV-2000.
XX PD
XX 25-MAY-1999; 99DE-01023966.
XX PF
XX 25-MAY-1999; 99DE-01023966.
XX PR

XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX PA
XX Boekenkamp D, Hoppe H, Burgstaller P;
XX PI
XX WPI; 2001-050938/07.
XX DR
XX Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
XX Example; Fig 1; 8pp; German.
XX PS
XX This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
XX Sequence 20 BP; 4 A; 1 C; 2 G; 13 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
|||||
RESULT 351
AAC82920/c
ID AAC82920 standard; DNA; 20 BP.
XX
XX AAC82920;
XX AC
XX 21-MAR-2001 (first entry)
XX DT
XX Human S-9 derived oligonucleotide #4.
XX DE
XX Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
XX Homo sapiens.
XX OS
XX DE19923966-A1.
XX PN
XX 30-NOV-2000.
XX PD
XX 25-MAY-1999; 99DE-01023966.
XX PF
XX 25-MAY-1999; 99DE-01023966.
XX PR
XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX PA
XX Boekenkamp D, Hoppe H, Burgstaller P;
XX PI
XX WPI; 2001-050938/07.
XX DR
XX Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
XX Example; Fig 1; 8pp; German.
XX PS
XX This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
XX Sequence 20 BP; 4 A; 1 C; 2 G; 13 T; 0 U; 0 Other;
SQ

CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides
 XX
 SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2573 TTTAAAAA 2588
 Db 16 TTTAAAAA 1
 RESULT 352
 ADA09834
 ID ADA09834 standard; DNA; 20 BP.
 AC ADA09834;
 XX
 DT 06-NOV-2003 (first entry)
 DE Antisense nested PCR primer #2 for amplification of rat P2X7 (P2Z).
 XX
 KW PCR; ss; primer; permeabilizing activity; P2X7 receptor; P2Z receptor;
 KW receptor; ATP; antigen presenting cell; T lymphocyte;
 KW mitogenic stimulation; multinucleated giant cell; adenosine triphosphate;
 KW 3'-O-(4-benzoyl)benzoyl ATP; BzATP; fluorescent dye; propidium iodide;
 KW nootropic; neuroprotective; immunosuppressive; cerebroprotective;
 KW vasotropic; arthritic disorder; respiratory disorder;
 KW neurodegenerative disease; Alzheimer's disease; inflammation;
 KW rheumatoid arthritis; amyloidosis; infection; tuberculosis;
 KW haematopoietic system; immune response; allergy;
 KW lymphoproliferative disorder; apoptosis; ischaemia; rat;
 KW autoimmune disorder.
 XX
 OS Rattus sp.
 XX
 PN US6509163-B1.
 XX
 PD 21-JAN-2003.
 XX
 PF 15-AUG-2000; 2000US-00638857.
 XX
 PR 28-APR-1997; 97US-00842079.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Buell GN, Surprenant A, Kawashima E;
 XX
 DR WPI; 2003-502654/47.
 XX
 PT Screening of compound for its ability to modulate permeabilizing activity
 PT of mammalian receptor useful for treating e.g. arthritis, and Alzheimer's
 PT disease.
 XX
 PS Example 1; SEQ ID NO 4; 43pp; English.
 XX
 CC The invention discloses a method for screening a compound for its ability
 CC to modulate the permeabilizing activity of a mammalian P2X7 (P2Z)
 CC receptor. The P2Z receptor is a cell surface receptor for ATP and has
 CC been implicated in the lysis of antigen presenting cells by cytotoxic T
 CC lymphocytes, in the mitogenic stimulation of human T lymphocytes, as well
 CC as in the formation of multinucleated giant cells. The preferred agonist
 CC is adenosine triphosphate (ATP) or 3'-O-(4-benzoyl)benzoyl ATP (BzATP)
 CC and the preferred method comprises monitoring the uptake into the cell of
 CC a detectable molecule, preferably a fluorescent dye (e.g. propidium

CC iodide). The inventive method is useful for screening a compound for its
 CC ability to modulate the permeabilizing activity of a mammalian P2X7
 CC receptor useful for treatment of arthritic and respiratory disorders and
 CC neurodegenerative diseases. It is particularly useful in the treatment of
 CC Alzheimer's disease, diseases involving acute or chronic inflammation
 CC including rheumatoid arthritis, amyloidosis, bacterial, viral and other
 CC microbial infections, e.g. tuberculosis, disorders of the haematopoietic
 CC system and immune response, including autoimmune disorders, allergies and
 CC lymphoproliferative disorders, diseases involving apoptotic cell death,
 CC such as cardiac and cerebral ischaemia. The sequence presented is a
 CC nested PCR primer used for the amplification of rat P2X7 cDNA.
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2102 GTCCAGCCGGCGAAG 2117
 Db 1 GTCCAGCCGGCGAAG 16
 RESULT 353
 ABZ91658
 ID ABZ91658 standard; DNA; 20 BP.
 AC ABZ91658;
 XX
 DT 17-OCT-2003 (first entry)
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIC-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 6900; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive, and
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2573 TTTAAAAA 2588
Db 3 TTTAAAAA 18

RESULT 354
ABZ98155/c
ID ABZ98155 standard; DNA; 20 BP.
XX
AC ABZ98155;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human CD23 + A1261 oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13397; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 306 CCAGGAGCGGTGTG 321
Db 20 CCAGGAGCGGTGTG 5
RESULT 355
ABZ89703
ID ABZ89703 standard; DNA; 20 BP.
XX
AC ABZ89703;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4945; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
D5 2 TTTAAAAA 17

RESULT 356
ABZ88813
ID ABZ88813 standard; DNA; 20 BP.
XX
AC ABZ88813;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
PN
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4055; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
D5 4 TTTAAAAA 19

RESULT 357
ABZ88694
ID ABZ88694 standard; DNA; 20 BP.
XX
AC ABZ88694;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
PN
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3936; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588

Db 1 TTTAAAAA 16

RESULT 358

ABD25043

ID ABD25043 standard; DNA; 20 BP.

XX

AC ABD25043;

XX

DT 29-JUL-2004 (first entry)

XX

DE A1128305-derived oligonucleotide SEQ ID 4055.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX

PN WO200285309-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013143.

XX

PR 24-APR-2001; 2001US-0286036P.

XX

XX (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

XX WPI; 2003-093058/08.

XX

XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 4055; 763pp; English.

XX

CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588

Db 4 TTTAAAAA 19

RESULT 359

ABD31186/c

ID ABD31186 standard; DNA; 20 BP.

XX

AC ABD31186;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human CD23-derived oligonucleotide SEQ ID 13397.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX

PN WO200285309-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013143.

XX

PR 24-APR-2001; 2001US-0286036P.

XX

XX (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

XX WPI; 2003-093058/08.

XX

PT Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
PS Claim 15; SEQ ID NO 13397; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 306 CCAGGAGCGCGTGTG 321
DB 20 CCAGGAGCGCGTGTG 5
RESULT 360
ABD27888
ID ABD27888 standard; DNA; 20 BP.
XX
AC ABD27888;
XX
DT 29-JUL-2004 (first entry)
DE AA258396-derived oligonucleotide SEQ ID 6900.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.

XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 6900; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
DB 3 TTTAAAAA 18
RESULT 361
ADJ60020/c
ID ADJ60020 standard; DNA; 20 BP.
XX
XX ADJ60020;
AC
XX
DT 06-MAY-2004 (first entry)
DE
DE Oligonucleotide associated to CD23-X04772 #14.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;

XX ss.
XX Homo sapiens.
XX WO2004011613-A2.
XX 05-FEB-2004.
XX 25-JUL-2003; 2003WO-US023509.
XX 29-JUL-2002; 2002US-0399076P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX NYCE JW, Tang L, Sandraasgra A, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-203534/19.
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX initiation codons and introns of respiratory disease-relevant genes e.g.,
XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
XX disease e.g., asthma.
XX Claim 2; SEQ ID NO 876; 85pp; English.
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
XX initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
XX end of nucleic acid target comprising gene(s) chosen from e.g.
XX interleukin (IL)-4 receptor, IL-5 receptor or salts of the
XX oligonucleotide and optionally surfactant operatively linked to the
XX oligonucleotide. The method is useful for preventing or treating a
XX respiratory or lung disease, which involves administering to the airways
XX of a subject an effective amount of an inhibitor. The oligonucleotide is
XX useful for production of a medicament for the prevention and/or treatment
XX of a respiratory or lung disease. The respiratory or lung disease is
XX chosen from airway inflammation, allergy(ies), asthma, impeded
XX respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
XX (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
XX (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
XX obstruction. The present sequence represents an oligonucleotide of the
XX invention.
XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 306 CCAGGAGCGCGGTGTG 321
Db 20 CCAGGAGCGCGGTGTG 5
RESULT 362
ADL58072/c
ID ADL58072 standard; DNA; 20 BP.
XX AC ADL58072;
XX AC
XX 03-JUN-2004 (first entry)
XX Human ESM-1 antisense oligonucleotide seqid 321.
XX cytotatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
XX gene therapy; endothelial specific molecule-1; ESM-1;
XX ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
XX angiogenic disorder; immunological disorder; cardiovascular disorder;
XX neurological disorder; antisense technology; ss.
XX Homo sapiens.
XX Key Location/Qualifiers

FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone. All cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2004021978-A2.
XX 19-MAR-2004.
XX 19-AUG-2003; 2003WO-US025833.
XX 19-AUG-2002; 2002US-0404495P.
XX (PHAA) PHARMACIA CORP.
XX Weinstein EJ, Griggs DW;
XX WPI; 2004-248358/23.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX composition for treating e.g., diabetes, cancer or cardiovascular
XX disorder.
XX Claim 3; SEQ ID NO 321; 555pp; English.
XX The invention describes a new antisense compound, having a sequence
XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX specific molecule-1 (ESM-1), that specifically hybridises with the
XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX treating an animal having a disease or condition associated with ESM-1.
XX The compound is useful for preparing a composition for treating diabetes,
XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX cardiovascular or neurological disorder. This sequence represents an
XX antisense oligonucleotide that can be used to modulate expression of
XX endothelial specific molecule-1 (ESM-1).
XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 362 TGGCGCGCTGGAGCAA 377
Db 17 TGGCGCGCTGGAGCAA 2
RESULT 363
ADL58071/c
ID ADL58071 standard; DNA; 20 BP.
XX AC ADL58071;
XX AC
XX 03-JUN-2004 (first entry)
XX Human ESM-1 antisense oligonucleotide seqid 320.
XX cytotatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
XX gene therapy; endothelial specific molecule-1; ESM-1;
XX ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
XX angiogenic disorder; immunological disorder; cardiovascular disorder;
XX neurological disorder; antisense technology; ss.
XX Homo sapiens.
XX Key Location/Qualifiers

XX Homo sapiens.
 OS Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone. All cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
 XX WO2004021978-A2.
 PN 18-MAR-2004.
 XX 19-AUG-2003; 2003WO-US025833.
 XX 19-AUG-2002; 2002US-0404495P.
 XX (PHAA) PHARMACIA CORP.
 XX Weinstein EJ, Griggs DW;
 PI WPI; 2004-248358/23.
 XX New antiense compound, having a sequence targeted to a nucleic acid
 XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
 XX composition for treating e.g., diabetes, cancer or cardiovascular
 XX disorder.
 PS Claim 3; SEQ ID NO 320; 555pp; English.
 XX The invention describes a new antiense compound, having a sequence
 XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
 XX specific molecule-1 (ESM-1), that specifically hybridises with the
 XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
 XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
 XX treating an animal having a disease or condition associated with ESM-1.
 XX The compound is useful for preparing a composition for treating diabetes,
 XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
 XX cardiovascular or neurological disorder. This sequence represents an
 XX antiense oligonucleotide that can be used to modulate expression of
 XX endothelial specific molecule-1 (ESM-1).
 SQ Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 362 TGCGCCGCTGGAGCAA 377
 Db 16 TGCGCCGCTGGAGCAA 1
 RESULT 364
 ID ADO45510/C
 XX ADO45510 standard; DNA; 20 BP.
 AC ADO45510;
 XX 15-JUL-2004 (first entry)
 DT Human oligonucleotide #876.
 XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;

KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease;
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX Homo sapiens.
 OS US2004049022-A1.
 PN 11-MAR-2004.
 XX 25-JUL-2003; 2003US-00627930.
 XX 23-APR-2002; 2002WO-US013135.
 XX 23-APR-2002; 2002WO-US013143.
 XX (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.
 PA (TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 PI WPI; 2004-293804/27.
 DR Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX Claim 2; SEQ ID NO 876; 174pp; English.
 PS The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.
 XX SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 CCAGGAGCGGTGTTG 321

```

Db          20 CCAGGAGCGCGTGTG 5
|||||
RESULT 365
AA59725/c
ID AAX59725 standard; DNA; 24 BP.
XX
AC AAX59725;
XX
XX
DT 22-JUL-1999 (first entry)
XX
DE DNA target used for the modified oligodeoxyribonucleotides.
XX
KW Oligodeoxyribonucleotide; intersubunit linkage;
KW phosphoramidate intersubunit; antisense activity; nuclease resistant;
KW in-vitro cell growth inhibition assay; infection;
KW smooth muscle cell proliferation disorder; inflammatory process;
KW genetic disorder; cancer; ss.
XX
OS Synthetic.
XX
XX WO9525814-A1.
XX
XX 28-SEP-1995.
XX
XX 20-MAR-1995; 95WO-US003575.
XX
XX 18-MAR-1994; 94US-00210505.
XX
XX 18-MAR-1994; 94US-00214599.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM, Schultz RG, Chen J;
XX
XX WPI; 1995-344627/44.
XX
XX Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance
XX toward phosphodiesterase digestion, and form stable duplexes with DNA and
XX RNA strands.
XX
XX Disclosure; Page 61; 101pp; English.
XX
XX The specification describes oligodeoxyribonucleotides having contiguous
XX nucleoside subunits joined by intersubunit linkages, where at least 3
XX contiguous subunits are joined by phosphoramidate intersubunits. The
XX oligodeoxyribonucleotides has a sequence of nucleoside subunits effective
XX to form a duplex with a target nucleic acid molecule. The
XX oligodeoxyribonucleotides are more resistant to nuclease digestion and
XX have improved RNA and dsDNA hybridisation characteristics, relative to
XX oligonucleotides not containing N3'-P5' phosphoramidate linkages. They
XX also have excellent antisense activity against complementary mRNA targets
XX in in-vitro cell growth inhibition assays. They also exhibit low
XX cytotoxicity. They may be used in diagnostic and therapeutic
XX applications, e.g., in combatting infections agents such as bacteria,
XX viruses, etc. or in treatment of smooth muscle cell proliferation
XX disorders, inflammatory processes, certain genetic disorders, cancers,
XX etc. The present sequence represents a target for the oligonucleotides
XX of the invention
XX
XX Sequence 24 BP; 10 A; 4 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAACAATCTTTT 2754
DB 24 AAAAAAAGGGGTTT 1

RESULT 366
ADH34300/c
ID AAH28312 standard; RNA; 25 BP.
XX
AC AAH28312;
XX
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from TGF-beta gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
XX WO200148480-A1.
XX

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```

ID ADH34300 standard; DNA; 24 BP.
XX
AC ADH34300;
XX
XX 11-MAR-2004 (first entry)
XX
DE Hairpin oligonucleotide.
XX
KW Nucleoside analogue; oligonucleotide synthesis; antisense therapy;
KW antigene method; hairpin oligonucleotide; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX stem_loop 1..24
XX /*tag= a
XX
XX WO2003068795-A1.
XX
XX 21-AUG-2003.
XX
XX 13-FEB-2003; 2003WO-JP001485.
XX
XX 13-FEB-2002; 2002JP-00035706.
XX
XX (IMAN/) IMANISHI T.
XX
XX Imanishi T, Obika S;
XX
XX WPI; 2003-689651/65.
XX
XX New nucleoside analogs for producing oligonucleotide analogs useful e.g.
XX as antisense compounds.
XX
XX Example 2; Page 48; 74pp; Japanese.
XX
XX The invention relates to nucleoside analogues and their salts. The
XX invention also encompasses oligonucleotides and their salts comprising at
XX least one nucleoside analogue of the invention. The nucleoside analogues
XX are produced by reducing an nucleoside azide derivative and optionally
XX further interconverting, or by reacting a nucleoside derivative with
XX formaldehyde and optionally deprotecting and/or interconverting. The
XX nucleoside analogues can be used for producing oligonucleotides useful as
XX antisense compounds and in antigene methods. The present sequence
XX represents a hairpin oligonucleotide used in an example of the invention.
XX
XX Sequence 24 BP; 10 A; 4 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAACAATCTTTT 2754
DB 24 AAAAAAAGGGGTTT 1

RESULT 367
AAH28312/c
ID AAH28312 standard; RNA; 25 BP.
XX
AC AAH28312;
XX
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from TGF-beta gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
XX WO200148480-A1.
XX

```

XX PD 05-JUL-2001.
 XX PF 28-DEC-2000; 2000WO-US035583.
 XX PR 28-DEC-1999; 99US-0173338P.
 XX PA (KEEN/) KEENE J D.
 XX PI Keene JD, Tenenbaum SA, Carson C;
 XX PT WPI; 2001-425706/45.
 XX PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
 PT sample comprising the complex with ligand that binds to a component of
 PT the complex and separating complex by binding ligand with a binding
 PT molecule.
 XX Example 6; Page 31; 49pp; English.
 XX The specification describes a method for partitioning endogenous cellular
 CC mRNA-protein (mRNP) complexes. The method comprises contacting a
 CC biological sample comprising mRNP complex with ligand that specifically
 CC binds a component of mRNP complex, separating mRNP complex by binding the
 CC ligand with a molecule specific for ligand, which is attached to the
 CC solid support and then collecting the mRNP complex by removing the
 CC complex from the support. The method is useful for in vivo partitioning
 CC of cellular mRNA protein complexes in a biological sample. The method is
 CC useful for determining the ribonomic profile of a cell which has numerous
 CC uses including monitoring of tumour development, state of growth or state
 CC of development, perturbations of a biological system such as disease,
 CC drug or toxin treatment and the state of cell aging or death,
 CC distinguishing ribonomic profiles among organisms, to discriminate
 CC between transcriptional and post-transcriptional contributions to gene
 CC expression and to track the movement of RNAs through RNP complexes,
 CC including the interactions of combinations of proteins with RNAs in RNP
 CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
 CC untranslated region (UTR) of mRNA of various genes. The sequences contain
 CC target sequences for RNA-binding proteins
 XX
 SQ Sequence 25 BP; 2 A; 1 C; 2 G; 1 T; 17 U; 2 Other;
 Query Match 0.4%; Score 16; DB 1; Length 25;
 Best Local Similarity 79.2%; Pred. No. 3.8e+02;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2576 AAAAAAAAAAATTCGAGNAAAA 2599
 Db | ||||| |||| |||||
 24 AAAAAAAAAACCAATTAAGAAAA 1
 RESULT 368
 AAV48959/C
 ID AAV48959 standard; DNA; 19 BP.
 AC AAV48959;
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-30.
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX EP856579-A1.
 PN 05-AUG-1998.
 XX
 PD 31-JAN-1997; 97EP-00101531.
 XX
 PF 31-JAN-1997; 97EP-00101531.
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

PR 31-JAN-1997; 97EP-00101531.
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA Schlingensiepen K, Brysch W;
 PI WPI; 1998-400910/35.
 XX Preparation of antisense oligonucleotide(s) which lack long runs of
 PT consecutive guanine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX Claim 10; Fig 8a; 286pp; English.
 PS
 XX AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 19 BP; 2 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2212 GGAAATGGATCCATGAACC 2230
 Db ||||| ||||| |||||
 19 GGAAATGGATACACGAACC 1
 RESULT 369
 AAV48939/C
 ID AAV48939 standard; DNA; 19 BP.
 XX
 AC AAV48939;
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-10.
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX EP856579-A1.
 PN 05-AUG-1998.
 XX
 PD 31-JAN-1997; 97EP-00101531.
 XX
 PF 31-JAN-1997; 97EP-00101531.
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Brysch W;
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligonucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX
XX Claim 10; Fig 8a; 286pp; English.
XX
XX AA48930-49007 represent antisense oligonucleotides directed against
XX transforming growth factor-beta2 (TGF-beta2). Of these, only
XX oligonucleotides AA48930-67 resulted in significant reduction in TGF-
XX beta 2 protein expression, while oligonucleotides AA48968-49007 had
XX little effect. The oligonucleotides exemplify the invention. The
XX specification describes oligonucleotides that contain 8-30 nucleotides,
XX which contain at most 8 nucleotides that can each form three hydrogen
XX bonds to cytosine; do not contain four consecutive nucleotides able to
XX form three H-bonds each to four consecutive cytosines; do not contain two
XX sequences of three consecutive nucleotides each able to form three H-
XX bonds to three consecutive cytosines, and the ratio between residues able
XX to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of
XX genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or
XX beta 2 to control proliferation of primary cell cultures (e.g. bone
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
XX keratinocytes). The oligonucleotides can also be used to analyse function
XX of proteins (by altering their expression or activity) and
XX therapeutically, e.g. in cases of cancer or (targeting TGF) for
XX stimulating the immune system
XX
XX Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 2.2e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 GGAGGTTTATAAATCGAC 1538
XX 19 GGAGGTTTACAAATAGAC 1
XX
XX Db
XX
XX RESULT 370
XX AAZ65447/C
XX ID AAZ65447 standard; DNA; 19 BP.
XX AC AAZ65447;
XX
XX DT 30-MAR-2000 (first entry)
XX
XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-7.
XX
XX KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
XX prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
XX glomerulonephritis; acute respiratory distress syndrome; ss;
XX atherosclerosis.
XX
XX OS Unidentified.
XX
XX PN WO9663975-A2.
XX
XX PD 16-DEC-1999.
XX
XX PF 10-JUN-1999; 99WO-EP004013.
XX
XX PR 10-JUN-1998; 98EP-00110709.
XX 25-JUL-1998; 98EP-00113974.
XX

PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
XX adversely affects the immune response, for treating cancers and
XX infections.
XX
XX Claim 5; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
XX used in the invention. The invention relates to a composition which
XX contains at least one inhibitor (less than 100 kD) of a substance (e.g.
XX transforming growth factor TGF-beta, vascular endothelial growth factor
XX VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
XX that adversely affects the immune response. The composition also includes
XX at least one stimulant that positively affects the immune response. This
XX oligonucleotide is an example of an inhibitor that is used in the
XX composition. The composition is used as an immunostimulant for the
XX treatment of neoplasms and infections, particularly hyperproliferation;
XX leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
XX colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
XX breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
XX malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
XX most of which are directed against TGFbeta or VEGF, are inhibitors of
XX monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
XX inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
XX colitis, diabetes, glomerulonephritis, acute respiratory distress
XX syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 2.2e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 GGAGGTTTATAAATCGAC 1538
XX 19 GGAGGTTTACAAATAGAC 1
XX
XX Db
XX
XX RESULT 371
XX AAA86481/C
XX ID AAA86481 standard; DNA; 19 BP.
XX XX
XX AC AAA86481;
XX
XX DT 04-DEC-2000 (first entry)
XX
XX DE PCBA HH ribozyme binding site #213.
XX
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX OS Mammalia.
XX
XX PN WO200032765-A2.
XX
XX PD 08-JUN-2000.
XX
XX PF 06-DEC-1999; 99WO-US028772.
XX
XX PR 04-DEC-1998; 98US-0110954P.
XX
XX PA (IMMU-) IMMUSOL INC.
XX
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX

```
PT PCNA and Cyclin B1.
XX Disclosure; Page 108; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 11 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
    Query Match      0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3591 TTTGGACTTTTCTTTTAA 3609
Db      ||||| ||||| |||||
      19 TTTGGACTTTTCTTTTAA 1

RESULT 372
AAF99013
ID AAF99013 standard; DNA; 19 BP.
XX
AC AAF99013;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #129.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 41; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 19 BP; 11 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
    Query Match      0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
    Query Match      0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGACGCG 633
Db      ||||| ||||| |||||
      1 GCGCGCGCGCGCGCGCG 19

RESULT 373
AAF99013/C
ID AAF99013 standard; DNA; 19 BP.
XX
AC AAF99013;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #129.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 41; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
    Query Match      0.4%; Score 15.8; DB 1; Length 19;
```

Best Local Similarity	89.5%;	Pred. No. 2.2e+02;	
Matches	17;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	616	CGCGCGCGCAGCAGCGCGC	634
Db	19	CGCGCGCGCGCGCGCGC	1
RESULT 374			
AAC83562/c			
ID	AAC83562	standard; DNA; 19 BP.	
XX	AC	AAC83562;	
XX	DT	28-FEB-2001	(first entry)
XX	DE	DNA synthesis method linker/primer sequence	SEQ ID NO: 1.
XX	XX	DNA synthesis; directional complementary DNA library; linker; PCR primer;	
XX	XX	ss.	
XX	OS	Synthetic.	
XX	XX	US6149531-A.	
XX	PN	07-NOV-2000.	
XX	PD	22-JUL-1997;	97US-00899029.
XX	PF	19-SEP-1988;	88US-00246567.
XX	PR	02-MAY-1991;	91US-00700066.
XX	PR	23-NOV-1992;	92US-00981931.
XX	PR	02-SEP-1993;	93US-00116049.
XX	XX	(STRA-) STRATAGENE.	
XX	XX	Hansen CJ, Huse WD;	
XX	XX	WPI; 2001-006435/01.	
XX	XX	Double stranded DNA synthesis with specific orientation comprises	
XX	XX	synthesizing a first strand of DNA complementary to a selected DNA or RNA	
XX	XX	template and synthesizing second strand complementary to first one.	
XX	XX	Example 1; Fig 1; 14pp; English.	
XX	XX	The present invention describes an improved method of DNA synthesis which	
XX	XX	provides double stranded DNA where the predetermined orientation of the	
XX	XX	sequence is preserved. This can be used in the construction of	
XX	XX	complementary DNA and directional DNA libraries	
XX	XX	Sequence 19 BP; 1 A; 2 C; 2 G; 14 T; 0 U; 0 Other;	
XX	XX	Query Match	0.4%; Score 15.8; DB 1; Length 19;
XX	XX	Best Local Similarity	89.5%; Pred. No. 2.2e+02;
XX	XX	Matches	17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2576	AAAAAAAAAAAAATTGCGAG	2594
Db	19	AAAAAAAAAAAAAACTCGAG	1
RESULT 375			
AAH61643/c			
ID	AAH61643	standard; DNA; 19 BP.	
XX	AC	AAH61643;	
XX	DT	10-SEP-2001	(first entry)
XX	DE	PCNA HH ribozyme binding site	SEQ ID NO:4067.
XX	DE	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;	
XX	DE	Angiogenesis inhibitory oligonucleotide #138.	

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 XX 14-DEC-2001; 2001WO-US048458.
 XX
 PF 14-DEC-2000; 2000US-0255534P.
 XX
 PR (COLE-) COLEY PHARM GROUP INC.
 XX
 PA Bratzler RL;
 XX
 PI WPI; 2002-566690/60.
 XX
 DR Inhibiting angiogenesis in a subject, involves administering at least one
 XX antiangiogenic nucleic acid molecule to the subject.
 XX
 PT Claim 2; Page 22; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 615 GCGCGCGCGCAGCGCGG 633
 DB 1 GCGCGCGCGCGCGCGG 19
 RESULT 377
 ABS77654/c
 ID ABS77654 standard; DNA; 19 BP.
 XX
 AC ABS77654;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #138.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;
 KW

KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 XX 14-DEC-2001; 2001WO-US048458.
 XX
 PF 14-DEC-2000; 2000US-0255534P.
 XX
 PR (COLE-) COLEY PHARM GROUP INC.
 XX
 PA Bratzler RL;
 XX
 PI WPI; 2002-566690/60.
 XX
 DR Inhibiting angiogenesis in a subject, involves administering at least one
 XX antiangiogenic nucleic acid molecule to the subject.
 XX
 PT Claim 2; Page 22; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 616 CGCGCGCGCAGCGCGG 634
 DB 19 CGCGCGCGCGCGCGG 1
 RESULT 378
 ABL38943
 ID ABL38943 standard; DNA; 19 BP.
 XX
 AC ABL38943;
 XX
 DT 16-APR-2002 (first entry)
 XX
 DE Immunostimulatory nucleic acid SEQ ID NO: 342.
 XX
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; ss.
 OS Synthetic.
 XX
 PN WO200197843-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US020154.
 XX
 XX 22-JUN-2000; 2000US-0213346P.
 PR

PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
XX WPI; 2002-154611/20.
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
XX Disclosure; Page 182; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
XX Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 615 GCGCGCGCGCACGCGCG 633
Db 1 GCGCGCGCGCGCGCGCG 19
RESULT 379
ABL38943/G
ID ABL38943 standard; DNA; 19 BP.
XX
XX ABL38943;
AC
XX 16-APR-2002 (first entry)
DT
XX Immunostimulatory nucleic acid SEQ ID NO: 342.
DE
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
XX Synthetic.
OS
XX WO200197843-A2.
PN
XX 27-DEC-2001.
PD
XX
XX 22-JUN-2001; 2001WO-US020154.
PF
XX 22-JUN-2000; 2000US-0213346P.
PR
XX (IOWA) UNIV IOWA RES FOUND.
PA
XX Weiner G, Hartmann G;
PI
XX WPI; 2002-154611/20.
DR
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX

PS Disclosure; Page 182; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
XX Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 GCGCGCGCGCACGCGCG 634
Db 19 GCGCGCGCGCGCGCGCG 1
RESULT 380
ACD99445
ID ACD99445 standard; DNA; 19 BP.
XX
XX ACD99445;
AC
XX 25-SEP-2003 (first entry)
DT
XX Immunostimulatory nucleic acid #131.
DE
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
XX Synthetic.
OS
XX US2003050268-A1.
PN
XX 13-MAR-2003.
PD
XX 29-MAR-2002; 2002US-00112653.
PF
XX 29-MAR-2001; 2001US-0279642P.
PR
XX (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
PA
XX Krieg AM, Berg DJ;
PI
XX WPI; 2003-521815/49.
DR
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 12; 229pp; English.
XX
XX The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.

CC This sequence represents an immunostimulatory nucleic acid
 XX
 SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 633
 DB 1 GCGCGCGCGCGCGCGCG 19

RESULT 381
 ACD9445/C
 ID ACD9445 standard; DNA; 19 BP.

XX ACD9445;
 AC ACD9445;
 XX
 DT 25-SEP-2003 (first entry)
 XX Immunostimulatory nucleic acid #131.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 OS Synthetic.

XX US2003050268-A1.
 PN
 XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.
 PF
 XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.
 PA (BERG/) BERG D J.

XX Krieg AM, Berg DJ;
 PI
 XX WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure; Page 12; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid

XX Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGCACGCGCG 634
 DB 19 GCGCGCGCGCGCGCGCG 1

RESULT 382
 ADB36515

ID ADB36515 standard; DNA; 19 BP.

XX ADB36515;
 AC
 XX 04-DEC-2003 (first entry)
 DT

XX Immunostimulatory nucleic acid #129.

XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX Synthetic.

XX US2003087848-A1.
 PN
 XX 08-MAY-2003.
 PD

XX 02-FEB-2001; 2001US-00776479.

XX 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;
 PI
 XX WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 PT Disclosure; Page 7; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.

XX Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 633
 DB 1 GCGCGCGCGCGCGCGCG 19

RESULT 383
 ADB36515/C
 ID ADB36515 standard; DNA; 19 BP.

XX ADB36515;
 AC

XX 04-DEC-2003 (first entry)
 DT

XX Immunostimulatory nucleic acid #129.

XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX Synthetic.

XX US2003087848-A1.
 PN
 XX 08-MAY-2003.
 PD

XX 02-FEB-2001; 2001US-00776479.

XX

```
PR 03-FEB-2000; 2000US-0179991P.
XX (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
XX Bratzler RL, Petersen DM, Fouron Y;
XX WPI; 2003-657977/62.
XX
XX Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX Disclosure; Page 7; 221pp; English.
XX
XX The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
XX Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCAGCAGCAGCGC 634
DB 19 CGCGCGCGCGCGCGCGC 1
RESULT 384
ADD42503
ID ADD42503 standard; DNA; 19 BP.
XX
XX ADD42503;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human infertility associated primer SEQ ID 364.
XX
XX primer; male infertility; infertility-associated mutation;
XX azoospermia factor; Y-chromosome;
XX cystic fibrosis transmembrane conductance regulator; CFTR;
XX Kallmann syndrome; KAL1; androgen resistance; steroid 21-hydroxylase;
XX CYP21; microarray; quantitative trait locus; in vitro fertilization;
XX oligospermia; ss.
XX
XX Homo sapiens.
XX
XX WO2003050299-A2.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2002; 2002WO-EF013995.
XX
XX 10-DEC-2001; 2001DE-01060563.
XX
XX (OGHA-) OGHAM GMBH.
XX
XX Cullen P, Seedorf U;
XX
XX WPI; 2003-505402/47.
XX
XX Investigating male genetic infertility, useful for diagnosis e.g. for
PT assessing suitability for in vitro fertilization, based on multifactorial
PT analysis of infertility-related mutations.
XX
XX Claim 13; SEQ ID NO 365; 110pp; German.
XX
XX This invention describes a novel method for investigating genetic
PA
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```
CC infertility or predisposition in males. The method involves selecting at
CC least two infertility-associated mutations which are recessive or
CC intermediate that are associated with infertility in the heterozygous
CC state and/or only in the homozygous state. Preferably at least one
CC azoospermia factor is detected which may be lost by microdeletions in
CC intervals 5 or 6 of the Y-chromosome. Also any of several hundred
CC mutations, listed, present in the cystic fibrosis transmembrane
CC conductance regulator (CFTR), Kallmann syndrome (KAL1), androgen
CC resistance (AR) or steroid 21-hydroxylase (CYP21) genes may be detected.
CC Probes for the mutated genes and/or native nucleic acid, or their
CC complementary strands, are fixed to a carrier, particularly as a
CC microarray, then tested for hybridization with oligonucleotides from or
CC synthesized from, a patient sample and hybridization detected.
CC Multifactorial analysis is by standard statistical methods, particularly
CC the quantitative trait locus method. The method is used to diagnose
CC inherited male infertility or predisposition to its, especially in
CC conjunction with in vitro fertilization programs, e.g. for assessing
CC subjects with oligospermia for possible application of the
CC intracytoplasmic sperm injection method. Analysis of many mutations
CC improves diagnosis of the genetic basis of male infertility, including
CC polygenic origins (complex interactions between different heterozygotic
CC mutations). A chip for analyzing genetic infertility in males comprises
CC oligonucleotides that represent known mutations (nonsense or missense,
CC insertions, allelic variants deletions or rearrangements) in the cystic
CC fibrosis transmembrane conductance regulator, Kallmann syndrome, androgen
CC resistance and steroid 21-hydroxylase genes. ADD42140-ADD42633 represent
CC oligonucleotides used in the microarray described in the method of the
CC invention. NOTE: there are no SEQ ID's 133, 472 or 473 represented in the
XX SEQ ID list of the specification.
XX
SQ Sequence 19 BP; 6 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3162 TCAAAGCCCCCAGCAACAC 3180
DB 1 TCACGTGCCCCAGCAACAC 19
RESULT 385
ADP50074
ID ADP50074 standard; RNA; 19 BP.
XX
XX ADP50074;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human BCL2 siNA lower sequence SEQ ID NO:802.
XX
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
XX cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
XX autoimmune disease; viral infection; HIV.
XX
XX Homo sapiens.
XX
XX WO2003070969-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-US004908.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 06-JUN-2002; 2002US-0386782P.
XX 18-JUL-2002; 2002US-0396905P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
```


CC that downregulates expression of the BCL2 gene by RNA interference. A
 CC siRNA of the invention has cytostatic, immunosuppressive, virucide, and
 CC anti-HIV activity. The siRNA are useful for modulation (inhibition) of
 CC expression or activity of BCL2 by RNA interference. siRNA are used to
 CC modulate expression of BCL2 genes, in cells, tissue explants or
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral
 CC infections (including by HIV) but also for drug screening, diagnosis,
 CC target identification and validation, genetic engineering,
 CC pharmacogenomics, studying gene function and gene mapping, (e.g. of single
 CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
 CC represent siRNA of the invention.

SQ Sequence 19 BP; 5 A; 5 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3748 AATGACATGAGCTACCTGG 3766
 DB 19 AATGAATGAGCTATCTGG 1

RESULT 388
 ADF49813/C
 ID ADF49813 standard; RNA; 19 BP.

XX AC ADF49813;
 XX DT 12-FEB-2004 (first entry)

XX DE Human BCL2 siRNA upper sequence SEQ ID NO:541.
 XX KW ss; siRNA; human; BCL2; short interfering nucleic acid; RNA interference;
 KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
 KW autoimmune disease; viral infection; HIV.

XX OS Homo sapiens.
 XX PN WO2003070969-A2.
 XX PD 28-AUG-2003.
 XX PF 18-FEB-2003; 2003WO-US0004908.
 XX PR 20-FEB-2002; 2002US-0358580P.
 XX PR 11-MAR-2002; 2002US-0363124P.
 XX PR 06-JUN-2002; 2002US-0386782P.
 XX PR 18-JUL-2002; 2002US-0396905P.
 XX PR 29-AUG-2002; 2002US-0406784P.
 XX PR 05-SEP-2002; 2002US-0408378P.
 XX PR 09-SEP-2002; 2002US-0409293P.
 XX PR 15-JAN-2003; 2003US-0440129P.

XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J, Beigelman L;
 XX WPI; 2003-712622/67.
 XX PT New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer or autoimmune disease, downregulates expression of
 PT the BCL2 gene.

XX PS Example 3; SEQ ID NO 541; 148pp; English.
 XX CC The invention relates to a novel short interfering nucleic acid (siRNA)
 CC that downregulates expression of the BCL2 gene by RNA interference. A
 CC siRNA of the invention has cytostatic, immunosuppressive, virucide, and
 CC anti-HIV activity. The siRNA are useful for modulation (inhibition) of
 CC expression or activity of BCL2 by RNA interference. siRNA are used to
 CC modulate expression of BCL2 genes, in cells, tissue explants or
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral

CC infections (including by HIV) but also for drug screening, diagnosis,
 CC target identification and validation, genetic engineering,
 CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
 CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
 CC represent siRNA of the invention.

SQ Sequence 19 BP; 5 A; 5 C; 2 G; 0 T; 7 U; 0 Other;
 Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4248 TGCAGGCTGATTAAGAAA 4266
 DB 19 TGCAGGCTGTTTAAGAAA 1

RESULT 389
 ADF31627/C
 ID ADF31627 standard; RNA; 19 BP.

XX AC ADF31627;
 XX DT 12-FEB-2004 (first entry)

XX DE Human IGF-1R siRNA lower strand, SEQ ID NO:292.
 XX KW RNA interference; short interfering nucleic acid; siRNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping; cancer;
 KW proliferative disease; restenosis; polycystic kidney disease;
 KW inflammatory disease; allergic disease; autoimmune disease;
 KW transplant rejection; cytostatic; vasotropic; nephrotropic;
 KW antiinflammatory; antiallergic; immunosuppressive; human;
 KW insulin-like growth factor 1 receptor; IGF-1R; ss.

XX OS Homo sapiens.
 XX PN WO2003070911-A2.
 XX PD 28-AUG-2003.
 XX PF 20-FEB-2003; 2003WO-US0005044.
 XX PR 20-FEB-2002; 2002US-0358580P.
 XX PR 11-MAR-2002; 2002US-0363124P.
 XX PR 06-JUN-2002; 2002US-0386782P.
 XX PR 29-AUG-2002; 2002US-0406784P.
 XX PR 05-SEP-2002; 2002US-0408378P.
 XX PR 09-SEP-2002; 2002US-0409293P.
 XX PR 15-JAN-2003; 2003US-0440129P.

XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J, Beigelman L, Chowrira B;
 XX WPI; 2003-721691/68.
 XX PT New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer, downregulates expression of the insulin-like growth
 PT factor-1 receptor gene.

XX PS Example 3; SEQ ID NO 292; 147pp; English.
 XX CC The invention relates to short interfering nucleic acids (siRNA) which
 CC downregulate expression of the human insulin-like growth factor 1
 CC receptor (IGF-1R) gene by RNA interference. The siRNAs may or may not
 CC comprise ribonucleotides and may be double or single stranded. They
 CC further comprise sense and antisense regions, or alternatively are
 CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
 CC Specifically, the siRNAs include short interfering RNA (siRNA), double-

CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
 CC can be unmodified or chemically modified, can contain
 CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
 CC vector or enzymatically synthesised. The invention also relates to kits
 CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
 CC of siNA; and vectors that express siNA. The siNAs are used to modulate
 CC expression of the IGF-1R gene in cells, tissue explants or organisms
 CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
 CC treatment of a variety of conditions. They may be used for treating
 CC cancer and other proliferative diseases (e.g., restenosis and polycystic
 CC kidney disease), inflammatory and/or allergic diseases, autoimmune
 CC diseases and transplant rejection. The siNAs are also useful for drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
 CC represents the lower strand of a human IGF-1R-targeted double-stranded
 CC siNA.

XX
 SQ Sequence 19 BP; 3 A; 3 C; 11 G; 0 T; 2 U; 0 Other;
 Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2332 CCGAAGCTTCCGCTTCCCC 2350
 Db 19 CCGCAGCTACCGCTTCCCC 1

RESULT 390
 ADF31350
 ID ADF31350 standard; RNA; 19 BP.
 AC ADF31350;
 XX
 DT 12-FEB-2004 (first entry)
 DE Human IGF-1R transcript target sequence/siNA upper strand, SEQ ID NO:15.
 DE
 DE RNA interference; short interfering nucleic acid; siNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping; cancer;
 KW proliferative disease; restenosis; polycystic kidney disease;
 KW inflammatory disease; allergic disease; autoimmune disease;
 KW transplant rejection; cytostatic; vasotropic; nephrotropic;
 KW antiinflammatory; antiallergic; immunosuppressive; human;
 KW insulin-like growth factor 1 receptor; IGF-1R; target sequence; ss.
 XX Homo sapiens.
 OS
 XX
 XX WO2003070911-A2.
 PN
 XX
 PD 28-AUG-2003.
 XX
 XX 20-FEB-2003; 2003WO-US005044.
 PF
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX
 XX Mcswiggen J, Beigelman L, Chowrira B;
 PI
 XX WPI; 2003-721691/68.
 DR
 XX
 XX New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of cancer, downregulates expression of the insulin-like growth
 PT factor-1 receptor gene.
 XX
 PS Example 3; SEQ ID NO 15; 147pp; English.
 XX
 CC The invention relates to short interfering nucleic acids (siNA) which
 CC downregulate expression of the human insulin-like growth factor 1
 CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not
 CC comprise ribonucleotides and may be double or single stranded. They
 CC further comprise sense and antisense regions, or alternatively are
 CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
 CC Specifically, the siNAs include short interfering RNA (siRNA), double-
 CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
 CC can be unmodified or chemically modified, can contain
 CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
 CC vector or enzymatically synthesised. The invention also relates to kits
 CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
 CC of siNA; and vectors that express siNA. The siNAs are used to modulate
 CC expression of the IGF-1R gene in cells, tissue explants or organisms
 CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
 CC treatment of a variety of conditions. They may be used for treating
 CC cancer and other proliferative diseases (e.g., restenosis and polycystic
 CC kidney disease), inflammatory and/or allergic diseases, autoimmune
 CC diseases and transplant rejection. The siNAs are also useful for drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
 CC represents the upper strand of a human IGF-1R-targeted double-stranded
 CC siNA, which is identical to the IGF-1R transcript target sequence.

XX
 SQ Sequence 19 BP; 2 A; 11 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 73.7%; Pred. No. 2.2e+02;
 Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2332 CCGAAGCTTCCGCTTCCCC 2350
 Db 1 CCGCAGCUACCGUCCCC 19

RESULT 391
 ADQ14537/c
 ID ADQ14537 standard; RNA; 22 BP.
 XX ADQ14537;
 AC ADQ14537;
 XX
 XX 23-SEP-2004 (first entry)
 DT
 XX
 XX TGF beta 2 3'-UTR consensus sequence SEQ ID NO:32.
 DE
 DE
 DE metabolic state; mRNA protein complex; mRNA complex; RNA binding protein;
 KW mRNA complex-associated protein; mRNA complex-associated protein;
 KW mRNA target; protein target; physiological pathway;
 KW TGF beta 2 3'-UTR consensus sequence; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX WO2004057032-A1.
 PN
 XX
 PD 08-JUL-2004.
 XX
 XX 04-DEC-2003; 2003WO-US038475.
 PF
 XX 04-DEC-2002; 2002US-00309788.
 PR
 XX (RIBO-) RIBONOMICS INC.
 PA
 XX
 XX Keene JD, Tenenbaum SA, Carson CC, Phelps WC;
 PI
 XX WPI; 2004-525445/50.
 DR
 XX
 XX Assessing the metabolic state of a cell comprises isolating at least one

PT mRNP complex comprising at least one RNA binding protein, and at least
PT one mRNA or at least one mRNP complex-associated protein.
PS Example 4; SEQ ID NO 32; 86pp; English.
XX
CC The present invention describes a method for assessing the metabolic
CC state of a cell. The method comprises isolating at least one mRNP complex
CC having at least one RNA binding protein, and at least one mRNA or at
CC least one mRNP complex-associated protein, and determining the expression
CC level of the mRNA or mRNP complex-associated protein, where the level of
CC expression of the at least one mRNA or the at least one mRNP complex-
CC associated protein is indicative of the metabolic state of the cell. The
CC method can be used for assessing the metabolic state in a cell, and for
CC identifying and evaluating mRNA and protein targets associated with mRNP
CC complexes and implicated in the expression of proteins involved in common
CC physiological pathways. The present sequence represents a TGF beta 2 3'-
CC UTR consensus sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 22 BP; 2 A; 1 C; 2 G; 0 T; 17 U; 0 Other;

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAAA 2599
DB ||||||| ||||| |||||||
22 AAAAAAACCAATTAAAGAAAAA 1

RESULT 392
AA63947
ID AAX63947 standard; RNA; 17 BP.
XX
AC AAX63947;
XX
DT 20-JUL-1999 (first entry)
DE Rabbit stromelysin hammerhead target SEQ ID NO:579.
XX
DE Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Oryctolagus cuniculus.
XX
PN WO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US015516.
XX
PR 13-DEC-1994; 94US-00354920.
PR 23-DEC-1994; 94US-00363253.
PR 23-DEC-1994; 94US-00363254.
PR 17-FEB-1995; 95US-00390850.
PR 20-APR-1995; 95US-00426124.
PR 02-MAY-1995; 95US-00432874.
PR 04-MAY-1995; 95US-00434509.
PR 07-JUL-1995; 95US-0000951P.
PR 07-JUL-1995; 95US-0000974P.
PR 07-AUG-1995; 95US-00512861.
PR 05-OCT-1995; 95US-00541365.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
PI Karpeisky A, Thompson JD, Modak A, Burgin A;
XX WPI; 1996-300653/30.

XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX
PS Example 1; Page 155; 307pp; English.
XX
CC The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC : (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention
XX
SQ Sequence 17 BP; 5 A; 1 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 1.9e+02;
Matches 7; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTTCTTTTAAAGGA 1048
DB ::::| ::::| :|||
1 UUUUCAUUUUUAAAGGA 17

RESULT 393
AA63948
ID AAX63948 standard; RNA; 17 BP.
XX
AC AAX63948;
XX
DT 20-JUL-1999 (first entry)
DE Rabbit stromelysin hammerhead target SEQ ID NO:580.
XX
DE Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Oryctolagus cuniculus.
XX
PN WO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US015516.
XX
PR 13-DEC-1994; 94US-00354920.
PR 23-DEC-1994; 94US-00363253.
PR 23-DEC-1994; 94US-00363254.
PR 17-FEB-1995; 95US-00390850.
PR 20-APR-1995; 95US-00426124.
PR 02-MAY-1995; 95US-00432874.
PR 04-MAY-1995; 95US-00434509.
PR 07-JUL-1995; 95US-0000951P.
PR 07-JUL-1995; 95US-0000974P.
PR 07-AUG-1995; 95US-00512861.
PR 05-OCT-1995; 95US-00541365.
XX

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PA (RIBO-) RIBOZYME PHARM INC.
XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
PI McSwiggan J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
PI Karpeisky A, Thompson JD, Modak A, Burgin A;
XX WPI; 1996-300653/30.
DR Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX
PS Example 1; Page 155; 307pp; English.
XX
CC The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention
XX
SQ Sequence 17 BP; 6 A; 1 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTCTTTTAAAGGAA 1049
Db 1 UUUCAUUUUUUAAAGGAA 17

RESULT 394
AAV93710
ID AAV93710 standard; RNA; 17 BP.
XX
AC AAV93710;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human B-raf substrate nucleotide position 2457.
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 03-JUL-1997; 97US-0049002P.
PR 22-AUG-1997; 97US-0051718P.
PR 02-OCT-1997; 97US-0061321P.

102-OCT-1997; 97US-0061324P.
05-NOV-1997; 97US-0064866P.
19-DEC-1997; 97US-0068212P.
(RIBO-) RIBOZYME PHARM INC.
Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
Parry T, Beigelman L, McSwiggan JA, Karpeisky A, Burgin A;
Thompson J, Workman CT, Beaudry A, Sweedler D;
WPI; 1999-009494/01.
Identifying new catalytic nucleic acid that modulates selected processes
- especially ribozymes that cleave Raf RNA for treating cancer,
restenosis, and also new ribozymes and modified nucleoside triphosphates
used as antiviral agents and synthons.
Claim 177; Page 172; 259pp; English.
A method has been developed for the identification of a nucleic acid
capable of modulating a process in a biological system. The method
comprises: (a) introducing into the system a random library of nucleic
acid catalysts (NAC) having a substrate binding domain (SBD), comprising
a random sequence, and a catalytic domain (CD); and (b) identifying NAC
in systems where modulation has occurred and/or determining the sequence
of at least part of the SBDs in such systems. Nucleic acid molecules with
endonuclease activity and catalytic activity, from the present invention,
are used to modulate gene expression in plant and mammalian cells and to
cleave target nucleic acid, particularly for treating systemic diseases
caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
ascites and infection. They may also be used to detect genetic drift and
mutations in diseased cells and to determine c-raf RNA. Specifically NACs
with RNA-cleaving activity that modulate expression of the Raf gene, are
used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
generally any condition associated with the level of c-raf. Introduction
of sugar/phosphate modifications increases stability against nuclease and
activity. AAV90922 to AAV93877 represent NACs that can be used in the
method, specifically for modulating the expression of a Raf gene
Sequence 17 BP; 2 A; 2 C; 2 G; 0 T; 11 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 29.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2743 TCCTTTTAAAGG 2759
Db 1 UCUCUUUUUUUUAAAGG 17

RESULT 395
AAZ65512/c
ID AAZ65512 standard; DNA; 17 BP.
XX
AC AAZ65512;
XX
DT 30-MAR-2000 (first entry)
XX
DE Immunosuppressant inhibitor oligonucleotide TGF-beta-23-2268.
XX
KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
KW glomerulonephritis; acute respiratory distress syndrome; ss;
KW atherosclerosis.
XX
OS Unidentified.
XX
PN WO9963975-A2.
XX
PD 16-DEC-1999.
XX

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PF 10-JUN-1999; 99WO-EP004013.
XX 10-JUN-1998; 98EP-00110709.
PR 25-JUL-1998; 98EP-00113974.
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
XX WPI; 2000-097470/08.
XX Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
XX infections.
XX Claim 10; Fig 1; 30pp; English.
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
XX syndrome and the formation of atherosclerotic plaque
XX
SQ Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2349 CCTGTGCTGTGTGCCA 2365
Db 17 CCTGTGCTGTGTGCCA 1
RESULT 396
ABZ59897
ID ABZ59897 standard; RNA; 17 BP.
XX ABZ59897;
AC
XX 21-MAR-2003 (first entry)
XX Human K-Ras DNazyme substrate #9.
DE
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
OS
XX WO200297114-A2.
PN
XX 05-DEC-2002.
PD
XX 29-MAY-2002; 2002WO-US016840.
PF
XX 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX Mcswiggen J;
XX WPI; 2003-140484/13.
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX Claim 58; Page 85; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59899 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 427 CAGCAGCGCGCGTCCA 443
Db 1 CAGCAGCGCGCGCGCA 17
RESULT 397
ADI49626/c
ID ADI49626 standard; DNA; 17 BP.
XX ADI49626;
AC
XX 15-APR-2004 (first entry)
XX Human tumour suppression/reversion-related DNA sequence SeqID2129.
DE
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX Homo sapiens.
OS
XX WO2003025177-A2.
PN
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004523.
PF
XX 17-SEP-2001; 2001FR-00011980.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-313354/30.
DR
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; SEQ ID NO 2129; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, indentifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration.
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publichedpct_sequences
 XX
 SQ Sequence 17 BP; 11 A; 1 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3598 TTTTCTTTTAAATGATC 3614
 Db 17 TTTCTTTTAAATGATC 1
 RESULT 398
 ADL49413/C
 ID ADL49413 standard; RNA; 17 BP.
 XX
 AC ADL49413;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #527.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; ikappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, ikappaB kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 2946; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC ikappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 XX
 SQ Sequence 17 BP; 4 A; 1 C; 1 G; 0 T; 11 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2570 GTGTTTAAAAA 2586
 Db 17 GTCTTTAAAAA 1
 RESULT 399
 ADL49412/C
 ID ADL49412 standard; RNA; 17 BP.
 XX
 AC ADL49412;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #526.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; ikappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, ikappaB kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 2945; 317pp; English.

CC protecting groups, deprotection of nucleobases and partial deprotection
 CC of phosphate linkages can be achieved in the reaction sequence. Suggested
 CC specific groups include S-pivaloylmercaptethyl (SPME) and
 CC cyanoethylcarbonyl (CEOC) groups. Spacer molecules include diglycolyl
 CC (COCH₂COCH₂CO) and its analogue with a catechol bisresidue replacing the
 CC oxygen atom (1,2-phenylenedioxy-diacetic acid). The present sequence
 CC represents a phosphorothioate oligonucleotide used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATGGAG 2594
 DB 18 AAAAAAAAAAATGGGG 2

RESULT 402
 ABL57541/C
 ID ABL57541 standard; DNA; 18 BP.

XX
 AC ABL57541;
 XX
 DT 26-JUL-2002 (first entry)

DE Nucleic acid probe f.

XX Concentration; quantification; mutation detection; polymorphic;
 KW polymerase chain reaction; PCR; probe; ss.

XX Unidentified.

XX EP1046717-A2.

XX 25-OCT-2000.

XX 20-APR-2000; 2000EP-00108643.

XX 20-APR-1999; 99JP-00111601.

XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.

PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

PA (KANK-) KANKYO ENG CO LTD.

XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX WPI; 2000-657765/64.

XX Determining the concentration of a target nucleic acid, useful e.g. for

PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.

XX Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a
 CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.
 CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for
 CC quantifying microbial cells in co-cultures or symbiotic systems, for
 CC detecting gene mutations or polymorphisms, and for analysing melting
 CC curves of target nucleic acids to determine a T_m value. Methods of the
 CC invention allow target nucleic acids to be quantified quickly, easily and
 CC accurately. Particularly there is no need to remove unbound probe, and no
 CC materials are introduced that inhibit amplification by Taq polymerase (so
 CC conventional PCR conditions can be used). The specificity of PCR is kept
 CC high (amplification of primer dimers is delayed), and the limit of
 CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis
 CC (automatically generated by a computer) has a higher correlation
 CC coefficient than conventional graphs so more accurate quantitation is
 CC possible. The current sequence represents a nucleic acid probe of the
 CC invention that was used for investigating the base selectivity of a
 CC target nucleic acid
 XX
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177

DB 17 TATATATTTTCTT 1

RESULT 403
 ABA97626/C
 ID ABA97626 standard; DNA; 18 BP.

XX
 AC ABA97626;

XX
 DT 11-APR-2002 (first entry)

XX Probe f.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

XX JP2001286300-A.

XX 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

XX 20-APR-1999; 99JP-00111601.

XX 24-AUG-1999; 99JP-00236666.

XX 30-AUG-1999; 99JP-00242693.

XX 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.

XX WPI; 2002-134193/18,

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

XX This invention relates to a method for measuring nucleic acids using a

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 2.2e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCTTTTATATATAT 1169

DB 18 TTCTTTTATATATAT 2

RESULT 404
 ABA97628/C

ID ABA97628 standard; DNA; 18 BP.
 AC ABA97628;
 XX
 DT 11-APR-2002 (first entry)
 XX
 DE Probe h.
 XX
 KW ss; fluorochrome; nucleic acid probe; fluorescence.
 XX
 OS Unidentified.
 XX
 PN JP2001286300-A.
 XX
 PD 16-OCT-2001.
 XX
 PF 20-APR-2000; 2000JP-00120097.
 XX
 PR 20-APR-1999; 99JP-00111601.
 PR 24-AUG-1999; 99JP-00236666.
 PR 30-AUG-1999; 99JP-00242693.
 PR 01-FEB-2000; 2000JP-00028896.
 XX
 PA (BIOI-) BIOINDUSTRY KYOKAI SH.
 PA (KANK-) KANKYO ENG KK.
 PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
 XX
 DR WPI; 2002-134193/18.
 XX
 PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
 PT the obtained data.
 XX
 PS Example 5; Page 17; 34pp; Japanese.
 XX
 CC This invention relates to a method for measuring nucleic acids using a
 CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
 CC decreases the fluorescence of the fluorochrome when hybridised with a
 CC target nucleic acid, the decrease in the fluorescence is measured. The
 CC method can be used for measuring a target nucleic acid
 XX
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1152 TTCTTTTATATATA 1168
 Db 17 TTTTATATATATA 1
 XX
 RESULT 405
 ABL95901/c
 ID ABL95901 standard; DNA; 18 BP.
 XX
 AC ABL95901;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Probe h for assaying nucleic acids.
 XX
 KW Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX
 OS Unidentified.
 XX
 PN WO200208414-A1.
 XX
 PD 31-JAN-2002.
 XX
 PF 27-JUN-2001; 2001WO-IB001147.
 XX
 PR 27-JUN-2000; 2000JP-00193133.
 PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PN Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PD Yokomaku T;
 XX
 PF WPI; 2002-195876/25.
 XX
 PR 27-JUN-2000; 2000JP-00193133.
 XX

PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;
 XX
 DR WPI; 2002-195876/25.
 XX
 XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 PT their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification.
 XX
 PS Example 12; Page 60; 152pp; Japanese.
 XX
 CC The present invention relates to nucleic acid probes, which are useful
 CC for assaying nucleic acids by hybridising with a target nucleic acid, in
 CC which a single-stranded oligonucleotide is labelled with a fluorescent
 CC substance and a quencher in a manner that the fluorescence intensity of
 CC the hybridisation reaction system is increased after completion of the
 CC hybridisation but no stem loop structure is formed. The probes are useful
 CC for assaying nucleic acids and their polymorphism and mutation.
 CC particularly useful for e.g. analytical applications, disease diagnosis
 CC and microbial identification. The present sequence was used to illustrate
 CC the invention
 XX
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1152 TTCTTTTATATATA 1168
 Db 17 TTTTATATATATA 1
 XX
 RESULT 406
 ABL95899/c
 ID ABL95899 standard; DNA; 18 BP.
 XX
 AC ABL95899;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Probe f for assaying nucleic acids.
 XX
 KW Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX
 OS Unidentified.
 XX
 PN WO200208414-A1.
 XX
 PD 31-JAN-2002.
 XX
 PF 27-JUN-2001; 2001WO-IB001147.
 XX
 PR 27-JUN-2000; 2000JP-00193133.
 PR 03-AUG-2000; 2000JP-00236115.
 PR 26-SEP-2000; 2000JP-00292483.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PN Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PD Yokomaku T;
 XX
 PF WPI; 2002-195876/25.
 XX

PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
PS Example 12; Page 60; 152pp; Japanese.
XX
XX The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
XX Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1161 TATATATATTTTCTT 1177
DB 17 TATATATATTTTCTT 1

RESULT 407
ABL95989/c
ID ABL95988 standard; DNA; 18 BP.
XX
XX ABL95898;
AC
DT 19-JUN-2002 (first entry)
XX
XX Probe d for assaying nucleic acids.
DE
XX Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
XX Unidentified.
OS
XX WO200208414-A1.
PN
XX 31-JAN-2002.
PD
XX 27-JUN-2001; 2001WO-IB001147.
PF
XX 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
PI
XX WPI; 2002-195876/25.
DR
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
PS
XX Example 12; Page 60; 152pp; Japanese.
XX
XX The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of

CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
XX Sequence 18 BP; 14 A; 0 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1152 TTCTTTTATATATA 1168
DB 17 TTTTATATATATA 1

RESULT 408
ABZ10862/c
ID ABZ10862 standard; DNA; 18 BP.
XX
XX ABZ10862;
AC
XX 16-JAN-2003 (first entry)
DT
XX
XX Haematopoietic cell proliferation disorder related oligonucleotide #1002.
DE
XX Human; haematopoietic cell proliferation disorder; cytostatic;
KW Gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX cytosine methylation state; probe; primer; ss.
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200277272-A2.
PN
XX 03-OCT-2002.
PD
XX 26-MAR-2002; 2002WO-EP003401.
PF
XX 26-MAR-2001; 2001US-0278333P.
PR
XX (EPTG-) EPIGENOMICS AG.
PA
XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwöpe I, Ziebarth H;
XX
XX WPI; 2003-018942/01.
DR
XX Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX Claim 15; Page 67; 117pp; English.
PS
XX The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the

CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferation disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAAAAACATCAAAAC 2823
 |||||
 Db 18 AAAAAAAAAACCAAAAC 2

RESULT 409
 AAV40352
 ID AAV40352 standard; DNA; 19 BP.

XX AC AAV40352;

DT 27-AUG-2003 (revised)
 DT 14-OCT-1998 (first entry)

XX DE Maize oligonucleotide marker S48F.

XX KW Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
 KW polymorphic site; corn; gramineae species; ss.

XX OS Synthetic.
 OS Zea.

XX PN W09830717-A2.

XX PD 16-JUL-1998.

XX PF 02-DEC-1997; 97WO-EP0071134.

XX PR 02-DEC-1996; 96US-0032069P.

XX PA (BIOC-) BIOCEM SA.

XX PI Murigneux A;

XX DR WPI; 1998-399160/34.

XX PT Vegetal sequences including single nucleotide polymorphism - useful, e.g.
 PT to determine polymorphisms in plants, determine strain in plant breeding
 PT and to correlate polymorphisms with phenotypic traits.

XX PS Example 2; Page 9; 32pp; English.

XX CC The present invention describes a nucleic acid segment comprising at
 CC least 10 contiguous nucleotides from a vegetal sequence including a
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
 CC complement of the segment. Also described are: (1) an allele-specific
 CC oligonucleotides hybridising to segment, or their complements, and (2) a
 CC method of analysing nucleic acids from a subject, by determining if a
 CC base is occupying any one (or a set) of polymorphic sites in 261
 CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
 CC segments are useful in fingerprint analysis in plants to determine which
 CC polymorphisms are present, which strain a plant belongs to and to
 CC distinguish between strains. The polymorphisms may correlate with
 CC phenotypic traits (e.g. plant growth rate or crop yield), and the
 CC segments are useful to determine the presence/absence of specific
 CC polymorphisms correlating with the existence/absence of particular
 CC traits. The segments are also useful in marker assisted back-cross
 CC techniques to select plants with a higher percentage of recurrent parent
 CC in a back-cross population. Segments incorporate SNPs which occur more

CC frequently than other polymorphism types and are therefore more likely to
 CC be located close to genetic loci of interest; different forms of
 CC characterised SNPs are also often easier to detect than other
 CC polymorphism types. AAV40304 to AAV40369 are used in an example from the
 CC present invention as markers and PCR primers. (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX

SQ Sequence 19 BP; 7 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3090 AGGGGGAAGGAGTCAT 3106
 |||||
 Db 2 AGGGGGAAGAGTCAT 18

RESULT 410
 AAA72748/c
 ID AAA72748 standard; DNA; 19 BP.

XX AC AAA72748;

XX DT 11-DEC-2000 (first entry)

XX DE PCR primer WB242 for bkt:npt construct fragment amplification.

XX KW Transgenic plant; potato; lepidopteran resistance; delta endotoxin;
 KW hornworm; pesticide; PCR primer; ss.

XX OS Bacillus thuringiensis.

XX PN US6100456-A.

XX PD 08-AUG-2000.

XX PF 16-MAR-1992; 92US-00851509.

XX PR 16-MAR-1992; 92US-00851509.

XX PA (UNMS) UNIV MICHIGAN STATE.

XX PI Sticklen MB, Cheng J;

XX DR WPI; 2000-542452/49.

XX PT New transgenic potato (Solanum tuberosum) plants resistant to
 PT lepidopteran insects comprise 5-10 copies of DNA encoding Bacillus
 PT thuringiensis endotoxin, for reducing synthetic pesticides in protecting
 PT potato crops.

XX PS Example 1; Col 5; 17pp; English.

XX CC A transformed potato (Solanum tuberosum) plant comprising 5-10 copies of
 CC a DNA, which encodes a Bacillus thuringiensis endotoxin integrated into
 CC the plant genome, has resistance to Lepidopteran insects. The DNA encodes
 CC the B. thuringiensis variety Kustaki (b.k.t.) HD-73 delta endotoxin
 CC (represented by sequence AAA72746). The potato plants are transformed
 CC using a vector containing the endotoxin gene fragment and neomycin
 CC phosphotransferase II (NPT II) in a translational fusion. The transgenic
 CC potato plants with higher endotoxin expression are more resistant to
 CC Lepidopteran insects e.g. hornworms, hence these transgenic plants are
 CC particularly useful in reducing the amount of synthetic pesticides used
 CC in protecting potato crops worldwide, and for producing Lepidopteran
 CC insect resistant potato varieties. The present sequence represents a PCR
 CC primer used to amplify a fragment of the HD-73 endotoxin and NPT II
 CC construct. The PCR product is used in the construction of the transgenic
 CC plant of the invention

SQ Sequence 19 BP; 6 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;

```
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2612 GTTCAACATTTTGCAA 2628
DB 19 GTTCAACATTTTGCAA 3

RESULT 411
AA85943/C
ID AAA85943 standard; DNA; 19 BP.
XX AC AAA85943;
XX DT 04-DEC-2000 (first entry)
XX DE Cdc 25 hs ribozyme binding site #51.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX DE Cdc 25 hs ribozyme binding site #51.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX DE New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 100; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker upstream amplification primer SEQ ID NO:4619.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX OS Homo sapiens.
XX PN WO954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
```

```
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX DE New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 100; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker upstream amplification primer SEQ ID NO:4619.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX OS Homo sapiens.
XX PN WO954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CAGGAGAAAAAACAAC 941
DB 19 CAGGAGAAAAAACAAC 3
```

```
RESULT 413
AAZ70263
ID AAZ70263 standard; DNA; 19 BP.
XX AC AAZ70263;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker upstream amplification primer SEQ ID NO:4619.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX OS Homo sapiens.
XX PN WO954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAAACA 940
DB 17 CCAGGAGAAAAAACA 1
```

```
RESULT 412
AA85940/C
ID AAA85940 standard; DNA; 19 BP.
XX AC AAA85940;
XX DT 04-DEC-2000 (first entry)
XX DE Cdc 25 hs ribozyme binding site #48.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
```

XX WPI; 2000-013267/01.
 DR Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome.
 PT
 PS Claim 8; Page 1216; 2745pp; English.
 XX
 CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 19 BP; 5 A; 2 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3126 GTTGTATAGGACTAAG 3142
 DB 2 GTTGTATAGGACTAAG 18
 RESULT 414
 AAZ29275
 ID AAZ29275 standard; DNA; 19 BP.
 AC AAZ29275;
 XX
 XX 28-FEB-2000 (first entry)
 DT
 DE Antisense nucleotide of sALG-2LP CDNA 3'UTR.
 XX
 KW Antisense nucleotide; sALG-2LP 3'UTR; programmed cell death; sALG-2LP;
 KW monkey apoptosis linked gene-2 like protein; apoptosis;
 KW Alzheimer's disease; Parkinson's disease; Lewy diffuse body disease;
 KW multiple sclerosis; proliferative disorder;
 KW amyotrophic lateral sclerosis; ss.
 XX
 OS Synthetic.
 XX
 XX WO9961459-A1.
 PN
 XX
 XX 02-DEC-1999.
 PD
 XX
 XX 13-MAY-1999; 99WO-US010581.
 PF
 XX
 XX 26-MAY-1998; 98US-00084749.
 PR
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX
 PI Curtis RAJ;
 XX
 DR WPI; 2000-086701/07.
 XX
 XX Genes useful for treating neurodegenerative disorders characterized by
 PT deregulated programmed cell death, such as Alzheimer's disease, multiple
 PT sclerosis and Parkinson's disease.
 XX
 XX Disclosure; Page 23; 108pp; English.
 PS
 XX

CC The present sequence is the antisense nucleotide to the 3'UTR region of
 CC monkey apoptosis linked gene-2 like protein (sALG-2LP) which modulates
 CC programmed cell death. This nucleotide when administered to a subject or
 CC generated in situ hybridises with cellular mRNA or genomic DNA encoding
 CC sALG-2LP to inhibit expression of the protein by inhibiting transcription
 CC or translation. sALG-2LP proteins are used for identifying compounds
 CC modulating the activity of a protein involved in apoptosis which may provide
 CC novel therapeutic approaches for treatment of disorders characterised by
 CC deregulated programmed cell death, e.g. Alzheimer's disease, Parkinson's
 CC and other Lewy diffuse body diseases, multiple sclerosis, amyotrophic
 CC lateral sclerosis, proliferative disorders etc
 XX
 SQ Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 158 CAACCCATCTGCGGAGA 174
 DB 3 CAACCCATCTGCGGAGA 19
 RESULT 415
 AAA71584/c
 ID AAA71584 standard; DNA; 19 BP.
 AC AAA71584;
 XX
 XX 11-DEC-2000 (first entry)
 DT
 DE Human MPROT13 forward PCR primer.
 XX
 KW MPROT13; human; metalloprotease; gene therapy; respiratory disease;
 KW arthritis; thrombosis; diabetes; cancer; inflammatory disorder;
 KW osteoporosis; cardiovascular disorder; neurodegenerative disease;
 KW central nervous system disorder; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200044913-A1.
 PN
 XX
 XX 03-AUG-2000.
 PD
 XX
 XX 17-JAN-2000; 2000WO-EP000344.
 PF
 XX
 XX 28-JAN-1999; 99GB-00001947.
 PR
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Southan CD, Palmer L, Zhu Y, Li X;
 XX
 XX WPI; 2000-505980/45.
 DR
 XX
 XX New metalloprotease (MPROT)13 polypeptides and polynucleotides, used to
 PT treat arthritis, diabetes, respiratory disorders, cancer, inflammation,
 PT and neurodegenerative disorders.
 XX
 XX Example; Page 22; 34pp; English.
 PS
 XX
 CC This invention describes a novel human metalloprotease (MPROT)13
 CC polypeptide (I), which can be used for gene therapy. (I) and
 CC polynucleotides encoding it can be used to treat arthritis, respiratory
 CC disease, thrombosis, diabetes, cancer, inflammatory disorders,
 CC osteoporosis, cardiovascular disorders, neurodegenerative diseases, and
 CC central nervous system disorders. Modulators of (I) can be used to treat
 CC conditions associated with MPROT13 imbalance. (I) can also be used in
 CC diagnostic assays to detect diseases associated with inappropriate
 CC MPROT13 activity, or levels. The polynucleotides can be used as
 CC hybridization probes for cDNA and genomic DNA and as primers for
 CC polymerase chain reaction, to isolate full length cDNAs and genomic
 CC clones of other genes which have high similarity to the polynucleotide

CC sequence encoding (I). This sequence represents a PCR primer used in the
CC amplification of the human MPROT13 protein described in the method of the
CC invention
XX
SQ Sequence 19 BP; 2 A; 2 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1748 AACATCTCCACCAGC 1764
Db 18 AACATCTCCAGCCAGC 2
RESULT 416
AAC89901
ID AAC89901 standard; DNA; 19 BP.
XX AC AAC89901;
XX 08-MAR-2001 (first entry)
XX
DE Oligonucleotide #2 used in a nucleic acid hybridisation assay.
XX
KW Fluorescence polarisation assay; polyion; binding assay;
KW enzyme activity assay; ss.
XX
OS Synthetic.
XX
PN WO200072016-A1.
PD
PP 30-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US013293.
XX
PR 21-MAY-1999; 99US-00316447.
PR 16-JUN-1999; 99US-0139562P.
PR 28-SEP-1999; 99US-0156366P.
XX
PA (CALI-) CALIPER TECHNOLOGIES CORP.
XX
PI Nikiforov TT;
XX
DR WPI; 2001-061370/07.
XX
PT Fluorescence polarization assays using polyions for detecting
PT phosphorylation of a phosphorylatable compound, and for identifying the
PT presence of a subsequence of nucleotides in a target sequence.
XX
PS Example 6; Page 38; 82pp; English.
XX
CC The present invention relates to a fluorescence polarisation assay
CC involving polyions. The assay of the present invention is useful for
CC identifying the presence of a subsequence of nucleotides in a target
CC nucleic acid sequence. In addition, the assay is useful in carrying out a
CC variety of binding assays and in assaying for enzymatic activity. The
CC present sequence is an oligonucleotide used in a nucleic acid
CC hybridisation assay, using the fluorescence polarisation detection assay
CC of the present invention
XX
SQ Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2123 CGCTTGGATGCTGCT 2139
Db 1 CGCTTGGATGCTGCT 17
RESULT 417

AAC61102/c
ID AAC61102 standard; DNA; 19 BP.
XX
AC AAC61102;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdc25 hs ribozyme binding site SEQ ID NO:3526.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PP 03-MAY-2001.
PD
PP 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 328; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seboreic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAC61102/c represents sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 1 A; 3 C; 4 G; 11 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 925 CAGGAGAAAAAAC 941
Db 19 CAGGAGAAAAAACAAAC 3

XX	Result 418
XX	AH61105/c
XX	ID AH61105 standard; DNA; 19 BP.
XX	AAH61105;
XX	10-SEP-2001 (first entry)
XX	Cdc25 hs ribozyme binding site SEQ ID NO:3529.
XX	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulneryar; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reducease; scarring; cytostatic; antiposiatric; dermatological; antisborrheic; antivirucide; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrhic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
XX	Homo sapiens.
OS	Synthetic.
OS	W0200130362-A2.
PB	03-MAY-2001.
PD	26-OCT-2000; 2000WO-US029500.
PF	26-OCT-1999; 99US-0161532P.
PR	(IMMU-) IMMUSOL INC.
PA	Robbins JW, Tritz R;
PI	WPI; 2001-300427/31.
PP	Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
PS	Example 1; Page 328; 408pp; English.
CC	The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatological, cytotstatic, antisborrheic, antidiabetic, antisickling, ophthalmological, vulneryar, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrhic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAH57577 to AAH62099 represent sequences used in the exemplification of the present invention
XX	Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
QQ	Query Match 0.4%; Score 15.4; DB 1; Length 19; Best Local Similarity 94.1%; Pred No. 2.5e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	924 CCAGGAGAAAAA 940

XX JP2001286300-A.
 PN 16-OCT-2001.
 PD
 PP 20-APR-2000; 2000JP-00120097.
 XX 20-APR-1999; 99JP-00111601.
 PR 24-AUG-1999; 99JP-00236666.
 PR 30-AUG-1999; 99JP-00242693.
 PR 01-FEB-2000; 2000JP-00028896.
 XX (BIOI-) BIOINDUSTRY KYOKAI SH.
 PA (KANK-) KANKYO ENG KK.
 PA (KEIZ-) KEIZAI SANGYOSHOU SANGYO GIJUTSU SOGO KEN.
 XX WPI; 2002-134193/18.
 DR
 XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
 PT the obtained data.
 PT
 PS Example 5; Page 17; 34pp; Japanese.
 XX
 CC This invention relates to a method for measuring nucleic acids using a
 CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
 CC decreases the fluorescence of the fluorochrome when hybridised with a
 CC target nucleic acid, the decrease in the fluorescence is measured. The
 CC method can be used for measuring a target nucleic acid
 XX
 SQ Sequence 19 BP; 15 A; 0 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1152 TTTCTTTTATATATA 1168
 Db 17 TTTTATATATATA 1
 RESULT 421
 ACA62440
 ID ACA62440 standard; DNA; 19 BP.
 AC ACA62440;
 XX
 DT 14-AUG-2003 (first entry)
 XX
 DE HCV core protein frameshift region DNA #2.
 XX
 KW HCV; hepatitis C infection; RNA frameshift; core protein; p17; virucide;
 KW hepatotropic; overlapping open reading frame; p21c; vaccine; ds.
 XX
 OS Hepatitis C virus.
 XX
 PN US2002076415-A1.
 XX
 PD 20-JUN-2002.
 XX
 PP 14-DEC-2000; 2000US-00736959.
 XX
 PR 14-DEC-1999; 99US-0170835P.
 XX
 PA (OUJ/) OU J.
 PA (XUZ/) XU Z.
 XX
 PI Ou J, Xu Z;
 XX
 DR WPI; 2003-479366/45.
 XX
 PT Isolated hepatitis C virus (HCV) proteins formed by expression of
 PT overlapping open reading frames in the core protein gene sequence through
 PT a frame shifting mechanism, useful for vaccinating against, and detecting

PT HCV infections.
 XX
 PS Example 5; Fig 6B; 37pp; English.
 XX
 CC The invention relates to an isolated and purified protein of the
 CC hepatitis C virus (HCV) that is formed by expression of an overlapping
 CC open reading frame in the core protein gene sequence through an RNA frame
 CC shifting mechanism. The protein is termed p17 (the full length, unshifted
 CC protein being p21c). Also included are a vaccine (including a DNA
 CC vaccine) for immunising a mammal against hepatitis C (producing a
 CC protective antibody) comprising at least 1 protein of p17 (or a nucleic
 CC acid encoding p17), an anti-viral composition (used to treat hepatitis C)
 CC comprising a compound that binds to p17, antibodies directed against an
 CC HCV core protein which are elicited by immunising an animal using the
 CC partially purified protein p17, a method for analysing an HCV antigen in
 CC a sample using the anti-p17 antibodies and detection of anti-HCV
 CC antibodies in a sample using the p17 proteins. The HCV p17 and the DNA
 CC sequences that encode it may be used as vaccines for immunising patients
 CC against HCV infection. The antibodies and the antiviral compound may also
 CC be used for treating HCV infections. HCV p17 and the antibodies may also
 CC be used in immunoassays for detecting HCV antigens and/or antibodies in
 CC samples for the diagnosis of HCV infections. The present sequence
 CC represents part of the an HCV core protein DNA from the frameshift region
 XX
 SQ Sequence 19 BP; 15 A; 2 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 931 AAAAAAAAAACAAACCT 947
 Db 1 AAAAAAAAAACAAACCT 17
 RESULT 422
 ADS90818
 ID ADS90818 standard; DNA; 19 BP.
 XX
 AC ADS90818;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Oligonucleotide of the invention SEQ ID NO:1834.
 KW ss; cell proliferative disorder; breast; methylation; cytostatic;
 KW gene therapy; single nucleotide polymorphism; SNP.
 XX
 OS Unidentified.
 XX
 PN WO2004035803-A2.
 PD 29-APR-2004.
 XX
 PP 01-OCT-2003; 2003WO-EP010881.
 XX
 PR 01-OCT-2002; 2002DE-01045779.
 PR 07-JAN-2003; 2003DE-01000096.
 PR 17-APR-2003; 2003DE-01017955.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
 PI Nimrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
 XX
 DR WPI; 2004-348468/32.
 XX
 PT Predicting responsiveness of a subject with breast cell proliferative
 PT disorder, useful for treating or differentiating breast cell
 PT proliferative disorders comprises analyzing methylation pattern of a
 PT genomic DNA from the subject.
 XX
 PS Disclosure; SEQ ID NO 1834; 104pp; English.

XX The invention relates to a novel method for predicting the responsiveness
 CC of a subject with a cell proliferative disorder of the breast tissues to
 CC a therapy comprising analysing the methylation pattern of a target
 CC nucleic acid by contacting at least one of the target nucleic acids in a
 CC biological sample obtained from the subject prior to or during treatment.
 CC The method of the invention has cytostatic activity, and may have a use
 CC in gene therapy. The set of oligonucleotides comprising at least two of
 CC the oligomers are useful for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
 CC methods, nucleic acid, oligonucleotide, and kit are useful for the
 CC treatment, characterisation, classification and/or differentiation, of
 CC breast cell proliferative disorders. The method is also useful for
 CC predicting the responsiveness of a subject with a cell proliferative
 CC disorder of the breast tissues to a therapy. The present sequence is used
 CC in the exemplification of the invention.

XX SQ Sequence 19 BP; 3 A; 0 C; 5 G; 11 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2959 GTTATTTATTGTCGTGTT 2975
 Db 1 GGTATTTATTGTCGTGTT 17
 |||||

RESULT 423
 ADS75429/c
 ID ADS75429 standard; DNA; 19 BP.
 XX
 AC ADS75429;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 XX TAK-1 gene PCR primer K-TRA13.
 XX
 DE ss; primer; antiinflammatory; antiasthmatic; respiratory;
 KW central nervous system; antiallergic; antiarthritic; antirheumatic;
 KW antiulcer; gastrointestinal.
 XX
 XX Homo sapiens.
 OS
 XX WO2004083854-A1.
 PN
 XX 30-SEP-2004.
 PD
 XX 16-MAR-2004; 2004WO-EP002712.
 PF
 XX 17-MAR-2003; 2003GB-00006071.
 PR
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 XX
 XX Dubois G;
 PI
 XX WPI; 2004-728516/71.
 DR
 XX
 XX Identifying substance which modulates activity of transforming growth
 PT factor beta-activated kinase 1 (TAK1) useful for treating inflammatory
 PT diseases, involves combining candidate substance with kinase and
 PT measuring activity of kinase.
 XX
 PS Example 1; Page 11; 17pp; English.
 XX
 CC The invention relates to a method of identifying (M1) a substance
 CC suitable for use in the treatment of an inflammatory disease which
 CC modulates the activity of transforming growth factor beta-activated
 CC kinase 1 (TAK1), by combining a candidate substance with the kinase and
 CC measuring the effect of the candidate substance on the activity of the
 CC kinase. (M1) is useful for identifying a substance suitable for use in
 CC the treatment of an inflammatory disease which modulates the activity of

CC TAK1. (II), (III) or (IV) is useful in preparation of a pharmaceutical
 CC that inhibits the accumulation of leukocytes in a human tissue or in
 CC preparation of pharmaceutical for the treatment of an inflammatory
 CC disease. The inflammatory disease is a respiratory disease which is
 CC asthma, chronic obstructive pulmonary disease, cystic fibrosis,
 CC adult/acute respiratory distress syndrome or allergic rhinitis. The
 CC respiratory disease is chronic obstructive pulmonary disease (COPD) (all
 CC claimed). The substance identified by (M1) is useful for treating
 CC inflammatory disease such as neutrophil associated inflammatory or
 CC obstructive airways diseases including COPD, chronic bronchitis and
 CC emphysema, cystic fibrosis and adult (or acute) respiratory distress
 CC syndrome (ARDS), rheumatoid arthritis and inflammatory bowel diseases
 CC such as Crohn's disease and ulcerative colitis. The substance identified
 CC by (M1) is useful for treating eosinophil-associated inflammatory or
 CC obstructive airways diseases such as asthma and allergic rhinitis. This
 CC sequence corresponds to a PCR primer to amplify the TAK1 gene from a
 CC retroviral insert following selection based on a reduction of ICAM-1
 CC expression in A549.tTA.G3 cells.

XX SQ Sequence 19 BP; 6 A; 3 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2927 CCTCCCGTCCCTTCCT 2943
 Db 19 CCTCCCGTCCCTTCCT 3
 |||||

RESULT 424
 AAF87713
 ID AAF87713 standard; DNA; 20 BP.
 XX
 AC AAF87713;
 XX
 DT 06-JUL-2001 (first entry)
 XX
 DE Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.
 XX
 KW Human; glutathione S-transferase pi; GSTP1; CpG island; diagnosis;
 KW hepatic cell proliferative disorder; liver cancer; anticancer;
 KW tumorigenesis; detection; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200126536-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 12-OCT-2000; 2000WO-US028427.
 XX
 PR 13-OCT-1999; 99US-0159168P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Nelson WG, Lin X, Tchou JC, Bakker J;
 XX
 XX WPI; 2001-290647/30.
 DR
 XX Detecting hepatic cell proliferative disorder useful for detecting
 PT hepatocellular carcinoma comprises detecting a methylated CpG-containing
 PT glutathione-S-transferase nucleic acid.
 XX
 PS Claim 83; Page 42; 64pp; English.
 XX
 CC The present invention describes a method for detecting hepatic cell
 CC proliferative disorders. The method comprises detecting a methylated CpG-
 CC containing glutathione-S-transferase (GST) nucleic acid (I) in a hepatic
 CC specimen or a biological fluid, where a methylated GST nucleic acid is
 CC indicative of a hepatic cell proliferative disorder. The method can be
 CC used to diagnose hepatocellular carcinoma, and to monitor progress of its
 CC treatment. Increasing the level of GST is useful in the treatment of

CC liver cancer, in humans or animals. The method can detect the early
 CC stages of tumorigenesis in liver cells simply. The present sequence
 CC represents a PCR primer which is used in the amplification of the human
 CC glutathione S-transferase pi gene (GSTP1) promoter in an example from the
 CC present invention for mapping somatic GSTP1 CpG island DNA
 CC hypermethylation changes by genomic sequencing after bisulfite treatment
 XX
 SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTAAAG 2758
 |||||
 Db 4 ATTTTAAAG 20

RESULT 425
 AAV48999/C
 ID AAV48999 standard; DNA; 15 BP.
 XX
 AC AAV48999;
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-N-32.
 XX
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN EP856579-A1.
 XX
 PD 05-AUG-1998.
 XX
 PF 31-JAN-1997; 97EP-00101531.
 XX
 PR 31-JAN-1997; 97EP-00101531.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Brysch W;
 XX
 DR WPI; 1998-400910/35.

XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 PS Example 6; Fig 8b; 286pp; English.
 XX
 CC AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, Erb-2, junB, jund, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function

CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 15 BP; 6 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1919 TAATAATTCATCAT 1933
 |||||
 Db 15 TAATAATTCATCAT 1

RESULT 426
 AAV48950/C
 ID AAV48950 standard; DNA; 15 BP.
 XX
 AC AAV48950;
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-21.
 XX
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN EP856579-A1.
 XX
 PD 05-AUG-1998.
 XX
 PF 31-JAN-1997; 97EP-00101531.
 XX
 PR 31-JAN-1997; 97EP-00101531.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Brysch W;
 XX
 DR WPI; 1998-400910/35.

XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 PS Claim 10; Fig 8a; 286pp; English.
 XX
 CC AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, Erb-2, junB, jund, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function

CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 15 BP; 6 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1919 TAATAATTCATCAT 1933
 |||||
 Db 15 TAATAATTCATCAT 1

RESULT 426
 AAV48950/C
 ID AAV48950 standard; DNA; 15 BP.
 XX
 AC AAV48950;
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-21.
 XX
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN EP856579-A1.
 XX
 PD 05-AUG-1998.
 XX
 PF 31-JAN-1997; 97EP-00101531.
 XX
 PR 31-JAN-1997; 97EP-00101531.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen K, Brysch W;
 XX
 DR WPI; 1998-400910/35.

XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 PS Claim 10; Fig 8a; 286pp; English.
 XX
 CC AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, Erb-2, junB, jund, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function

XX SQ Sequence 15 BP; 4 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1968 GCAGGTATTGATGAC 1982
 Db 15 GCAGGTATTGATGAC 1

RESULT 427
 AAV48951/c
 ID AAV48951 standard; DNA; 15 BP.
 XX AC AAV48951;
 XX DT 15-OCT-1998 (first entry)
 XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-22.
 XX KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 XX KW modulate; gene expression; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN EP856579-A1.
 XX PD 05-AUG-1998.
 XX PF 31-JAN-1997; 97EP-00101531.
 XX PR 31-JAN-1997; 97EP-00101531.
 XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX PI Schlingensiepen K, Brysch W;
 XX DR WPI; 1998-400910/35.
 XX PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
 consecutive guanosine or inosine - and have specific ratio of residues
 able to form two or three hydrogen bonds, have greater activity and
 reduced toxicity, used therapeutically or to modulate growth of cells in
 culture.
 XX PS Claim 10; Fig 8a; 286pp; English.

XX CC AAV48930-49007 represent antisense oligonucleotides directed against
 transforming growth factor-beta2 (TGF-beta2). Of these, only
 oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 little effect. The oligonucleotides exemplify the invention. The
 specification describes oligonucleotides that contain 8-30 nucleotides,
 which contain at most 8 nucleotides that can each form three hydrogen
 bonds to cytosine; do not contain four consecutive nucleotides able to
 form three H-bonds each to four consecutive cytosines; do not contain two
 sequences of three consecutive nucleotides each able to form three H-
 bonds to three consecutive cytosines, and the ratio between residues able
 to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 = 0.33-0.72. The oligonucleotides are used to modulate expression of
 genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or
 beta 2 to control proliferation of primary cell cultures (e.g. bone
 marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 keratinocytes). The oligonucleotides can also be used to analyse function
 of proteins (by altering their expression or activity) and
 therapeutically, e.g. in cases of cancer or (targeting TGF) for
 stimulating the immune system

XX SQ Sequence 15 BP; 4 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1971 GGTATTGATGGCACC 1985
 Db 15 GGTATTGATGGCACC 1

RESULT 428
 AAF53238/c
 ID AAF53238 standard; DNA; 15 BP.
 XX AC AAF53238;
 XX DT 30-MAR-2001 (first entry)
 XX DE TGF-I oligonucleotide #4198.
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pteryiasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wraight CJ, Werther GA, Edmondson SR;
 XX DR WPI; 2001-041421/05.
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 inhibits or reduces growth factor mediated cell proliferation and/or
 inflammation.

XX PS Example 8; Page 88; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of
 skin disorders. The method comprises contacting the skin with an
 antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 inhibiting or reducing growth factor mediated cell proliferation,
 inflammation and/or other disorders. The present sequence is an
 oligonucleotide which can be used to design the antisense
 oligonucleotides of the present invention (see AAF45151 and AAF45153-
 F45161). The method is useful for ameliorating the effects of psoriasis,
 ichthyosis, pteryiasis, ruba, pilaris, serborrhea, keloids, keratosis,
 neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 hyperneovascular condition such as a neovascular condition of the retina,
 brain or skin, growth factor-mediated malignancies, other sclerotic
 disease, kidney disease, hyperproliferation of the inside of blood
 vessels or any other hyperplasia

XX SQ Sequence 15 BP; 1 A; 1 C; 12 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 972 TCCCCCCCCACCCCG 986
Db 15 TCCCCCCCCACCCCG 1

RESULT 429
AAF45320/c
ID AAF45320 standard; DNA; 15 BP.
XX
XX AAF45320;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP2 oligonucleotide #159.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 6; Page 35; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 8 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 GCGAGCAGCGCGGC 439
Db 15 GCGAGCAGCGCGGC 1

RESULT 431
AAF60455/c
ID AAF60455 standard; DNA; 15 BP.

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XX AC AAF60455;
XX DT 27-APR-2001 (first entry)
XX DE Oligonucleotide clamp #10.
XX KW Oligonucleotide clamp; ds.
XX OS Unidentified.
XX PN US6180777-B1.
XX PD 30-JAN-2001.
XX PF 03-JAN-1997; 97US-00787321.
XX PR 12-JAN-1996; 96US-0009918P.
XX PA (FARB ) BAYER CORP.
XX PI Horn T;
XX DR WPI; 2001-201911/20.
XX PT Synthesizing branched nucleic acids useful as diagnostic and molecular
XX PT probes, involves combining first units having haloalkylamino groups and
XX PT second units having thiol or phosphorothioate groups.
XX PS Example 5; Col 17-18; 20pp; English.
XX CC The present invention relates to a method for synthesising a branched or
XX CC multiply connected macromolecular structure, comprising oligonucleotide
XX CC clamps (OC). The macromolecular structure is capable of specifically
XX CC binding to a target molecule, and can therefore be used as probes. At
XX CC least one OC comprises a target binding sequence that binds specifically
XX CC and stably with the target molecule, and at least two OCs comprise signal
XX CC generation moieties capable of generating a detectable signal in the
XX CC presence of the target molecule. In addition the OCs are connected to one
XX CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
XX CC present sequence is an OC used in the present invention
XX SQ Sequence 15 BP; 1 A; 2 C; 0 G; 12 T; 0 U; 0 Other;
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAAATAAAA 2814
DB 15 GTGAAAAAATAAAA 1

RESULT 432
ABK96652/c
ID ABK96652 standard; DNA; 15 BP.
XX AC ABK96652;
XX DT 24-SEP-2002 (first entry)
XX DE Interleukin-3 (IL-3) allele specific oligonucleotide primer #3.
XX KW Interleukin 3; colony-stimulating factor; IL3; transgenic animal;
XX KW IL3 isogene; central nervous system disorder; multiple sclerosis;
XX KW Alzheimer's disease; Parkinson's disease; CNS injury; immune disorder;
XX KW inflammatory disorder; allele specific oligonucleotide; A50; PCR; primer;
XX ss.
XX OS Homo sapiens.
XX PN WO200244410-A1.
XX PT

PD 06-JUN-2002.
XX PF 28-NOV-2000; 2000WO-US032381.
XX PR 28-NOV-2000; 2000WO-US032381.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Chew A, Denton RR, Nandabalan K, Stephens JC;
XX DR WPI; 2002-519590/55.
XX PT Novel isolated polynucleotide comprising a sequence which is a
XX PT polymorphic variant for a reference sequence for interleukin 3 gene
XX PT useful for studying the expression and biological function of the
XX PT protein.
XX PS Claim 11; Page 16; 62pp; English.
XX CC The invention describes an isolated polynucleotide (I) comprising a
XX CC sequence which is a polymorphic variant for a reference sequence for
XX CC interleukin 3 (colony-stimulating factor) (IL3) gene or its fragment. (I)
XX CC is useful for studying the expression and biological function of IL3, as
XX CC well as in developing drugs targeting the IL3 protein. A transgenic
XX CC animal is useful for studying expression of IL3 isogenes in vivo, for in
XX CC vivo screening and testing of therapeutic agents and compounds for diseases of
XX CC testing the efficacy of therapeutic agents and compounds for diseases of
XX CC the central nervous system e.g. multiple sclerosis, Alzheimer's disease,
XX CC Parkinson's disease and CNS injury, and immune or inflammatory disorders.
XX CC The method described in the invention is useful in developing diagnostic
XX CC tests and therapeutic treatments for diseases of the central nervous
XX CC system and immune or inflammatory disorders. This sequence represents an
XX CC allele specific oligonucleotide primer for detecting polymorphisms in the
XX CC IL-3 gene
XX SQ Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 CTGAGAGCTGAGCTC 101
DB 15 CTGAGAGCTGAGCTC 1

RESULT 433
AAK18370/c
ID AAK18370 standard; DNA; 17 BP.
XX AC AAK18370;
XX DT 11-MAY-1999 (first entry)
XX DE RT-PCR primer of the invention SEQ ID 11.
XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX OS Synthetic.
XX PN JPI1032765-A.
XX PD 09-FEB-1999.
XX PF 18-JUL-1997; 97JP-00208312.
XX PR 18-JUL-1997; 97JP-00208312.
XX PA (TAKI ) TAKARA SHUZO CO LTD.
XX DR WPI; 1999-183822/16.
XX PT Peptides having at least two new nucleotides - useful as primers in RT-

```


PT PCR.
 PS Disclosure; Page 11; 19pp; Japanese.
 XX
 CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2574 TTAATAAAAAAAAAA 2588
 DB 17 TTAATAAAAAAAAAA 3
 RESULT 434
 ABT35106/c
 ID ABT35106 standard; DNA; 17 BP.
 XX
 AC ABT35106;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 743.
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX
 OS Homo sapiens.
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004208.
 XX
 PR 17-SEP-2001; 2001PR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Anson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 120; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3922 CTGTGTGAACACAGA 3936
 DB 17 CTGTGTGAACACAGA 3
 RESULT 435
 ADL49409/c
 ID ADL49409 standard; RNA; 17 BP.
 XX
 AC ADL49409;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #523.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
 XX
 XX WPI; 2003-058513/05.
 DR
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 2942; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor

CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC I-kappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.

XX
 SQ Sequence 17 BP; 2 A; 1 C; 0 G; 0 T; 14 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAA 2588
 |||||
 Db 17 TTAATAAAAAAATAAAAA 3

RESULT 436

ADP86176
 ID ADP86176 standard; DNA; 17 BP.

XX

AC ADP86176;

XX

DT 09-SEP-2004 (first entry)

XX

DE CpG immunostimulatory oligonucleotide #47.

XX

KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
 KW viral infection; bacterial infection; cancer; lymphoma;
 KW intraepithelial neoplasia; melanoma; neuroblastoma; Hodgkin's lymphoma;
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

XX modified_base 1..17

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

XX

PN WO2004053104-A2.

XX

PD 24-JUN-2004.

XX

PF 11-DEC-2003; 2003WO-US039775.

XX

PR 11-DEC-2002; 2002US-0432409P.

XX

PR 25-SEP-2003; 2003US-0506108P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PA (COLE-) COLEY PHARM GMBH.

XX

PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;

XX

DR WPI; 2004-487902/46.

XX

PT New oligonucleotides, useful for treating allergy or asthma, viral and

XX

PT bacterial infections, and cancer, e.g. biliary tract cancer, breast

XX

PT cancer, cervical cancer.

XX

PS Example; SEQ ID NO 47; 104pp; English.

XX

XX The invention relates to a class of CpG immunostimulatory

CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that

CC are useful for stimulating an immune response. Oligonucleotides and
 CC compositions of the invention are useful for treating allergy or asthma,
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasias,
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
 CC testicular cancer, as well as other carcinomas and sarcomas. The
 CC invention is also useful in gene therapy. The present sequence is a CpG
 CC immunostimulatory oligonucleotide.

XX
 SQ Sequence 17 BP; 11 A; 1 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2572 GTTTAAAAAATAAAAA 2586
 |||||
 Db 3 GTTTAAAAAATAAAAA 17

RESULT 437

AAT41540

ID AAT41540 standard; DNA; 18 BP.

XX

AC AAT41540;

XX

DT 24-JUN-1997 (first entry)

XX

DE Human apolipoprotein-J gene exon 8-specific 5' PCR primer.

XX

KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;
 KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;
 KW diagnosis; ss.

XX

OS Synthetic.

XX

PN WO9632502-A1.

XX

PD 17-OCT-1996.

XX

PF 02-APR-1996; 96WO-US004510.

XX

PR 11-APR-1995; 95US-00420291.

XX

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Mayeux R, Tycko B;

XX

DR WPI; 1996-477152/47.

XX

PT New oligonucleotide specific for apolipoprotein-J polymorphisms - used
 PT to identify patients susceptible to Alzheimer's disease or prostate
 PT cancer.

XX

PS Example 1; Page 20; 62pp; English.

XX

AAT41527-T41541 are exon-specific PCR primers used for the amplification
 CC of exons 2-8 of the human apolipoprotein-J (ApoJ) gene. The primers were
 CC used in a method for detecting polymorphisms associated with an allelic
 CC variation in the ApoJ gene. The oligonucleotide (OG) detects the
 CC probability of a person developing Alzheimer's disease (AD), preferably
 CC in patients of African or Hispanic descent. The OG also detects the
 CC probability of a person developing a cognitive disorder, or a prostatic
 CC carcinoma. Transgenic mammals expressing an allelic variant of an ApoJ
 CC gene may be used as a prognostic and diagnostic means for studying AD,
 CC and to determine the effectiveness of therapeutic drugs

XX

SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

```

Query Match      0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3845 CCACAGTGTTCAGC 3859
DB 1 CCACAGTGTTCAGC 15

RESULT 438
AAV54164/c
ID AAV54164 standard; cDNA; 18 BP.
XX AC
XX AAV54164;
DT 21-DEC-1998 (first entry)
XX DE
XX Nucleotide sequence PCR primer 1.
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX OS
XX Synthetic.
XX WO9839437-A1.
PN 11-SEP-1998.
XX PD
XX 05-MAR-1998; 98WO-JP000905.
XX PF
XX 05-MAR-1997; 97JP-00050302.
XX PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA
XX Sakaki Y;
XX PI
XX WPI; 1998-495844/42.
XX DR
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX PS
XX Example 1; Page 47; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX SQ
Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match      0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2588
DB 18 TTAATAAAAAAAAAA 4

RESULT 439
AAV18372/c
ID AAV18372 standard; DNA; 18 BP.
XX AC
XX AAV18372;
DT 11-MAY-1999 (first entry)
XX DE
XX RT-PCR primer of the invention SEQ ID 13.
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
```

```

XX OS
XX Synthetic.
XX JP11032765-A.
XX PN
XX 09-FEB-1999.
XX PD
XX 18-JUL-1997; 97JP-00208312.
XX PF
XX 18-JUL-1997; 97JP-00208312.
XX PR
XX (TAKI ) TAKARA SHUZO CO LTD.
XX PA
XX WPI; 1999-183822/16.
XX DR
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX PS
XX Disclosure; Page 11; 19pp; Japanese.
XX This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX SQ
Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match      0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2588
DB 18 TTAATAAAAAAAAAA 4

RESULT 440
AAZ90646/c
ID AAZ90646 standard; DNA; 18 BP.
XX AC
XX AAZ90646;
XX DT
XX 13-JUN-2000 (first entry)
XX DE
XX Human adipose tissue gene amplifying primer #7.
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS
XX Homo sapiens.
XX JP2000037190-A.
XX PN
XX 08-FEB-2000.
XX PD
XX 23-JUL-1998; 98JP-00225228.
XX PF
XX 23-JUL-1998; 98JP-00225228.
XX PR
XX (NISB ) JAPAN TOBACCO INC.
XX PA
XX WPI; 2000-306578/27.
XX DR
XX A physiologically active protein specifically derived from mammal tissue.
XX PT
XX
```

PS Example 2; Page 18; 50pp; Japanese.
 XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAI67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2574 TTTAAAAA 2588
 DB 18 TTTAAAAA 4
 RESULT 441
 ADL95317
 ID ADL95317 standard; DNA; 18 BP.
 XX
 AC ADL95317;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Anti-proliferative oligonucleotide #8.
 XX
 KW ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;
 CC cancer; malignant tumour.
 KW
 KW
 KW
 XX
 OS Synthetic.
 XX
 FH Key modified_base 8 Location/Qualifiers
 FT FT /*tag= a
 FT FT /mod_base= OTHER
 FT FT /note= "Optionally 32-P labelled"
 XX
 PN US2004067197-A1.
 XX
 PD 08-APR-2004.
 XX
 PF 02-FEB-2001; 2001US-00775479.
 XX
 PR 26-NOV-1997; 97WO-CA000892.
 PR 24-MAY-1999; 99US-00318106.
 XX
 PA (LECL/) LECLERC G.
 PA (MART/) MARTEL R.
 XX
 PI Leclerc G, Martel R;
 XX
 WPI; 2004-314974/29.
 XX
 XX New anti-proliferative substance comprising a radiolabelled DNA carrier,
 PT useful for preventing or treating uncontrolled cellular proliferation
 PT e.g. restenosis, cancer or malignant tumors.
 PT
 PS Claim 13; SEQ ID NO 8; 28pp; English.
 XX
 XX The invention relates to an anti-proliferative substance for preventing
 CC uncontrolled cellular proliferation comprising a radiolabelled DNA
 CC carrier, where a radioisotope is located internally within the DNA
 CC sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier
 CC penetrates the cell membrane and is retained intracellularly for a time
 CC sufficient for the radio-isotope to effect a dose therapy. The carrier in
 CC the anti-proliferative substance is an oligonucleotide, which is linear
 CC or a plasmid, which is circular. The plasmid is of viral or bacterial
 CC origin. The oligonucleotide is a double- or a single-stranded DNA

CC functional allele profiles of various genes. The primers are specific for
CC genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene
XX
SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAA 2588
Db 15 TTAAAAAATAAAAAA 1

RESULT 443
ADA45244/c
ID ADA45244 standard; DNA; 20 BP.

XX AC ADA45244;

XX DT 20-NOV-2003 (first entry)

XX DE Human MSH2 gene PCR primer #3.

XX KW Functional allele profile; genetic inheritance; haplotype; population;
KW disease; pharmacogenetic application; selective pressure; human; MSH2;
KW MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.

XX OS Homo sapiens.

XX PN US2003096236-A1.

XX PD 22-MAY-2003.

XX PF 08-AUG-2001; 2001US-00923327.

XX PR 12-FEB-1996; 96US-00598591.

XX PR 12-FEB-1997; 97US-00798691.

XX PR 04-AUG-1997; 97US-00905772.

XX PR 22-MAY-1998; 98US-00084471.

XX PR 04-AUG-1998; 98US-00129134.

XX PR 14-MAR-2000; 2000US-00524794.

XX PA (ONCO-) ONCORMED INC.

XX PI Murphy PD;

XX WPI; 2003-576875/54.

XX Determining a functional allele profile of a gene in a population by
PT identifying the nucleotide sequence of a gene of genomic DNA from each of
PT the individuals with a family history of functional alleles of the gene
PT of interest.

XX Example 1; Page 9; 28pp; English.

XX The present invention relates to a method for determining a functional
XX allele profile of a gene in a population. The method comprises
XX identifying the nucleotide sequence of a gene of interest out of genomic
XX DNA from each of a population of individuals identified as having a
XX family history which indicates inheritance of functional alleles of the
XX gene of interest, and rank ordering the frequency of occurrence of each
XX haplotype, where the identity of the alleles containing each haplotype
XX and the determination of their relative frequencies constitutes the
XX functional allele profile of the gene of interest in the population. The
XX method is useful for determining functional allele profiles which are
XX useful in the treatment and diagnosis of diseases, for genetic and
XX pharmacogenetic applications, and for evaluating the degree to which the
XX gene(s) are under selective pressure. The present sequence represents a
XX PCR primer used in the method of the invention.

XX Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAA 2588
Db 15 TTAAAAAATAAAAAA 1

RESULT 444
ADQ14575/c
ID ADQ14575 standard; RNA; 23 BP.

XX AC ADQ14575;

XX DT 23-SEP-2004 (first entry)

XX DE TGF beta 2 3'-UTR consensus sequence.

XX KW metabolic state; mRNA protein complex; mRNA complex; RNA binding protein;
KW mRNA complex-associated protein; mRNA complex-associated protein;
KW mRNA target; protein target; physiological pathway;
KW TGF beta 2 3'-UTR consensus sequence; ss.

XX OS Synthetic.

XX PN WO2004057032-A1.

XX PD 08-JUL-2004.

XX PF 04-DEC-2003; 2003WO-US038475.

XX PR 04-DEC-2002; 2002US-00309788.

XX PA (RIBO-) RIBONOMICS INC.

XX PI Keene JD, Tenenbaum SA, Carson CC, Phelps WC;

XX WPI; 2004-525445/50.

XX Assessing the metabolic state of a cell comprises isolating at least one
PT mRNA complex comprising at least one RNA binding protein, and at least
PT one mRNA or at least one mRNA complex-associated protein.

XX Example 4; Page 35; 86pp; English.

XX The present invention describes a method for assessing the metabolic
XX state of a cell. The method comprises isolating at least one mRNA complex
XX having at least one RNA binding protein, and at least one mRNA or at
XX least one mRNA complex-associated protein, and determining the expression
XX level of the mRNA or mRNA complex-associated protein, where the level of
XX expression of the at least one mRNA or the at least one mRNA complex-
XX associated protein is indicative of the metabolic state of the cell. The
XX method can be used for assessing the metabolic state in a cell, and for
XX identifying and evaluating mRNA and protein targets associated with mRNA
XX complexes and implicated in the expression of proteins involved in common
XX physiological pathways. The present sequence represents a TGF beta 2 3'-
XX UTR consensus sequence, which is used in an example from the present
XX invention.

XX Sequence 23 BP; 2 A; 1 C; 2 G; 1 T; 16 U; 1 Other;

Query Match 0.4%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2577 AAAAAAATAATTCGAGAAAA 2599
Db 23 AAAAAAACCAATTAAGAAAA 1

RESULT 445
AAQ70698

```

ID AAQ70698 standard; DNA; 18 BP.
XX AC
XX AAQ70698;
XX (INMR ) BIO MERIEUX.
DT 25-MAR-2003 (revised)
DT 15-MAR-1995 (first entry)
XX PI
XX C-Rich oligonucleotide used to inhibit c-myc transcription.
DE DE
XX c-myc; upstream region; regulatory element; gene expression; triplex;
KW antiseize; inhibition; screening; identification; ss.
XX OS
XX Synthetic.
XX WO9417086-A1.
XX 04-AUG-1994.
XX 10-JAN-1994; 94WO-US000348.
XX 25-JAN-1993; 93US-00008897.
XX (APOL-) APOLLON INC.
XX Yoon K, Lu M;
XX WPI; 1994-264018/32.
XX Composition for decreasing gene transcription - comprises
PT oligo:nucleotide or deriv. complementary to target gene region.
XX Example 1; Page 28; 71pp; English.
XX A number of oligonucleotides were screened for their ability to inhibit c
CC -myc transcription. They were tested on the substrate molecule described
CC in AAQ70670. This substrate molecule is a nuclease sensitive element
CC which has been shown to bind transcriptional factors, be involved in
CC transcriptional regulation and form H-DNA in vitro. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGGCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 446
AAQ57781/C
ID AAQ57781 standard; DNA; 18 BP.
XX AC
XX AAQ57781;
XX 25-MAR-2003 (revised)
DT 15-AUG-1994 (first entry)
XX DE
XX M.avium-intracellular complex-specific probe (640-657).
XX Mycobacterium avium-intracellular complex; species specific; detection;
KW polymerase chain reaction; amplification; MAIC; PCR primer; probe;
KW 65kd mycobacterial antigen; ss.
XX OS
XX Synthetic.
XX EP584023-A1.
XX 23-FEB-1994.
PD 12-AUG-1993; 93EP-00420339.
PF 12-AUG-1993; 93EP-00420339.

XX 12-AUG-1992; 92EP-00010094.
XX (INMR ) BIO MERIEUX.
XX Mabilat C, Pechere J;
XX WPI; 1994-058892/08.
XX Mycobacterium DNA fragments - corresp. to 65-kD antigen sequences, and
PT primers and probes for detecting Mycobacterium spp.
XX Claim 14; Page 34; 40pp; French.
XX The region corresponding to nucleotides 438-751 encoding the
CC M.tuberculosis 65kD antigen is highly conserved among mycobacteria. DNA
CC fragments having at least 70 per cent homology to this region and to the
CC corresponding region from other species are claimed. PCR amplification of
CC the appropriate region is performed using oligonucleotides AAQ57768 and
CC AAQ57769 as primers. The primers were designed to be "universal", i.e. to
CC amplify DNA from all Mycobacteria. Oligonucleotide AAQ57781 is a probe
CC specific to species belonging to the Mycobacterium avium-intracellular
CC complex; it hybridises to a species-specific sequence within the
CC amplified region. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 359 CCTTGGCGCGCTTGAGCA 376
Db 18 CTTGGCGCGACTTGAGCA 1

RESULT 447
AAQ79242
ID AAQ79242 standard; DNA; 18 BP.
XX AC
XX AAQ79242;
XX 25-MAR-2003 (revised)
DT 19-JUL-1995 (first entry)
XX DE
XX Guanosine rich oligonucleotide (sic) used to treat viral infection.
XX Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;
KW infection; herpes simplex virus; human papilloma virus;
KW Epstein-Barr virus; HIV, adenovirus; respiratory syncytial virus;
KW hepatitis B virus; human cytomegalovirus; ss.
XX OS
XX Synthetic.
XX Key Location/Qualifiers
FH misc_feature 18
FT /tag= a
FT /mod_base
FT /note= "Amine moiety attached to this base."
XX WO9425037-A1.
XX 10-NOV-1994.
XX 25-APR-1994; 94WO-US004529.
XX 23-APR-1993; 93US-00053027.
XX 28-OCT-1993; 93US-00145704.
XX (TRIP-) TRIPLEX PHARM CORP.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX Rando RF, Fennwald S, Zendegui JG, Ojwang JO, Hogan ME;
PI 12-AUG-1993; 93EP-00420339.

```

XX WPI; 1994-357890/44.
 XX
 PT Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used
 PT to treat viral infections, e.g. herpes-virus and HIV.
 XX
 PS Claim 41; Page 66; 101pp; English.
 XX
 CC The oligonucleotides (See AAQ79201-52) can be used to treat viral
 CC infections. The oligonucleotides inhibit viral replication by forming
 CC guanosine tetrads which form a stabilised 3D structure. Preferred
 CC oligonucleotides contain at least 2 runs of at least 2 guanosine bases
 CC and may be capped at the 3' terminus with a modifier selected from
 CC polyamine, poly-L-lysine, cholesterol and propanolamine. They may also
 CC have a modified phosphodiester linkage or be modified to contain a
 CC phosphorothioate linkage. They are used to treat infections with viruses
 CC such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,
 CC HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human
 CC cytomegalovirus. NOTE: This poly C sequence is a claimed sequence and
 CC given in Table 1 in the specification (Page 14) as a guanosine rich
 CC oligonucleotide although clearly it is not. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 973 CCCCCCCCCACCGGCC 990
 Db 1 CCCCCCCCCCCCCCCC 18
 RESULT 448
 AAQ79243
 ID AAQ79243 standard; DNA; 18 BP.
 AC AAQ79243;
 DT 25-MAR-2003 (revised)
 DT 19-JUL-1995 (first entry)
 XX
 DE Guanosine rich oligonucleotide (sic) used to treat viral infection.
 KW Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;
 KW infection; herpes simplex virus; human papilloma virus;
 KW Epstein-Barr virus; HIV, adenovirus; respiratory syncytial virus;
 KW hepatitis B virus; human cytomegalovirus; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..18
 FT /*tag= b
 FT /note= "Phosphorothioate backbone."
 FT misc_feature 18
 FT /*tag= a
 FT /mcd_base
 FT /note= "Amine moiety attached to this base."
 XX
 PN WO9425037-A1.
 PD 10-NOV-1994.
 XX
 PF 25-APR-1994; 94WO-US0004529.
 XX
 PR 23-APR-1993; 93US-00053027.
 PR 28-OCT-1993; 93US-00145704.
 XX
 PA (TRIP-) TRIPLEX PHARM CORP.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX

PI Rando RF, Fennewald S, Zengdeui JG, Ojwang JO, Hogan ME;
 DR WPI; 1994-357890/44.
 XX
 PT Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used
 PT to treat viral infections, e.g. herpes-virus and HIV.
 XX
 PS Claim 41; Page 67; 101pp; English.
 XX
 CC The oligonucleotides (See AAQ79201-52) can be used to treat viral
 CC infections. The oligonucleotides inhibit viral replication by forming
 CC guanosine tetrads which form a stabilised 3D structure. Preferred
 CC oligonucleotides contain at least 2 runs of at least 2 guanosine bases
 CC and may be capped at the 3' terminus with a modifier selected from
 CC polyamine, poly-L-lysine, cholesterol and propanolamine. They may also
 CC have a modified phosphodiester linkage or be modified to contain a
 CC phosphorothioate linkage. They are used to treat infections with viruses
 CC such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,
 CC HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human
 CC cytomegalovirus. NOTE: This poly C sequence is a claimed sequence and
 CC given in Table 1 in the specification (Page 14) as a guanosine rich
 CC oligonucleotide although clearly it is not. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 973 CCCCCCCCCACCGGCC 990
 Db 1 CCCCCCCCCCCCCCCC 18
 RESULT 449
 AAQ78447/c
 ID AAQ78447 standard; DNA; 18 BP.
 AC AAQ78447;
 DT 25-MAR-2003 (revised)
 DT 27-JUN-1995 (first entry)
 XX
 DE TGF-beta gene phosphorothioate antisense oligonucleotide.
 KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX
 OS Synthetic.
 XX
 PN WO9425588-A2.
 XX
 PD 10-NOV-1994.
 XX
 PF 29-APR-1994; 94WO-EP001362.
 XX
 PR 30-APR-1993; 93EP-00107089.
 PR 13-MAY-1993; 93EP-00107849.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 PI Bogdahn U;
 XX
 DR WPI; 1994-358266/44.
 XX
 PT New transforming growth factor beta anti-sense oligo:nucleotide(s) - for
 PT treating immunosuppression, tumours, etc.
 XX
 PS Claim 6; Page 51; 74pp; English.

XX The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 5 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1880 AATAAGTTTACATGCC 1897
Db 18 AATAAGCTTACATGTC 1

RESULT 450
AAQ78430/c
ID AAQ78430 standard; DNA; 18 BP.
XX
AC AAQ78430;
XX
XX 25-MAR-2003 (revised)
DT 27-JUN-1995 (first entry)
XX
DE TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX
OS Synthetic.
XX
XX WO9425588-A2.
XX
PD 10-NOV-1994.
XX
PF 29-APR-1994; 94WO-EP001362.
XX
PR 30-APR-1993; 93EP-00107089.
PR 13-MAY-1993; 93EP-00107849.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;
PI
XX WPI; 1994-358266/44.
XX
XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT treating immunosuppression, tumours, etc.
XX
XX Claim 6; Page 46; 74pp; English.
XX
XX The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 5 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1636 ATGCTTCGAATCTGGTGA 1653
Db 18 ATGCTTCCAATTTGGTGA 1

RESULT 451
AAQ78479/c
ID AAQ78479 standard; DNA; 18 BP.
XX
AC AAQ78479;
XX
XX 25-MAR-2003 (revised)
DT 27-JUN-1995 (first entry)
XX
DE TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX
OS Synthetic.
XX
XX WO9425588-A2.
XX
PD 10-NOV-1994.
XX
PF 29-APR-1994; 94WO-EP001362.
XX
PR 30-APR-1993; 93EP-00107089.
PR 13-MAY-1993; 93EP-00107849.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;
PI
XX WPI; 1994-358266/44.
XX
XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT treating immunosuppression, tumours, etc.
XX
XX Claim 6; Page 60; 74pp; English.
XX
XX The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 6 A; 0 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

RESULT 453

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX Synthetic.
 XX WO9425588-A2.
 PN
 XX
 XX 10-NOV-1994.
 PD
 XX
 XX 29-APR-1994; 94WO-EP001362.
 PF
 XX
 XX 30-APR-1993; 93EP-00107089.
 PR
 XX 13-MAY-1993; 93EP-00107849.
 PR
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 PI Bogdahn U;
 PI
 XX WPI; 1994-358266/44.
 DR
 XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
 XX treating immunosuppression, tumours, etc.
 PT
 XX
 XX Claim 6; Page 44; 74pp; English.
 PS
 XX The antisense oligonucleotides are useful in the treatment of tumours in
 XX which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1527 TATATAATCGACATGCCG 1544
 DB 18 TACAAAAATAGACATGCCG 1
 RESULT 455
 AAQ78483/C
 ID AAQ78483 standard; DNA; 18 BP.
 XX
 XX AAQ78483;
 AC
 XX
 XX 25-MAR-2003 (revised)
 DT 27-JUN-1995 (first entry)
 DT
 XX TGF-beta gene phosphorothioate antisense oligonucleotide.
 DE
 XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX Synthetic.
 OS
 XX WO9425588-A2.
 PN

XX 10-NOV-1994.
 PD
 XX 29-APR-1994; 94WO-EP001362.
 PF
 XX
 XX 30-APR-1993; 93EP-00107089.
 PR
 XX 13-MAY-1993; 93EP-00107849.
 PR
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 PI Bogdahn U;
 PI
 XX WPI; 1994-358266/44.
 DR
 XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
 XX treating immunosuppression, tumours, etc.
 PT
 XX
 XX Claim 6; Page 62; 74pp; English.
 PS
 XX The antisense oligonucleotides are useful in the treatment of tumours in
 XX which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2439 GTCAGTCTTGTAAATGC 2456
 DB 18 GTAAAGTCTTGCAATGC 1
 RESULT 456
 AAQ75026/C
 ID AAQ75026 standard; DNA; 18 BP.
 XX
 XX AAQ75026;
 AC
 XX
 XX 25-MAR-2003 (revised)
 DT 03-AUG-1995 (first entry)
 DT
 XX PCR primer.
 DE
 XX Synthetic oligo; solid phase immunoassay; ss.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH misc_difference 1
 FT /tag= a
 FT /note= "Linked to biotin"
 FT
 XX WO9426932-A1.
 PN
 XX 24-NOV-1994.
 PD
 XX 13-MAY-1994; 94WO-US005407.
 PF
 XX 13-MAY-1993; 93US-00061694.
 PR
 XX

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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fields HA, Khudyakov YE;
XX
XX WPI; 1995-006819/01.
XX
XX Solid phase immunoassay using oligo:nucleotide as label - also new
PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT diagnosing hepatitis C or E virus infection.
XX
XX Example; Page 12; 34pp; English.
XX
XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC They are used in a method for detecting an antigen in a subject. The
CC method involves binding the antigen to a solid support and then reacting
CC it with an immunoreactive ligand (L) bound to an oligo; removing any
CC unreacted L, and then detecting the presence of the oligo. A similar
CC method can be used to detect Ab, in which case the ligand is an oligo-
CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC to be detected at very low levels. An exemplary oligo is AAQ75024 which
CC can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC a synthetic peptide. In the example, peptide AAR62941 was coupled to
CC oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
CC contain HEV Abs were immobilised on plastic tubes or wells, then
CC incubated for 30-60 mins with the peptide-oligo product. The vessels were
CC washed; bound oligo was released with 0.2M glycine and amplified in a
CC separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
CC The amplification product - AAQ75031 - was treated with uracil DNA
CC glycosylase to remove the U18 fragment, and the product captured by
CC immobilised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 1 A; 10 C; 0 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 254 AGGAGAAGCTAGGGAGG 271
DB 18 AGGAGAAGATAGGGAGG 1
RESULT 457
AAT51660
ID AAT51660 standard; DNA; 18 BP.
XX
XX AAT51660;
AC
XX
XX 12-NOV-1997 (first entry)
DT
XX
XX Viral integrase inhibiting oligonucleotide.
DE
XX
XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;
KW herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;
KW respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;
KW integrase inhibition; guanosine tetrad; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 18
FT /*tag= a
FT /note= "amine moiety attached to 3' end"
XX
XX W09703997-A1.
PN
XX
XX 06-FEB-1997.
PD
XX
XX 17-JUL-1996; 96WO-US011786.
XX
XX 19-JUL-1995; 95US-0001505P.
PR 23-OCT-1995; 95US-00535168.
PR 19-MAR-1996; 96US-0013688P.
XX

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PR 25-MAR-1996; 96US-0014007P.
PR 17-APR-1996; 96US-0015714P.
PR 23-APR-1996; 96US-0016271P.
XX
XX (ARON-) ARONEX PHARM INC.
XX
XX Rando RF, Fennewald S, Zendequi JG, Ojwang JO, Hogan MB;
PI Pommier Y, Mazumder A;
XX
XX WPI; 1997-132569/12.
XX
XX Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit viral
PT enzyme responsible for integrating viral nucleic acid into the host
PT genome.
XX
XX Claim 3; Page 164; 245pp; English.
XX
XX AAT51619-T51698 are oligonucleotides used to inhibit the production of
CC viruses within a host cell. The oligonucleotides may form guanosine
CC tetrads (structures formed of eight hydrogen bonds by coordination of the
CC four oxygen atoms of guanine with alkali cations believed to bind to the
CC centre of a quadruplex, and by strong stacking interactions) and are used
CC to prevent the integration of viral nucleic acid into a host genome. The
CC oligonucleotides inhibit functioning of the integrase enzyme and hence
CC prevent viral infection. Viral infections that may be treated include
CC human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes
CC simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory
CC syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),
CC especially HIV-1 infection
XX
XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 973 CCCCCCCCCACCGCCCC 990
DB 1 CCCCCCCCCCCCCCCCC 18
RESULT 458
AAV54166/C
ID AAV54166 standard; cDNA; 18 BP.
XX
XX AAV54166;
AC
XX
XX 21-DEC-1998 (first entry)
DT
XX
XX Nucleotide sequence PCR primer 3.
DE
XX
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
XX Synthetic.
OS
XX
XX W09839437-A1.
PN
XX
XX 11-SEP-1998.
PD
XX
XX 05-MAR-1998; 98WO-JP000905.
PR
XX
XX 05-MAR-1997; 97JP-00050302.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX
XX Sakaki Y;
PI
XX
XX WPI; 1998-495844/42.
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX

```

PS Example 1; Page 48; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method of the

CC invention, involving the use of novel apoptosis-related DNAs and

CC proteins. The inventions can be used as diagnostic reagents for apoptosis

CC e.g. (monoclonal) antibodies for the protein, as a reagent in

CC immunohistological staining, as apoptosis inhibitors. It can also be used

CC for treatment of apoptosis-related diseases

XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2801 TGAAGAAAAAACAATC 2818

DB 18 TGAAGAAAAAACAATC 1

RESULT 459

AAV54169/C

ID AAV54169 standard; cDNA; 18 BP.

AC AAV54169;

XX 21-DEC-1998 (first entry)

DT Nucleotide sequence PCR primer 6.

DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;

XX immunohistological staining.

KW Synthetic.

OS WO9839437-A1.

XX 11-SEP-1998.

PD 05-MAR-1998; 98WO-JP000905.

PF 05-MAR-1997; 97JP-00050302.

PR (KYOW) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

PI WPI; 1998-495844/42.

DR Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or

XX treating diseases associated with apoptosis.

PT Example 1; Page 49; 70pp; Japanese.

PS This is the nucleotide sequence of a PCR primer used in the method of the

CC invention, involving the use of novel apoptosis-related DNAs and

CC proteins. The inventions can be used as diagnostic reagents for apoptosis

CC e.g. (monoclonal) antibodies for the protein, as a reagent in

CC immunohistological staining, as apoptosis inhibitors. It can also be used

CC for treatment of apoptosis-related diseases

XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 929 AGAAGAAAAAACAAC 946

DB 18 AGAAGAAAAAACAAC 1

RESULT 460

AAV21971

ID AAV21971 standard; DNA; 18 BP.

XX AAV21971;

AC 14-JUL-1998 (first entry)

DT Nuclease resistant antisense oligo NBT 143 targeted against (C)18.

XX Nuclease resistant; bacterial infection; antibiotic; target;

XX veterinary medicine; treatment; human; industrial process;

KW bacterial control; ss.

KW Synthetic.

OS WO9803533-A1.

PN 29-JAN-1998.

PD 23-JUL-1997; 97WO-US012961.

PF 24-JUL-1996; 96US-00685575.

XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.

XX Arrow A, Dale RMK, Thompson TL;

PI WPI; 1998-120687/11.

DR Treating bacterial infections in humans or animals with

XX oligo:nucleotide(s) - resistant to nuclease and targeted to bacterial

PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)

PT with antibiotics.

XX Claim 49; Page 87; 163pp; English.

XX This antisense oligonucleotide is nuclease resistant and can be used in

CC the treatment of animals, including humans, having a bacterial infection.

CC The treatment comprises administration of such nuclease resistant

CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,

CC and formulated with a carrier. A compound comprising this nuclease

CC resistant oligonucleotide can be covalently linked to an antibiotic. The

CC method is used to treat infections by a wide variety of Gram-positive and

CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.

CC The methods are particularly used in immuno-compromised individuals (e.g.

CC patients with acquired immunodeficiency syndrome or those receiving

CC chemotherapy or radiation therapy), optionally in combination with, or

CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from

CC therapeutic use, the oligonucleotides can be used to control bacteria in

CC laboratory cultures, foods, beverages and industrial processes. The

CC oligonucleotides are specific for bacteria, without affecting metabolism

CC in mammalian cells. They may also activate RNase H and have a general,

CC non-specific immune-stimulating effect. The oligonucleotides can be

CC administered orally, intranasally, rectally, topically or by injection,

CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that

XX enhances cellular uptake

SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCCCC 990

DB 1 CCCCCCCCCCGCCCC 18

RESULT 461

AAV79242

ID AAV79242 standard; DNA; 18 BP.

XX AAV79242;

XX 21-OCT-2004 (revised)

DT 31-AUG-1999 (first entry)

XX

DE Oligonucleotide #35 forms an intramolecular stacked tetrad structure.

XX

XX Column; box; stacked tetrad; inhibition; replication; pathophysiological;

KW herpes simplex virus; HSV; human papilloma virus; Epstein Barr Virus;

KW HPV; EBV; HIV; human immunodeficiency virus; adenovirus; RSV; HBV; HCMV;

KW respiratory syncytial virus; hepatitis B virus; human cytomegalovirus;

KW human T-cell leukaemia virus; HTLV; ss.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc_structure 1. .18

FT /tag= a

FT /notes= "forms intramolecular stacked tetrad or 3D

FT columnar box structure"

FT modified_base 1. .18

FT /tag= b

FT /mod_base= optionally contains phosphodiester

FT internucleotide linkages

XX

XX WO9833807-A1.

PN

XX

XX 06-AUG-1998.

PD

XX

XX 03-FEB-1998; 98WO-US001974.

PF

XX

XX 04-FEB-1997; 97US-0037374P.

PR

XX

XX 09-DEC-1997; 97US-00987574.

PR

XX

XX (ARON-) ARONEX PHARM INC.

PA

XX

XX Rando RF, Ojwang JO, Hogan ME, Wallace TL, Cossum PA;

PI

XX

XX WPI; 1998-446809/38.

DR

XX

XX New guanosine-rich tetrad forming oligonucleotide(s) - used for

PT inhibiting virus replication for treating e.g. herpes simplex, papilloma,

PT HIV, adenovirus or hepatitis B virus infection.

PT

XX

PS Disclosure; Page 146; 140pp; English.

PS

XX

XX Sequences AAX79210-X79275 represent oligonucleotides (ON) which are able

CC to form a columnar box or "stacked tetrad" structure by intramolecular

CC internucleotide binding. The ONs are used to inhibit the replication of

CC viruses. They are able to suppress virus production for prolonged periods

CC after an initial short treatment regimen. They can be used for treating

CC pathophysiological states caused by viruses such as herpes simplex virus,

CC human papilloma virus, Epstein Barr Virus, HIV, adenovirus, respiratory

CC syncytial virus, hepatitis B virus, human cytomegalovirus and HTLV I and

CC II

CC

CC Revised record issued on 21-OCT-2004 : Correction to feature table key

XX

XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

SQ

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCCCC 990

DB 1 CCCCCCCCCCCCCCCCCC 18

RESULT 462

AAZ65449/C

ID AAZ65449 standard; DNA; 18 BP.

XX

AC AAZ65449;

XX 30-MAR-2000 (first entry)

DT

XX

DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-9.

XX

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;

KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;

KW prostaglandin E2; PGE2; immune response; tumour; aethma; Crohn's disease;

KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;

KW glomerulonephritis; acute respiratory distress syndrome; ss;

KW atherosclerosis.

XX

OS Unidentified.

OS

XX

XX WO963975-A2.

PN

XX

XX 16-DEC-1999.

PD

XX

XX 10-JUN-1999; 99WO-EP004013.

PF

XX

XX 10-JUN-1998; 98EP-00110709.

PR

XX

XX 25-JUL-1998; 98EP-00113974.

PR

XX

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

PA

XX

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

PI

XX

XX WPI; 2000-097470/08.

DR

XX

XX Composition containing immune stimulant and inhibitor of agent that

PT adversely affects the immune response, for treating cancers and

PT infections.

PT

XX

XX Claim 5; Fig 1; 30pp; English.

PS

XX

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is

CC used in the invention. The invention relates to a composition which

CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.

CC transforming growth factor TGF-beta, vascular endothelial growth factor

CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)

CC that adversely affects the immune response. The composition also includes

CC at least one stimulant that positively affects the immune response. This

CC oligonucleotide is an example of an inhibitor that is used in the

CC composition. The composition is used as an immunostimulant for the

CC treatment of neoplasms and infections, particularly hyperproliferation;

CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,

CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,

CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,

CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,

CC most of which are directed against TGFbeta or VEGF, are inhibitors of

CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-

CC inflammatory for treating e.g. aethma, Crohn's disease, ulcerative

CC colitis, diabetes, glomerulonephritis, acute respiratory distress

CC syndrome and the formation of atherosclerotic plaque

XX

XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

SQ

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TATAAATCGACATGCCG 1544

DB 18 TACAAAATAGACATGCCG 1

RESULT 463

AAZ65505/C

ID AAZ65505 standard; DNA; 18 BP.

XX

AC AAZ65505;

XX

XX 30-MAR-2000 (first entry)

DT

XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-98-8.
 DE Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX Unidentified.
 OS
 XX WO9963975-A2.
 XX
 XX 16-DEC-1999.
 XX
 XX 10-JUN-1999; 99WO-EP004013.
 XX
 XX 10-JUN-1998; 98EP-00110709.
 PR
 XX 25-JUL-1998; 98EP-00113974.
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX WPI; 2000-097470/08.
 XX
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 PT
 XX Claim 10; Fig 1; 30pp; English.
 PS
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 XX Sequence 18 BP; 0 A; 10 C; 6 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1462 CAGCCGAGCGGCGCGC 1479
 DB 18 CGAGCCGAGCGGCGCGC 1
 RESULT 464
 AA265456/C
 ID AA265456 standard; DNA; 18 BP.
 XX
 XX AA265456;
 AC
 XX 30-MAR-2000 (first entry)
 DT
 XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-16.
 DE

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX Unidentified.
 OS
 XX WO9963975-A2.
 XX
 XX 16-DEC-1999.
 XX
 XX 10-JUN-1999; 99WO-EP004013.
 XX
 XX 10-JUN-1998; 98EP-00110709.
 PR
 XX 25-JUL-1998; 98EP-00113974.
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX WPI; 2000-097470/08.
 XX
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 PT
 XX Claim 5; Fig 1; 30pp; English.
 PS
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 XX Sequence 18 BP; 5 A; 5 C; 2 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1711 GGATTGAACTCTATCAGA 1728
 DB 18 GGATTGAGCTATATCAGA 1
 RESULT 465
 AA265453/C
 ID AA265453 standard; DNA; 18 BP.
 XX
 XX AA265453;
 AC
 XX 30-MAR-2000 (first entry)
 DT
 XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-13.
 DE
 XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW

KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX Unidentified.

OS WO9963975-A2.

PN 16-DEC-1999.

PD 10-JUN-1999; 99WO-EP004013.

XX 10-JUN-1998; 98EP-00110709.

PR 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

PA Schlingensiepen K, Schlingensiepen R, Brysch W;

PI WPI; 2000-097470/08.

DR Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1636 ATGCTTCGAATCTGGTGA 1653

DB 18 ATGCTTCCAATTGGTGA 1

RESULT 466

AAZ90648/c

ID AAZ90648 standard; DNA; 18 BP.

XX AAZ90648;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #9.

DE Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

OS Homo sapiens.

PN JP2000037190-A.

XX 08-FEB-2000.

XX 23-JUL-1998; 98JP-00225228.

XX 23-JUL-1998; 98JP-00225228.

XX (NISR) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes

XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAACATC 2818

DB 18 TGAATAAAAAAAACATC 1

RESULT 467

AAZ90645/c

ID AAZ90645 standard; DNA; 18 BP.

XX AAZ90645;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #6.

DE Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.

PN JP2000037190-A.

XX 08-FEB-2000.

XX 23-JUL-1998; 98JP-00225228.

XX 23-JUL-1998; 98JP-00225228.

XX (NISR) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention

CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
 SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 929 AGAAAAAACAACACC 946
 Db 18 AGAAAAAACAAC 1

RESULT 468
 AAA58387/c
 ID AAA58387 standard; DNA; 18 BP.
 XX
 AC AAA58387;
 XX
 DT 01-NOV-2000 (first entry)
 XX
 DE Polynucleotide # 3 used in a biomolecule detection system.
 XX
 KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
 XX
 XX Synthetic.
 OS
 XX WO200028088-A1.
 PN
 PD 18-MAY-2000.
 XX
 PF 10-NOV-1999; 99WO-US026612.
 XX
 PR 10-NOV-1998; 98US-0107828P.
 PR 09-NOV-1999; 99US-00437076.
 XX
 XX (BIOC-) BIOCRYSTAL LTD.
 PA
 XX Barbera-Guillem E, Nelson MB, Castro S;
 PI
 XX WPI; 2000-376593/32.
 DR
 XX Functionalized nanocrystal carrying polynucleotide, used for detecting
 PT target analyte, forms dendrimers with complementary nanocrystals to
 PT amplify the fluorescent signal.
 PT
 XX Example 3; Page 69; 72pp; English.
 PS
 XX The present invention relates to functionalised nanocrystals for use in
 CC nonisotopic detection systems for biomolecules e.g. nucleic acids, proteins,
 CC lipids or drugs. The nanocrystals have polynucleotide strands
 CC attached to their surfaces with one end of the polynucleotide extending
 CC outwardly from the nanocrystal. The present sequence is one such
 CC polynucleotide. These nanocrystals are used with a second series of
 CC nanocrystals, which have polynucleotides complementary to the first
 CC polynucleotides, so that the respective complementary strands hybridise
 CC to each other and form a dendrimer. This dendrimer produces a signal
 CC which can then be detected e.g. fluorescence. The present sequence is
 CC composed of Guanine bases. This sequence may therefore be used with a
 CC polynucleotide composed mainly of Cytosine bases (AAA58388)
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 18 G; 0 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 973 CCCCCCCCCCCCCCCCCC 990
 Db 18 CCCCCCCCCCCCCCCCCC 1

RESULT 469
 ABL57543/c
 ID ABL57543 standard; DNA; 18 BP.
 XX
 AC ABL57543;
 XX
 DT 26-JUL-2002 (first entry)
 XX
 DE Nucleic acid probe h.
 XX
 KW Concentration; quantification; mutation detection; polymorphic;
 KW polymerase chain reaction; PCR; probe; ss.
 XX
 OS Unidentified.
 XX
 PN EP1046717-A2.
 XX
 PD 25-OCT-2000.
 XX
 PF 20-APR-2000; 2000EP-00108643.
 XX
 PR 20-APR-1999; 99JP-00111601.
 XX
 XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kanagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX
 DR WPI; 2000-657765/64.
 XX
 PT Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.
 XX
 PS Example 5; Page 21; 55pp; English.
 XX
 CC The invention relates to the determination of the concentration of a
 CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.
 CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for
 CC quantifying microbial cells in co-cultures or symbiotic systems, for
 CC detecting gene mutations or polymorphisms, and for analysing melting
 CC curves of target nucleic acids to determine a Tm value. Methods of the
 CC invention allow target nucleic acids to be quantified quickly, easily and
 CC accurately. Particularly there is no need to remove unbound probe, and no
 CC materials are introduced that inhibit amplification by Taq polymerase (so
 CC conventional PCR conditions can be used). The specificity of PCR is kept
 CC high (amplification of primer dimers is delayed), and the limit of
 CC quantitation is reduced. Complex probes are not needed, and amplification
 CC can be monitored in real time. The working graph for data analysis
 CC (automatically generated by a computer) has a higher correlation
 CC coefficient than conventional graphs so more accurate quantitation is
 CC possible. The current sequence represents a nucleic acid probe of the
 CC invention that was used for investigating the base selectivity of a
 CC target nucleic acid
 XX
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1162 ATATATATTTTCTTCTAC 1179
 Db 18 ATATATATTTTCTTCTAC 1

RESULT 470
 AAS13708


```

ID AAS13708 standard; DNA; 18 BP.
XX
AC AAS13708;
XX
DT 08-MAY-2002 (first entry)
XX
DE Simple sequence repeat, SSR, #5.
XX
KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
KW cereal profiling; grass profiling; seed batch purity testing.
XX
OS Poae.
XX
PN NZ509193-A.
XX
PD 25-MAY-2001.
XX
PF 03-JAN-2001; 2001NZ-00509193.
XX
PR 24-DEC-1999; 99AU-00004906.
PR 04-MAY-2000; 2000AU-00007310.
XX
XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
PA (UYSC-) UNIV SOUTHERN CROSS.
PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
PA (UYAD-) UNIV ADELAIDE.
PA (ITWA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX
PI Forster JW, Jones ES;
XX
XX WPI; 2001-512563/56.
XX
XX New simple sequence repeats having 2 or more tandemly repeated nucleotide
PT core elements isolated from ryegrass and fescue, useful for selecting of
PT genes in grass or cereal breeding or profiling grass or cereal species
PT varieties.
XX
PS Claim 6; Page 51; 72pp; English.
XX
XX The invention relates to a substantially purified or isolated nucleic
CC acid (1) from ryegrass or fescue species including a simple sequence
CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
CC 2-6 nucleotides in length. Also included are a nucleic acid primer
CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
CC library of ryegrass or fescue genomic DNA enriched for SSRs and
CC identifying clones in the library containing SSRs, a library of ryegrass
CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
CC a gene in grass or cereal breeding by identifying an SSR that is closely
CC associated with the gene such that the SSR and the gene are
CC preferentially co-inherited, and selecting for the SSR in the breeding, a
CC method for DNA profiling grass or cereal species varieties by assessing
CC variation between SSR varieties and testing the purity of grass or cereal
CC seed batches by assessing variation within seed batch of an SSR. The SSRs
CC may be used in the selection of genes in grass or cereal breeding, for
CC profiling grass or cereal species varieties, for testing the purity of
CC grass or cereal seed batches, and for DNA profiling to establish the
CC distinct identity, uniformity and/or stability of a cultivar. The present
CC sequence is a ryegrass or fescue SSR
XX
SQ Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2667 CAGCAACAACACCAACAA 2684
DB 1 CAACAACAACACCAACAA 18
|||
|||

RESULT 471
AAD12565/C
ID AAD12565 standard; DNA; 18 BP.
XX
XX
AC AAD12565;
XX
DT 25-SEP-2001 (first entry)
XX
DE Pinorensinol/lariciresinol reductase DNA cloning linker PCR primer.
XX
KW Dirigent protein; pinorensinol/lariciresinol reductase; stereospecificity;
KW lignan biosynthetic pathway; secoisolariciresinol; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200149833-A2.
XX
PD 12-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US035265.
XX
PR 30-DEC-1999; 99US-00475316.
XX
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.
PA (MINU ) UNIV MINNESOTA.
XX
XX Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;
PI Ford JD, Sarkanen S;
XX
XX WPI; 2001-465260/50.
XX
XX Dirigent and/or pinorensinol/lariciresinol reductase proteins useful for
PT producing optically-pure lignans.
XX
XX Example 24; Page 72; 183pp; English.
XX
XX The present invention relates to an isolated dirigent and/or pinorensinol
CC /lariciresinol reductase protein from a lignan biosynthetic pathway.
CC Dirigent and/or pinorensinol/lariciresinol reductase protein and the
CC nucleic acids that encode it may be expressed either in vivo or in vitro
CC to produce enzymes involved in the biosynthesis of lignans. The 78-KD
CC dirigent protein confers stereospecificity in 8'-linked lignan
CC formation and binds to and orients coniferyl alcohol-derived free
CC radicals, which then under go stereospecific coupling to form (+)-
CC pinorensinol. Pinorensinol/lariciresinol reductase catalyses the conversion
CC of pinorensinol to lariciresinol and then to secoisolariciresinol. The
CC present sequence is a PCR primer used for cloning
CC pinorensinol/lariciresinol reductase DNA
XX
SQ Sequence 18 BP; 1 A; 2 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2577 AAAAAAAAAAATTCGAG 2594
DB 18 AAAAAAAAAAATTCGAG 1
|||
|||

RESULT 472
AAD18718/C
ID AAD18718 standard; DNA; 18 BP.
XX
XX
AC AAD18718;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human oligonucleotide #4, useful in drug target validation.
XX
KW Human; TGF-beta; erbB-2; MTA; c-jun; junB; c-fos; VCAM; NF-kappaB p65;
KW NF-kappaB p50; ICAM; VEGF; NF-kB 2; therapy; tumour; immune disorder;
KW organ transplantation; cell expansion; drug target validation;
KW antitumour; immunosuppressive; ss.
XX
XX Homo sapiens.
OS
```

XX EP1133988-A1.
 XX
 XX 19-SEP-2001.
 XX
 XX 11-MAR-2000; 2000EP-00105190.
 XX
 XX 11-MAR-2000; 2000EP-00105190.
 XX
 XX (BIOG-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 XX Schlingensiepen K, Schlingensiepen R;
 XX WPI; 2001-604124/69.
 XX
 XX Mixture useful in preparation of medicament for treating tumors and
 PT immune disorders, comprises an inhibitor or suppressor of expression of a
 PT gene, and a molecule binding to expression product of the gene.
 XX
 XX Claim 16; Page 2; 16pp; English.
 XX
 XX The invention relates to a mixture comprising an inhibitor or suppressor
 CC of a gene and a molecule binding to an expression product of that gene.
 CC The gene is selected from the group consisting of TGF-beta, erbB-2, MIA,
 CC c-jun, junB, c-fos, VCAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF
 CC -kappa B 2. Molecules including drugs are used to modulate biological
 CC functions through gene products and their derivatives - like e.g.
 CC glycosylated, phosphorylated or otherwise modified gene products, have
 CC either stimulated or inhibited gene products and/or their derivatives.
 CC The mixture is useful in the preparation of a medicament for treating
 CC tumours, immune disorders or for improving organ or cell transplantation
 CC or cell expansion, where inhibition of tumour growth, improvement of
 CC organ or cell transplantation or cell expansion and enhancement or
 CC inhibition of immune response is enhanced in a supra-additive manner. The
 CC mixture is useful in drug target validation, i.e., to identify genes that
 CC are relevant for certain pathological state by testing the effect of the
 CC mixture on a cell system or organism. The present sequence is a human
 CC oligonucleotide useful in drug target validation
 XX
 XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1527 TATAAATCGACATGCG 1544
 DB 18 TACAAATAGACATGCG 1
 RESULT 473
 AAF23524
 ID AAF23524 standard; DNA; 18 BP.
 XX
 XX AAF23524;
 AC
 XX 22-MAR-2001 (first entry)
 DT
 XX Primer #2.
 DE
 XX Primer; mRNA; amplification; ss.
 KW
 XX Unidentified.
 OS
 XX WO200075356-A1.
 PN
 XX 14-DEC-2000.
 PD
 XX 04-JUN-1999; 99WO-US012461.
 XX
 XX 04-JUN-1999; 99WO-US012461.
 PR
 XX (LINS/) LIN S.
 PA

PA (YING/) YING S.
 PA (CHUO/) CHUONG C.
 PA (WIDE/) WIDELITZ R B.
 XX
 XX Lin S, Ying S, Chuong C, Widelitz RB;
 PI WPI; 2001-061734/07.
 XX
 XX Generating amplified messenger RNA sequences from single cells, involves
 PT cycling steps of reverse transcription, denaturation, double-stranded DNA
 PT sequences and in vitro transcription.
 PT
 XX Disclosure; Page 17; 31pp; English.
 PS
 XX The present invention relates to generating amplified messenger RNAs with
 CC polymerase reaction activity, comprising cycling steps of reverse
 CC transcription, denaturation, double-stranded cDNA synthesis and in vitro
 CC transcription. The invention is used for generating amplified mRNAs from
 CC limited mRNAs from single cells
 XX
 XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 973 CCCCCCCCCACCCGCCCC 990
 DB 1 CCCCCCCCCCCCCCCCCC 18
 RESULT 474
 ABL30793/c
 ID ABL30793 standard; DNA; 18 BP.
 XX
 XX ABL30793;
 AC
 XX 21-MAR-2002 (first entry)
 DT
 XX Human HLA genotyping oligonucleotide SEQ ID NO 282.
 DE
 XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW immunogenetic; transplantation; genetic disease; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200192572-A1.
 PN
 XX 06-DEC-2001.
 PD
 XX 01-JUN-2001; 2001WO-JP004662.
 PF
 XX 01-JUN-2000; 2000JP-00164798.
 PR
 XX (NISN) NITSSHINO IND INC.
 PA (SYST-) SYSTEM RES INC.
 XX
 XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 PI WPI; 2002-122074/16.
 XX
 XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when
 PT transplanting between them.
 PT
 XX Claim 10; Page 146; 345pp; Japanese.
 PS
 XX The invention relates to a typing kit for judging human leukocyte antigen
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
 CC genes e.g. belonging to HLA class I antigens on human genome and
 CC containing gene polymorphisms as alloantigens have been immobilised as
 CC primers for amplification of cleaved nucleic acids relating to gene

CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC between them, providing genetic information to decide compatibility of
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals
 XX
 SQ Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2914 CTGCAGTGGGTGCCCTCC 2931
 Db 18 CTGCAGTAGGTGCCACC 1
 RESULT 475
 ACA62280
 ID ACA62280 standard; DNA; 18 BP.
 XX
 AC ACA62280;
 XX
 DT 12-AUG-2003 (first entry)
 DE
 DE Oligo (dC) primer.
 XX
 XX ss; PCR; primer; antisense therapy; mRNA expression profile;
 KW promoter containing primer.
 KW
 OS Synthetic.
 OS
 XX US2003022318-A1.
 PN
 XX 30-JAN-2003.
 PD
 XX 07-SEP-2001; 2001US-00949305.
 XX
 PR 25-JAN-2000; 2000US-00494212.
 XX
 XX (EPIC-) EPICLONE INC.
 PA
 XX Lin S, Ying S;
 PI
 XX WPI; 2003-479488/45.
 DR
 XX Improved polymerase thermocycling reaction for nucleic acid
 PT amplification, by thermal cycling of promoter-linked nucleic acid
 PT template synthesis and in vitro transcriptional amplification of nucleic
 PT acid sequences.
 XX
 PS Example 3; Page 14; 28pp; English.
 XX
 CC The invention relates to an improved polymerase thermocycling reaction
 CC (M1) for linear amplification of nucleic acid sequences, involves
 CC denaturing a number of nucleic acid templates (I), combining the
 CC denatured (I) with a promoter-containing primer (P1), a primer (P2), a
 CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
 CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
 CC polymerase, contacting P1 with (I) to generate a number of promoter-
 CC containing templates, denaturing the promoter-containing templates,
 CC contacting P2 with the denatured promoter-containing templates to
 CC generate a number of promoter-containing double-stranded DNA templates,
 CC where the double-stranded nucleic acid templates are flanked by P1 in one
 CC end and P2 in the other end of the other orientation, transcribing the
 CC promoter-containing double-stranded DNA templates to form a number of
 CC amplified RNA sequences, including the primer region of the promoter-
 CC containing double-stranded DNA templates, contacting the amplified RNA
 CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA
 CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
 CC is useful for improved polymerase thermocycling reaction for linear
 CC amplification of nucleic acid sequences, and thus for producing mRNA

CC expression profile of a cell by M1 to generate multiple copies of the
 CC mRNA. M1 is also useful for determining aberrant protein production of
 CC cells in a diseased state, by generating an expression profile by the
 CC above method, of cells in both normal and diseased states, comparing the
 CC expression profile of the cells in the normal and diseased states, the
 CC determining the differences in mRNA composition of the cell(s) in the
 CC diseased state, isolating the mRNA sequences of cell(s) in the diseased
 CC state that differ from mRNA in cell(s) in non-diseased state, amplifying
 CC the isolated mRNA by M1, and determining aberrant protein function of the
 CC protein coded for by the isolated mRNA. M1 is also useful for treating a
 CC cell in a diseased state caused by aberrant protein production, by
 CC determining protein expression of a cell in a diseased state, determining
 CC the mRNA sequence for the aberrant proteins, synthesising an antisense
 CC sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and
 CC delivering a pharmaceutically effective dosage of a composition
 CC comprising the anti-sense mRNA and a compatible lipid based biological
 CC carrier. M1 is also useful for predicting the efficacy of a proposed drug
 CC targeted against an aberrant protein, by determining aberrant protein
 CC production of cell in a diseased state by the above method, amplifying
 CC the aberrant protein by M1 and using recombinant techniques to determine
 CC the effect of proposed drug on the aberrant protein. M1 is also useful
 CC for differential screening of tissue-specific gene expression at a
 CC cellular level, for preparing labeled RNA/DNA probes for a gene chip
 CC technology, and for determining the efficacy of a drug regimen against a
 CC gene or its cDNAs. The present sequence is an Oligo (dC) primer used to
 CC produce second strand cDNA in the method of the invention
 XX
 SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 973 CCCCCCAGCGCGCC 990
 Db 1 CCCCCCCCCCCCCCCCC 18
 RESULT 476
 ADB54824/C
 ID ADB54824 standard; DNA; 18 BP.
 XX
 AC ADB54824;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Hybridisation oligonucleotide 362 used to analyse genomic DNA region.
 XX
 KW colon cell proliferative disorder; non methylated CpG dinucleotide;
 KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;
 KW probe.
 XX
 OS Unidentified.
 XX
 XX WO2003072821-A2.
 PN
 XX 04-SEP-2003.
 PD
 XX 27-FEB-2003; 2003WO-EP002035.
 PF
 XX 27-FEB-2003; 2002EP-00004551.
 PR
 XX (EPIC-) EPICENOMICS AG.
 PA
 XX Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Lesche R;
 PI Rujan T, Schmitt A;
 PI
 XX WPI; 2003-731620/69.
 DR
 XX Detecting and differentiating between colon cell proliferative disorders
 PT associated with a gene or its regulatory regions comprises contacting a
 PT target nucleic acid in a biological sample obtained from the subject with
 PT a reagent.

```

XX
PS Claim 36; Page 46; 74pp; English.
CC
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the hybridisation
CC oligonucleotide of the invention which was used to analyse the genomic
CC DNA region.
XX
SQ Sequence 18 BP; 0 A; 0 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2808 AAAAAAAAAATCAAAACAA 2825
Db 18 AAAAAACCAACCAAAACAA 1

RESULT 477
ADC64808/c
ID ADC64808 standard; DNA; 18 BP.
XX
AC ADC64808;
XX
DT 18-DEC-2003 (first entry)
XX
DE
XX
DE B4 clone cDNA library linker primer SEQ ID NO:29.
XX
XX humanised; polypeptide antigen; protein antigen; decreased antigenicity;
XX CD8; T lymphoblast; CD8 T cell; cancer; linker; primer; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX KR2002066383-A.
XX
XX 16-AUG-2002.
XX
XX 07-FEB-2002; 2002KR-00006974.
XX
XX 08-FEB-2001; 2001KR-00006212.
XX
XX (IMMU-) IMMUNOMICS CO LTD.
XX
XX Kwon BS;
XX
XX WPI; 2003-145050/14.
XX
XX New humanized polypeptide antigen with decreased antigenicity and it's
XX encoding gene, for the treatment of tumors and AIDS.
XX
XX Disclosure; Page 3; 18pp; Korean.
XX
XX The present invention describes a humanised polypeptide antigen with
XX decreased antigenicity, which binds to 4-1BB of CD8 T lymphoblasts to
XX activate CD8 T cells, and it's encoding gene. The humanised polypeptide
XX antigen can be used in the treatment of cancer. The present sequence
XX represents a linker primer which is used in the exemplification of the
XX present invention.
XX
XX Sequence 18 BP; 1 A; 2 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAACTCGAG 1

RESULT 478
ADL06307/c
ID ADL06307 standard; DNA; 18 BP.
XX
AC ADL06307;
XX
DT 06-MAY-2004 (first entry)
XX
DE
XX
DE Kid lingual tissue cDNA library associated linker #1.
XX
XX kid pregastric esterase; kPGE; rennet; enzyme-modified cheese; kosher;
XX vegetarian; polyHis-enterokinase; esterase expression; lipase expression;
XX goat; linker; cDNA library; lingual tissue; ss.
XX
XX Synthetic.
XX
XX US6582948-B1.
XX
XX 24-JUN-2003.
XX
XX 14-JAN-2002; 2002US-00043665.
XX
XX 05-NOV-1998; 98US-00186489.
XX
XX (INFL ) INT FLAVORS & FRAGRANCES INC.
XX
XX Bolen PL, Cihak PL, Scharpf LG;
XX
XX WPI; 2003-656428/62.
XX
XX Recombinant kid pregastric esterase useful for producing of enzyme
XX modified cheeses acceptable to kosher and vegetarian consumers.
XX
XX Disclosure; Fig 6; 35pp; English.
XX
XX The invention describes an isolated kid pregastric esterase (kPGE)
XX polynucleotide (I) encoding a fully defined sequence of 378 amino acids
XX as given in the specification. Also described are: a transforming nucleic
XX acid molecule comprising a plasmid or vector comprising (i); a non-kid
XX cell capable of recombinantly expressing the kid pregastric esterase,
XX which has been transformed with the transforming nucleic acid; and
XX recombinantly producing kid pregastric esterase. The polynucleotides and
XX methods are useful for producing kPGE in very pure form free of the other
XX substances found in the present commercial rennet formulations. The
XX uncontaminated kPGE is also useful for producing enzyme-modified cheeses
XX (EMC's) acceptable to kosher and vegetarian consumers. The fusion
XX polynucleotide of kid pregastric esterase and polyHis-enterokinase
XX increases expression of esterases and lipases when fused to the N
XX terminal of the enzyme. This sequence represents a linker or primer
XX oligonucleotide used in the creation of a kid lingual tissue cDNA library
XX used in the isolation of a kid pregastric esterase.
XX
XX Sequence 18 BP; 1 A; 2 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAACTCGAG 1
```

RESULT 479
ADL06309
ID ADL06309 standard; DNA; 18 BP.
XX
AC ADL06309;
XX
DT 06-MAY-2004 (first entry)
XX
DE Kid lingual tissue cDNA library associated linker #3.
XX
DE kid pregastric esterase; kPGE; rennet; enzyme-modified cheese; kosher;
KW
KW vegetarian; polyHis-enterokinase; esterase expression; lipase expression;
KW
KW goat; linker; cDNA library; lingual tissue; ss.
XX
OS Synthetic.
XX
XX US6582948-B1.
PN
XX 24-JUN-2003.
PD
XX 14-JAN-2002; 2002US-00043665.
PF
XX 05-NOV-1998; 98US-00186489.
PR
XX (INFL) INT FLAVORS & FRAGRANCES INC.
PA
XX Bolen PL, Cihak PL, Scharpf LG;
PI
XX WPI; 2003-656428/62.
DR
XX
XX Recombinant kid pregastric esterase useful for producing of enzyme
PT modified cheeses acceptable to kosher and vegetarian consumers.
PT
PS Disclosure; Fig 6; 35pp; English.
XX
XX The invention describes an isolated kid pregastric esterase (kPGE)
CC polynucleotide (I) encoding a fully defined sequence of 378 amino acids
CC as given in the specification. Also described are: a transforming nucleic
CC acid molecule comprising a plasmid or vector comprising (I); a non-kid
CC cell capable of recombinantly expressing the kid pregastric esterase,
CC which has been transformed with the transforming nucleic acid; and
CC recombinantly producing kid pregastric esterase. The polynucleotides and
CC methods are useful for producing kPGE in very pure form free of the other
CC substances found in the present commercial rennet formulations. The
CC uncontaminated kPGE is also useful for producing enzyme-modified cheeses
CC (EMC's) acceptable to kosher and vegetarian consumers. The fusion
CC polynucleotide of kid pregastric esterase and polyHis-enterokinase
CC increases expression of esterases and lipases when fused to the N
CC terminal of the enzyme. This sequence represents a linker or primer
CC oligonucleotide used in the creation of a kid lingual tissue cDNA library
CC used in the isolation of a kid pregastric esterase.
XX
SQ Sequence 18 BP; 13 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAAAAAATTCGAG 2594
DB 1 AAAAAAAAAAATTCGAG 18

RESULT 480
ADF31330/C
ID ADF31330 standard; DNA; 18 BP.
XX
AC ADF31330;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human MEGSIN gene related primer seq id 13.
KW

KW nephrotropic; antidiabetic; antiinflammatory; dermatological;
KW immunosuppressive; gene therapy; MEGSIN gene expression supressor;
KW positive transcription regulatory activity; human; MEGSIN;
KW transcriptional regulatory agent; transcription promoter;
KW transcription inhibitor; renal disease;
KW kidney mesangial cell proliferation; Iga glomerulonephritis;
KW systemic lupus erythematosus; SLE; nephropathy; diabetic nephropathy;
KW cryoglobulin; nephropathy; renal disease; PCR; primer; ss.
XX
OS Unidentified.
XX
XX JP2003310268-A.
PN
XX 05-NOV-2003.
PD
XX 23-APR-2002; 2002JP-00121315.
PF
XX 23-APR-2002; 2002JP-00121315.
PR
XX (KURO/) KUROKAWA K.
PA (MIYA/) MIYATA T.
XX
XX WPI; 2004-015356/02.
DR
XX Novel transcriptional regulatory DNA sequence of MEGSIN gene, useful for
PT regulating mesangial cell specific transcription, and for identifying
PT compounds which control expression of MEGSIN gene.
XX
XX Disclosure; SEQ ID NO 13; 20pp; Japanese.
XX
CC The invention describes DNA (I) which has positive transcription
CC regulatory activity having at least 15 continuous bases containing a
CC specific 9 base pair sequence of a fully defined human MEGSIN gene
CC sequence of 4230 nucleotides as given in specification, or a sequence of
CC at least 15 continuous bases of (SI) in which one or more bases are
CC substituted, deleted and/or added other than the specific 9 base pair
CC sequence. (I) is useful for screening of compound which couples with (I),
CC which controls coupling of (I) and AP-1, and which controls
CC transcriptional activity, respectively. A transcriptional regulatory
CC agent (II) containing (I) is useful for regulating transcription of
CC MEGSIN gene. (II) is useful either as a transcription promoter or
CC transcription inhibitor of the MEGSIN gene, and transcription inhibitor
CC is useful for treating renal diseases associated with proliferation of
CC kidney mesangial cells such as Iga glomerulonephritis, systemic lupus
CC erythematosus (SLE), nephropathy, diabetic nephropathy, cryoglobulin and
CC nephropathy. (I) allows identification of compounds that regulate
CC transcription of human MEGSIN gene, and thus for treating MEGSIN gene
CC associated renal diseases. This sequence represents a primer associated
CC with the human MEGSIN gene.
XX
SQ Sequence 18 BP; 9 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3611 GATCATTTCAGTTGTATA 3628
DB 18 GTTCATTTCAGTTGTATA 1

RESULT 481
ADO28562
ID ADO28562 standard; DNA; 18 BP.
XX
AC ADO28562;
XX
DT 12-AUG-2004 (first entry)
XX
DE Displacement oligo for immuno-PCR assay for PSA protein.
XX
XX ss; analyte; detection; prostate specific antigen; peptide nucleic acid;
KW prostate specific antigen.

AC ADO26652;
XX 12-AUG-2004 (first entry)
DE Synthetic leader sequence encoding DNA SEQ ID NO:45.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
KW Synthetic.
XX WO2004042059-A1.
XX 21-MAY-2004.
XX 10-NOV-2003; 2003WO-AU001487.
XX 08-NOV-2002; 2002US-0425163P.
XX (UYQU) UNIV QUEENSLAND.
XX Frazer IH;
XX WPI; 2004-411519/38.
XX P-PSDB; ADO26653.
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX Example 1; SEQ ID NO 45; 86pp; English.
XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX Sequence 18 BP; 0 A; 0 C; 18 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 973 CCCCCCCCCACCGCGCCC 990
DB 18 CCCCCCCCCCCCCCCCCC 1
RESULT 484
ADO26640/C
ID ADO26640 standard; DNA; 18 BP.
XX ADO26640;
XX 12-AUG-2004 (first entry)
XX Synthetic leader sequence encoding DNA SEQ ID NO:33.
DE phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX Synthetic.
XX WO2004042059-A1.
XX 21-MAY-2004.
XX 10-NOV-2003; 2003WO-AU001487.
XX 08-NOV-2002; 2002US-0425163P.
XX (UYQU) UNIV QUEENSLAND.
XX Frazer IH;
XX WPI; 2004-411519/38.
XX P-PSDB; ADO26641.
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX Example 1; SEQ ID NO 33; 86pp; English.
XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX Sequence 18 BP; 0 A; 0 C; 18 G; 0 T; 0 U; 0 Other;

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CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2666 ACAGCAACACCAACCA 2683
Db 18 ACAACACACCAACCA 1

RESULT 485
AD026688
ID AD026688 standard; DNA; 18 BP.
XX
AC AD026688;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:81.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX (UYQU ) UNIV QUEENSLAND.
XX Frazer IH;
XX WPI; 2004-411519/38.
XX P-PSDB; AD026689.
XX
PT Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS Example 1; SEQ ID NO 81; 86pp; English.
XX
CC The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism of interest or part containing a

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CC synthetic polynucleotide constructed from the method above; (4) an
CC organism of interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCC 990
Db 1 CCCCCCCCCCCCCCCCC 18

RESULT 486
AD026708
ID AD026708 standard; DNA; 18 BP.
XX
AC AD026708;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:101.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX (UYQU ) UNIV QUEENSLAND.
XX Frazer IH;
XX WPI; 2004-411519/38.
XX P-PSDB; AD026709.
XX
PT Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS Example 1; SEQ ID NO 101; 86pp; English.
XX
CC The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different

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CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.

XX Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2666 ACAGCAACACCAACCA 2683

DB 1 ACAACAACACCAACACA 18

RESULT 487

ID ADO26642

XX ADO26642 standard; DNA; 18 BP.

AC ADO26642;

XX 12-AUG-2004 (first entry)

XX Synthetic leader sequence encoding DNA SEQ ID NO:35.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

OS Synthetic.

XX WO2004042059-A1.

PD 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

XX (UYQU) UNIV QUEENSLAND.

PA Frazer IH;

XX WPI; 2004-411519/38.
DR P-PSDB; ADO26643.
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
XX codon with a synonymous codon to construct the synthetic polynucleotide.
XX Example 1; SEQ ID NO 35; 86pp; English.

CC The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.

XX Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2667 CAGCAACACCAACCA 2684

DB 1 CAACAACACCAACACA 18

RESULT 488

ID ADS90816

XX ADS90816 standard; DNA; 18 BP.

AC ADS90816;

XX 18-NOV-2004 (first entry)

XX Oligonucleotide of the invention SEQ ID NO:1832.

XX ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.

XX OS Unidentified.
 XX PN WO2004035803-A2.
 XX PD 29-APR-2004.
 XX PF 01-OCT-2003; 2003WO-EP010881.
 XX PR 01-OCT-2002; 2002DE-01045779.
 XX PR 07-JAN-2003; 2003DE-01000096.
 XX PR 17-APR-2003; 2003DE-01017955.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Roekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
 XX PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
 XX DR WPI; 2004-348468/32.
 XX PT Predicting responsiveness of a subject with breast cell proliferative
 XX PT disorder; useful for treating or differentiating breast cell
 XX PT proliferative disorders comprises analyzing methylation pattern of a
 XX FT genomic DNA from the subject.
 XX PS Disclosure; SEQ ID NO 1832; 104pp; English.
 XX CC The invention relates to a novel method for predicting the responsiveness
 XX CC of a subject with a cell proliferative disorder of the breast tissues to
 XX CC a therapy comprising analysing the methylation pattern of a target
 XX CC nucleic acid by contacting at least one of the target nucleic acids in a
 XX CC biological sample obtained from the subject prior to or during treatment.
 XX CC The method of the invention has cytostatic activity, and may have a use
 XX CC in gene therapy. The set of oligonucleotides comprising at least two of
 XX CC the oligomers are useful for detecting the cytosine methylation state
 XX CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
 XX CC methods, nucleic acid, oligonucleotide, and kit are useful for the
 XX CC treatment, characterization, classification and/or differentiation, of
 XX CC breast cell proliferative disorders. The method is also useful for
 XX CC predicting the responsiveness of a subject with a cell proliferative
 XX CC disorder of the breast tissues to a therapy. The present sequence is used
 XX CC in the exemplification of the invention.
 XX SQ Sequence 18 BP; 3 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3275 TTTTAATTGTAATGGTT 3292
 ||||| ||||| |||||
 Db 1 TTTTGATTGTAGATGGTT 18
 RESULT 489
 ABN87920/C
 ID ABN87920 standard; DNA; 15 BP.
 XX AC ABN87920;
 XX AC
 XX DT 12-AUG-2002 (first entry)
 XX DE Human GSR allele specific oligonucleotide primer SEQ ID NO:39.
 XX KW Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;
 XX KW gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;
 XX KW primer; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 XX FT misc_feature 14
 XX FT /*tag= a

FT XX /note= "polymorphic base"
 XX PN WO200242320-A2.
 XX PD 30-MAY-2002.
 XX PF 13-NOV-2001; 2001WO-US046473.
 XX PR 10-NOV-2000; 2000US-0247202P.
 XX PA (GENA-) GENAISANCE PHARM INC.
 XX PI Bieglecki KM, Sanchis A, Sausker EA, Sun X;
 XX PI WPI; 2002-471719/50.
 XX DR New genetic variants of Glutathione reductase isogenes, useful for
 XX PT improving efficiency and reliability in drug development for treating
 XX PT hemolytic anemia.
 XX PS Claim 14; Page 14; 137pp; English.
 XX CC The present invention describes genetic variants of the human glutathione
 XX CC reductase (GSR) gene (I). (I) has antianaemic activity and can be used in
 XX CC gene therapy. (I) can be used in screening for drugs targeting (I) that
 XX CC are useful for treating haemolytic anaemia. Methods from the present
 XX CC invention can be used: for improving the efficiency and reliability of
 XX CC several steps in the discovery and development of drugs for treating
 XX CC diseases associated with GSR activity; for haplotyping, which is also
 XX CC used by the pharmaceutical research scientist to validate GSR as a
 XX CC candidate target for treating a specific condition or disease predicted
 XX CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the
 XX CC design of clinical trials for treating a specific condition of disease
 XX CC associated with GSR activity; and for screening compounds targeting GSR.
 XX CC (I) is useful in studying the expression and function of GSR, and in
 XX CC expressing GSR protein for use in screening for candidate drugs to treat
 XX CC diseases related to GSR activity. (I) is also useful in studying the
 XX CC effect of the variation on the biological activity of GSR as well as on
 XX CC the binding affinity of candidate drugs targeting GSR for the treatment
 XX CC of haemolytic anaemia. The present sequence represents an allele specific
 XX CC oligonucleotide (ASO) primer for the human GSR gene, which is given in
 XX CC the exemplification of the present invention. N.B. The polymorphic base
 XX CC (showing a single nucleotide polymorphism) in the ASO primer is shown
 XX CC using an IUPAC ambiguity code (as given in the present invention)
 XX SQ Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 1 Other;
 Query Match 0.3%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2574 TTTAAAAA 2588
 ||:|||||
 Db 15 TTTAAAAA 1
 RESULT 490
 AAQ78445/C
 ID AAQ78445 standard; DNA; 16 BP.
 XX AC AAQ78445;
 XX AC
 XX DT 25-MAR-2003 (revised)
 XX DT 27-JUN-1995 (first entry)
 XX DE TGF-beta gene phosphorothioate antisense oligonucleotide.
 XX KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 XX KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 XX KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 XX KW immunosuppression; oligonucleotide; ss.
 XX OS Synthetic.

XX WO9425588-A2.
 PN 10-NOV-1994.
 PD
 XX
 XX 29-APR-1994; 94WO-EP001362.
 XX
 XX 30-APR-1993; 93EP-00107089.
 XX 13-MAY-1993; 93EP-00107849.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 PI Bogdahn U;
 XX WPI; 1994-358266/44.
 DR
 XX New transforming growth factor beta anti-sense oligo:nucleotide(s) - for
 PT treating immunosuppression, tumours, etc.
 PT
 XX Claim 6; Page 51; 74pp; English.
 PS
 XX The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 16 BP; 1 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
 SQ Query Match 0.3%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1851 CACCACAAAGACAGGA 1866
 Db 16 CACCATAAAGACAGGA 1
 RESULT 491
 AAV48961/c
 ID AAV48961 standard; DNA; 16 BP.
 XX
 XX AAV48961;
 AC
 XX 15-OCT-1998 (first entry)
 DT
 XX TGF-beta2 antisense oligonucleotide TGF-beta2-32.
 DE
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX EP856579-A1.
 PN
 XX 05-AUG-1998.
 PD
 XX 31-JAN-1997; 97EP-00101531.
 PF
 XX 31-JAN-1997; 97EP-00101531.
 XX
 XX 31-JAN-1997; 97EP-00101531.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Brysch W;
 PI WPI; 1998-400910/35.
 DR

PI Schlingensiepen K, Brysch W;
 XX WPI; 1998-400910/35.
 XX
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 XX Claim 10; Fig 8a; 286pp; English.
 PS
 XX AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 16 BP; 5 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2245 CTAACCTTCGTGCTGG 2260
 Db 16 CCAACTTCGTGCTGG 1
 RESULT 492
 AAV48954/c
 ID AAV48954 standard; DNA; 16 BP.
 XX
 XX AAV48954;
 AC
 XX 15-OCT-1998 (first entry)
 DT
 XX TGF-beta2 antisense oligonucleotide TGF-beta2-25.
 DE
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 KW modulate; gene expression; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX EP856579-A1.
 PN
 XX 05-AUG-1998.
 PD
 XX 31-JAN-1997; 97EP-00101531.
 PF
 XX 31-JAN-1997; 97EP-00101531.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Brysch W;
 PI WPI; 1998-400910/35.
 DR

XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 XX
 PS Claim 10; Fig 8a; 286pp; English.
 XX
 CC AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 16 BP; 4 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2078 CTCTACAGACTGAG 2093
 Db 16 CTCTACAGACTTGAG 1

RESULT 493
 AAX18362/c
 ID AAX18362 standard; DNA; 16 BP.
 AC AAX18362;
 XX
 XX 11-MAY-1999 (first entry)
 DT
 XX
 DE RT-PCR primer of the invention SEQ ID 3.
 XX
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 XX JP11032765-A.
 PN
 XX 09-FEB-1999.
 PD
 XX 18-JUL-1997; 97JP-00208312.
 PF
 XX 18-JUL-1997; 97JP-00208312.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX WPI; 1999-183822/16.
 DR
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX
 PS Disclosure; Page 10; 19pp; Japanese.
 XX
 XX This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta = thymine; n =
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 SQ Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAAACA 2816
 Db 16 TGAATAAAAAAAAAAAAA 1

RESULT 494
 AAX18363/c
 ID AAX18363 standard; DNA; 16 BP.
 XX
 AC AAX18363;
 XX
 XX 11-MAY-1999 (first entry)
 DT
 XX
 DE RT-PCR primer of the invention SEQ ID 4.
 XX
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 XX JP11032765-A.
 PN
 XX 09-FEB-1999.
 PD
 XX 18-JUL-1997; 97JP-00208312.
 PF
 XX 18-JUL-1997; 97JP-00208312.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX WPI; 1999-183822/16.
 DR
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX
 PS Disclosure; Page 10; 19pp; Japanese.
 XX
 XX This sequence represents a primer of the invention. The invention relates

Query Match 0.3%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	929	AGAAAAAACAACAAA	944
DB	16	AGAAAAAACAACAAA	1
RESULT 495			
ADL46313/C			
ID	ABL46313	standard; DNA; 16 BP.	
XX	AC	ABL46313;	
XX	DT	26-APR-2002 (first entry)	
XX	DE	Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:280.	
XX	KW	Nucleic acid accessible hybridisation site; detection; hybridisation;	
XX	KW	characterisation; identification; nucleic acid structure; diagnosis;	
XX	KW	PCR primer; probe; ss.	
XX	OS	Mus sp.	
XX	OS	Synthetic.	
XX	PN	WO200198537-A2.	
XX	XX	27-DEC-2001.	
XX	PD		
XX	PF	15-JUN-2001; 2001WO-US019401.	
XX	XX		
XX	PR	17-JUN-2000; 2000US-0212308P.	
XX	PR	15-JUN-2001; 2001US-00212308.	
XX	XX	(THIR-) THIRD WAVE TECHNOLOGIES INC.	
XX	PI	Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;	
XX	XX	WPI; 2002-049698/06.	
XX	DR		
XX	PT	Identifying oligonucleotides hybridizing to nucleic acids containing	
XX	PT	secondary structure, useful in clinical diagnosis, comprises identifying	
XX	PT	primers that interact with the target to form an extension product under	
XX	PT	amplification conditions.	
XX	XX		
XX	PS	Claim 48; Fig 79A; 409pp; English.	
XX	CC	The present invention describes a method for identifying oligonucleotides	
XX	CC	with desired hybridisation properties to nucleic acid targets containing	
XX	CC	acid having at least one accessible and one inaccessible site. Primers	
XX	CC	that form an extension product are identified as the oligonucleotides	
XX	CC	which can interact with the folded target nucleic acid. Oligonucleotides	
XX	CC	from the present invention can be used in novel detection methods for	
XX	CC	clinical diagnostic purposes, including the detection and identification	
XX	CC	of pathogenic organisms (e.g. HIV). The method allows the ability to	
XX	CC	rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent	
XX	CC	sequences used in the exemplification of the present invention	
XX	XX		
SQ	Sequence 16 BP; 1 A; 7 C; 1 G; 7 T; 0 U; 0 Other;		
Query Match	0.3%;	Score 14.4; DB 1; Length 16;	
Best Local Similarity	93.8%;	Pred. No. 2.3e+02;	
Matches	15; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	65	TGGGAGAGAAAGAGAG	80
DB	16	TGGGAGAGAAACAGAG	1
RESULT 496			
ADL49413			
ID	ADL49413	standard; RNA; 17 BP.	
XX	XX		
AC	ADL49413;		
XX	XX		
DT	20-MAY-2004	(first entry)	
XX	DE	Human PKR substrate sequence #527.	
XX	XX		
XX	KW	antisense oligonucleotide; neurite growth inhibitor; NOGO;	
XX	KW	prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;	
XX	KW	protein kinase PKR; cerebrovascular accident;	
XX	KW	central nervous system injury; CNS injury; spinal cord injury; cancer;	
XX	KW	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;	
XX	KW	restenosis; asthma; Crohn's disease; diabetes; obesity;	
XX	KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;	
XX	KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;	
XX	KW	allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;	
XX	KW	substrate; ds.	
XX	OS	Unidentified.	
XX	XX		
XX	PN	WO200281628-A2.	
XX	XX		
XX	PD	17-OCT-2002.	
XX	XX		
XX	PF	03-APR-2002; 2002WO-US010512.	
XX	XX		
XX	PR	05-APR-2001; 2001US-00827395.	
XX	PR	29-MAY-2001; 2001US-0294412P.	
XX	PR	28-AUG-2001; 2001US-0315315P.	
XX	XX	(RIBO-) RIBOZYME PHARM INC.	
XX	PA		
XX	XX		
XX	PI	Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;	
XX	XX	WPI; 2003-058513/05.	
XX	DR		
XX	XX		
XX	PT	Novel enzymatic nucleic acid that down-regulates expression of neurite	
XX	PT	growth inhibitor receptor, prostaglandin D2 receptor. IkappaB kinase or	
XX	PT	protein kinase PKR genes, for treating cancer and inflammatory disease.	
XX	XX		
XX	PS	Claim 59; SEQ ID NO 2946; 317pp; English.	
XX	CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)	
XX	CC	that down regulate the expression or inhibit the function of a receptor	
XX	CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),	
XX	CC	IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the	
XX	CC	invention are useful for treating: cerebrovascular accident, central	
XX	CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,	
XX	CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,	
XX	CC	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune	
XX	CC	disease, lupus, multiple sclerosis, transplant/graft rejection, and allergic	
XX	CC	ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic	
XX	CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The	
XX	CC	nucleic acids of the invention are also useful for down-regulating the	
XX	CC	expression of a target gene and as a diagnostic tool to examine genetic	
XX	CC	drifts and mutations within diseased cells or to detect the presence of a	
XX	CC	target RNA in a cell. The present RNA sequence represents a human PKR	
XX	CC	substrate sequence.	
XX	XX		
SQ	Sequence 17 BP; 4 A; 1 C; 1 G; 0 T; 11 U; 0 Other;		
Query Match	0.3%;	Score 14.4; DB 1; Length 17;	
Best Local Similarity	25.0%;	Pred. No. 2.6e+02;	
Matches	4; Conservative	11; Mismatches 1; Indels 0; Gaps 0;	
QY	2745	TTTTTTTTTTTAAAGGA	2760
DB	1	UUUUUUUUUUUAAAGA	16
RESULT 497			
ADL49412			
ID	ADL49412	standard; RNA; 17 BP.	
XX	XX		
AC	ADL49412;		
XX	XX		

```
DT 20-MAY-2004 (first entry)
XX Human PKR substrate sequence #526.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX restenosis; asthma; Crohn's disease; diabetes; obesity;
XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX substrate; ds.
XX
XX Unidentified.
XX
XX WO200281628-A2.
XX
XX 17-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010512.
XX
XX 05-APR-2001; 2001US-00827395.
XX
XX 23-MAY-2001; 2001US-0294412P.
XX
XX 28-AUG-2001; 2001US-0315315P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
XX WPI; 2003-058513/05.
XX
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX Claim 59; SEQ ID NO 2945; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX disease, lupus, multiple sclerosis, transplant/graft rejection, and allergic
XX ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX nucleic acids of the invention are also useful for down-regulating the
XX expression of a target gene and as a diagnostic tool to examine genetic
XX drifts and mutations within diseased cells or to detect the presence of a
XX target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.
XX
XX
XX Sequence 17 BP; 4 A; 0 C; 1 G; 0 T; 12 U; 0 Other;
XX
XX Query Match 0.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 25.0%; Pred. No. 2.6e+02;
XX Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2745 TTTTTCCTTTTAAAGGA 2760
XX : : : : : : : : : :
XX 2 UUUUUUUUUUAAAGA 17
XX
XX
XX RESULT 498
XX AAQ26183
XX ID AAQ26183 standard; DNA; 17 BP.
XX
XX AC AAQ26183;
XX
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```
DT 25-MAR-2003 (revised)
XX 04-JAN-1993 (first entry)
XX
XX HLA-DR beta sub-type tailed probe DRB79 hybridising region.
XX
XX Tissue typing; identity determination; disease susceptible; ss.
XX Synthetic.
XX
XX WO9210589-A1.
XX
XX 25-JUN-1992.
XX
XX 06-DEC-1991; 91WO-US009294.
XX
XX 06-DEC-1990; 90US-00623098.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Erlich HA, Begovich AB, Bugawan T, Griffith RL, Scharf SJ;
XX Apple RJ;
XX
XX WPI; 1992-234644/28.
XX
XX Method for determining HLA-DR beta sub-type in DNA sample - comprises
XX amplification and hybridisation with probes and primers, useful in tissue
XX typing.
XX
XX Example; Page 39; 90pp; English.
XX
XX The sequence is that of the hybridising region of tailed probe DRB79 for
XX use in a method for determining HLA-DR beta sub-type in a nucleic acid
XX sample. The method allows specific nucleic acid sequences of the second
XX exon of HLA-DR beta genes to be amplified then probed for identification
XX of polymorphic sequences. The amplified DNA is useful for typing
XX homozygous or heterozygous samples from a variety of sources and for
XX detecting allelic variants not distinguishable by serological methods.
XX The typing system can be used in a reverse dot blot format which is
XX simple and rapid to perform, produces detectable signals in minutes and
XX can be utilised in tissue typing, determination of individual identity
XX and identifying disease susceptible individuals. See also AAQ26092 -
XX Q26367. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 365 CCGCCTGGAGCAAGAA 380
XX : : : : : : : : : :
XX 1 CCTCCTGGAGCAAGAA 16
XX
XX
XX RESULT 499
XX AAQ52216/c
XX ID AAQ52216 standard; RNA; 17 BP.
XX
XX AC AAQ52216;
XX
XX 25-MAR-2003 (revised)
XX 26-MAY-1994 (first entry)
XX
XX Neuroblastoma specific mRNA ribozyme cleavable nucleotide (1471).
XX
XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
XX actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
XX adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
XX human; chronic myelogenous leukemia; CML; follicular lymphoma;
XX B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
XX neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
XX hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.
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OS Homo sapiens.
XX WO9323057-A1.
XX 25-NOV-1993.
XX 13-MAY-1993; 93WO-US004573.
XX 14-MAY-1992; 92US-00882822.
XX 14-MAY-1992; 92US-00882885.
XX 26-AUG-1992; 92US-00936110.
XX 26-AUG-1992; 92US-00936421.
XX 26-AUG-1992; 92US-00936422.
XX 26-AUG-1992; 92US-00936531.
XX 26-AUG-1992; 92US-00936532.
XX 07-DEC-1992; 92US-00987131.
XX 19-JAN-1993; 93US-00006122.
XX 19-JAN-1993; 93US-00008910.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Draper KG;
XX WPI; 1993-386203/48.
XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
XX with tumours or mRNA expressed from gene encoding multiple drug
XX resistance.
XX Claim 3; Fig 10; 69pp; English.
XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are
XX associated with development or maintenance of chronic myelogenous
XX leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
XX lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
XX leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
XX The full length mRNAs containing these target sequences, encode aberrant
XX cellular proteins which are able to control cellular proliferation and
XX are directly linked to a leukemic phenotype. These target sequences are
XX identified by the ribozyme of the invention. The ribozymes is formed in a
XX hammerhead motif, but may also be formed in the motif of a hairpin,
XX hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
XX may be used to inhibit the development or expression of a transformed
XX phenotype in man and other animals by modulating expression of the
XX corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
XX and transformed cells elicits inhibition of the transformed state.
XX Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
XX mechanism of drug resistance used by transformed cells and thus enhances
XX drug therapies for tumours. The ribozymes may also be used to study
XX genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX Sequence 17 BP; 9 A; 2 C; 5 G; 0 T; 1 U; 0 Other;
XX Query Match 0.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 869 TCATTCTCTCTCTT 884
DB 16 TCATTCTCTCTCTT 1
RESULT 500
AAQ51975/c
ID AAQ51975 standard; RNA; 17 BP.
XX AAQ51975;
AC AAQ51975;
XX 25-MAR-2003 (revised)
DT 26-MAY-1994 (first entry)
XX
DE B-cell mRNA ribozyme cleavable nucleotide 297.
XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
XX actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
XX adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
XX human; chronic myelogenous leukemia; CML; follicular lymphoma;
XX B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
XX neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
XX hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX Homo sapiens.
OS WO9323057-A1.
XX 25-NOV-1993.
XX 13-MAY-1993; 93WO-US004573.
XX 14-MAY-1992; 92US-00882822.
XX 14-MAY-1992; 92US-00882885.
XX 26-AUG-1992; 92US-00936110.
XX 26-AUG-1992; 92US-00936421.
XX 26-AUG-1992; 92US-00936422.
XX 26-AUG-1992; 92US-00936531.
XX 26-AUG-1992; 92US-00936532.
XX 07-DEC-1992; 92US-00987131.
XX 19-JAN-1993; 93US-00006122.
XX 19-JAN-1993; 93US-00008910.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Draper KG;
XX WPI; 1993-386203/48.
XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
XX with tumours or mRNA expressed from gene encoding multiple drug
XX resistance.
XX Claim 3; Fig 7; 69pp; English.
XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are
XX associated with development or maintenance of chronic myelogenous
XX leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
XX lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
XX leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
XX The full length mRNAs containing these target sequences, encode aberrant
XX cellular proteins which are able to control cellular proliferation and
XX are directly linked to a leukemic phenotype. These target sequences are
XX identified by the ribozyme of the invention. The ribozymes is formed in a
XX hammerhead motif, but may also be formed in the motif of a hairpin,
XX hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
XX may be used to inhibit the development or expression of a transformed
XX phenotype in man and other animals by modulating expression of the
XX corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
XX and transformed cells elicits inhibition of the transformed state.
XX Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
XX mechanism of drug resistance used by transformed cells and thus enhances
XX drug therapies for tumours. The ribozymes may also be used to study
XX genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX Sequence 17 BP; 4 A; 7 C; 4 G; 0 T; 2 U; 0 Other;
XX Query Match 0.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2915 TGCAGTGGTGCCCTC 2930
DB 17 TGAAGTGGTGCCCTC 2

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Best Local Similarity	37.5%	Pred. No. 2.6e+02;	Mismatches	6;	Conservative	9;	Mismatches	1;	Indels	0;	Gaps	0;
RESULT 501												
AAAG3946												
ID	AAAG3946	standard; RNA; 17 BP.										
XX	AC											
XX	AC	AAAG3946;										
XX	XX											
DT	DT	20-JUL-1999 (first entry)										
XX	DE											
XX	DE	Rabbit stromelysin hammerhead target SEQ ID NO:578.										
XX	XX											
XX	KW	Arthritic condition; graft tolerance; immune response; target; cleavage;										
XX	KW	hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;										
XX	KW	stromelysin; synovial membrane; joint; arthritis; osteoarthritis;										
XX	KW	rheumatoid arthritis; autoimmune disease; allergy; inflammation;										
XX	KW	diagnosis; ss.										
XX	XX											
XX	OS	Oryctolagus cuniculus.										
XX	XX											
XX	PN	WO9618736-A2.										
XX	XX											
PD	PD	20-JUN-1996.										
XX	XX											
XX	PF	22-NOV-1995; 95WO-US015516.										
XX	XX											
XX	PR	13-DEC-1994; 94US-00354920.										
XX	PR	23-DEC-1994; 94US-00363253.										
XX	PR	23-DEC-1994; 94US-00363254.										
XX	PR	17-FEB-1995; 95US-00390850.										
XX	PR	20-APR-1995; 95US-00426124.										
XX	PR	02-MAY-1995; 95US-00432874.										
XX	PR	04-MAY-1995; 95US-00434509.										
XX	PR	07-JUL-1995; 95US-0000951P.										
XX	PR	07-JUL-1995; 95US-0000974P.										
XX	PR	07-AUG-1995; 95US-00512861.										
XX	PR	05-OCT-1995; 95US-00541365.										
XX	XX	(RIBO-) RIBOZYME PHARM INC.										
XX	PA											
XX	PI	Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;										
XX	PI	Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;										
XX	PI	Karpeisky A, Thompson JD, Modak A, Burgin A;										
XX	XX	WPI; 1996-300653/30.										
XX	DR											
XX	XX	Enzymatic nucleic acid molecules having a hammer-head motif - used for										
XX	PT	the treatment of arthritis, induction of graft tolerance or treatment of										
XX	PT	auto-immune diseases.					</					

CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention

SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;
 Query Match 0.3%; Score 14.4; DS 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.6e+02;
 Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1034 TTCTTTTAAAGGAA 1049
Db 1 UUCAUUUUAAAGGAA 16

RESULT 503
AAX71256

ID AAX71256 standard; RNA; 17 BP.

AC AAX71256;

DT 28-JUL-1999 (first entry)

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XX DE Human B-raf substrate nucleotide position 2458.
XX DE
XX DE Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9850530-A2.
XX
XX PD 12-NOV-1998.
XX
XX PF 05-MAY-1998; 98WO-US009249.
XX
XX PR 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
XX PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX DR WPI; 1999-009494/01.
XX
XX DR Identifying new catalytic nucleic acid that modulates selected processes
XX - especially ribozymes that cleave Raf RNA for treating cancer,
XX restenosis, and also new ribozymes and modified nucleoside triphosphates
XX used as antiviral agents and synthons.
XX
XX PS Claim 177; Page 172; 259pp; English.
XX
XX CC A method has been developed for the identification of a nucleic acid
XX capable of modulating a process in a biological system. The method
XX comprises: (a) introducing into the system a random library of nucleic
XX acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX in systems where modulation has occurred and/or determining the sequence
XX of at least part of the SBDs in such systems. Nucleic acid molecules with
XX endonuclease activity and catalytic activity, from the present invention,
XX are used to modulate gene expression in plant and mammalian cells and to
XX cleave target nucleic acid, particularly for treating systemic diseases
XX caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX ascites and infection. They may also be used to detect genetic drift and
XX mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX with RNA-cleaving activity that modulate expression of the Raf gene, are
XX used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX generally any condition associated with the level of c-raf. Introduction
XX of sugar/phosphate modifications increases stability against nuclease and
XX activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 17 BP; 2 A; 2 C; 2 G; 0 T; 11 U; 0 Other;
Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 31.2%; Pred. No. 2.6e+02;
Matches 5; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
QY 2744 CTTTCTTTTAAAGG 2759
|: ::::::::::|||
Db 1 CUCUUUUUUUAAGG 16
RESULT 506

```

```

AAV93709
ID AAV93709 standard; RNA; 17 BP.
XX
AC AAV93709;
XX
XX DT 18-FEB-1999 (first entry)
XX
DE Human B-raf substrate nucleotide position 2456.
XX
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9850530-A2.
XX
XX PD 12-NOV-1998.
XX
XX PF 05-MAY-1998; 98WO-US009249.
XX
XX PR 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
XX PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX DR WPI; 1999-009494/01.
XX
XX DR Identifying new catalytic nucleic acid that modulates selected processes
XX - especially ribozymes that cleave Raf RNA for treating cancer,
XX restenosis, and also new ribozymes and modified nucleoside triphosphates
XX used as antiviral agents and synthons.
XX
XX PS Claim 177; Page 172; 259pp; English.
XX
XX CC A method has been developed for the identification of a nucleic acid
XX capable of modulating a process in a biological system. The method
XX comprises: (a) introducing into the system a random library of nucleic
XX acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX in systems where modulation has occurred and/or determining the sequence
XX of at least part of the SBDs in such systems. Nucleic acid molecules with
XX endonuclease activity and catalytic activity, from the present invention,
XX are used to modulate gene expression in plant and mammalian cells and to
XX cleave target nucleic acid, particularly for treating systemic diseases
XX caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX ascites and infection. They may also be used to detect genetic drift and
XX mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX with RNA-cleaving activity that modulate expression of the Raf gene, are
XX used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX generally any condition associated with the level of c-raf. Introduction
XX of sugar/phosphate modifications increases stability against nuclease and
XX activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 17 BP; 2 A; 3 C; 1 G; 0 T; 11 U; 0 Other;
Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

```

QY	2743 TCTTTTTCCTTAAG 2758 : : :::: Db 2 UCUCUUUUUUUAAG 17
 RESULT 507 AAx14708 ID AAX14708 standard; DNA; 17 BP. XX AC XX AAX14708; DT DT XX 24-MAR-1999 (first entry) XX DE Triple helix forming nucleotides 1205-1218 of superoxide dismutase gene. XX KW Triple-helix forming region; Triplex formation; DNA detection; KW identification; bacteria; oncogene; virus; ds. XX AC XX Homo sapiens. OS XX PN US5861244-A. XX 19-JAN-1999. XX 24-MAR-1999 (first entry) XX DE Triple helix forming nucleotides 1205-1218 of superoxide dismutase gene. XX KW Triple-helix forming region; Triplex formation; DNA detection; KW identification; bacteria; oncogene; virus; ds. XX AC XX Homo sapiens. OS XX PN US5861244-A. XX 19-JAN-1999. XX 24-MAR-1999 (first entry)	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	975 CCCCCCACCCTCC 990 Db 2 CCCCCCACCCTCC 17
 RESULT 508 AAx14705 ID AAX14705 standard; DNA; 17 BP. XX AC XX AAX14705; AC AC XX 24-MAR-1999 (first entry) DT DT XX	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 RESULT 509 AAZ57107 ID AAZ57107 standard; DNA; 17 BP. XX AC XX AAZ57107; DT DT XX 24-MAR-2000 (first entry) XX DE Human FCMD-causing protein related oligonucleotide. XX KW Fukuyama-type congenital muscular dystrophy-causing protein; FCMD; KW detection; muscular dystrophy; diagnosis; ss. XX OS XX Homo sapiens. XX PN JP11313682-A. XX	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 1 A; 14 C; 0 G; 2 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16
 Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;	
 Query Match 0.3%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2930 CCCCGTCCCTTCCTCC 2945 Db 1 CCCCCCCTTCCTCC 16

[illegible]

PD 16-NOV-1999.
 XX 30-APR-1998; 98JP-00137703.
 XX 30-APR-1998; 98JP-00137703.
 PR (SAKA) OTSUKA PHARM CO LTD.
 XX WPI; 2000-090363/08.
 XX A Fukuyama-type congenital muscular dystrophy-causing protein - for
 PT preparing its specific antibody.
 XX
 XX Example 2; Page 13; 32pp; Japanese.
 XX The present invention describes a Fukuyama-type congenital muscular
 CC dystrophy (FCMD)-causing protein isolated from human. Also described in
 CC the present invention is a method for the detection of gene abnormality
 CC for FCMD diagnosis by detecting the presence of a mutated FCMD-causing
 CC DNA having a mutation causing functional insufficiency of the FCMD-
 CC causing protein coded in the base sequence of 7389 nucleotides in the
 CC gene of a person to be tested. The FCMD-causing protein is useful in the
 CC preparation of its specific antibody. The present sequence represents an
 CC oligonucleotide used in the exemplification of the present invention
 XX
 XX Sequence 17 BP; 12 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2576 AAAAAAAAAAAATTG 2591
 DB 1 AAAAAAAAAAAATTG 16
 RESULT 510
 ID AAF05267 standard; DNA; 17 BP.
 AC AAF05267;
 XX 16-FEB-2001 (first entry)
 DT Hammerhead ribozyme substrate #2486.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 OS WO200061729-A2.
 PN 19-OCT-2000.
 PD 11-APR-2000; 2000WO-US009721.
 PF 12-APR-1999; 99US-0129390P.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Zwick M, Pavco P, Mcswiggen J;
 PI WPI; 2000-647423/62.
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX Claim 18; Page 113; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes

CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 XX Sequence 17 BP; 3 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 424 AGCAGCAGCGGGCGC 439
 DB 2 AGCAGTAGCGGGCGC 17
 RESULT 511
 ID AAF06339/c
 XX AAF06339 standard; DNA; 17 BP.
 AC AAF06339;
 XX 16-FEB-2001 (first entry)
 DT Hammerhead ribozyme substrate #3136.
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 OS WO200061729-A2.
 PN 19-OCT-2000.
 PD 11-APR-2000; 2000WO-US009721.
 PF 12-APR-1999; 99US-0129390P.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Zwick M, Pavco P, Mcswiggen J;
 PI WPI; 2000-647423/62.
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX Claim 42; Page 127; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 XX Sequence 17 BP; 2 A; 1 C; 1 G; 0 T; 13 U; 0 Other;
 SQ
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3805 AAAAGATAAAACCAA 3820
 DB 17 AAAAGATAAAACCAA 2

RESULT 512
 AAF03387/c
 ID AAF03387 standard; DNA; 17 BP.
 XX
 AC AAF03387;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #1682.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 37; Page 94; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SI Sequence 17 BP; 3 A; 2 C; 2 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1620 TCAACAATGGAGAAA 1635
 DB ||||||| |||||
 17 TCACAATGAAGAAA 2
 XX
 RESULT 513
 AAF06340/c
 ID AAF06340 standard; DNA; 17 BP.
 XX
 AC AAF06340;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #3137.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1620 TCAACAATGGAGAAA 1635
 DB ||||||| |||||
 17 TCACAATGAAGAAA 2
 XX
 RESULT 514
 AAF03071/c
 ID AAF03071 standard; DNA; 17 BP.
 XX
 AC AAF03071;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #1366.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 37; Page 87; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid

XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 42; Page 127; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SI Sequence 17 BP; 1 A; 2 C; 1 G; 0 T; 13 U; 0 Other;
 XX
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 3805 AAAAGATAAAACCAA 3820
 DB ||||||| |||||
 16 AAAAGATAAAACCAA 1
 XX
 RESULT 514
 AAF03071/c
 ID AAF03071 standard; DNA; 17 BP.
 XX
 AC AAF03071;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #1366.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 37; Page 87; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid

CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 826 GAGTTCAGATCAGCCA 841
 Db 16 GACTTCAGATCAGCCA 1

RESULT 515
 AAH95613
 ID AAH95613 standard; RNA; 17 BP.

XX AAH95613;
 AC
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human Chk1 ribozyme substrate SEQ ID NO: 1038.

XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 KW RNA cleavage; cancer; ss.

OS Homo sapiens.
 XX
 XX WO200157206-A2.

XX 09-AUG-2001.
 PD
 PF 02-FEB-2001; 2001WO-US003504.
 XX
 PR 03-FEB-2000; 2000US-0179983P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (FATT/) FATTAEY A R.

XX Fattaey AR, Jarvis T, Mcswiggen J, Boohar RN, Holman PS;
 XX
 DR WPI; 2001-496922/54.

XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 PT molecules, which downregulates expression of a checkpoint kinase-1 gene,
 PT useful for treating colorectal, lung, breast or prostate cancers.

XX Claim 4; Page 79; 115pp; English.

XX The present invention provides nucleic acid molecules capable of
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
 CC gene. These may be antisense or ribozyme sequences, and are useful in the
 CC treatment of diseases associated with conditions affected by Chk1 levels,
 CC including cancer. The present sequence is an oligonucleotide described in
 CC the exemplification of the invention

XX Sequence 17 BP; 11 A; 4 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.6e+02;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 932 AAAAAAAAAAACCT 947
 Db 1 AAAAAAAAAACUACCU 16

RESULT 516
 ABK00233
 ID ABK00233 standard; RNA; 17 BP.
 XX
 AC ABK00233;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Hammerhead Ribozyme #233.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI
 DR WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 PS
 XX Claim 88; Page 69; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA motif) or
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1587 AGACCTCTTTCAGAA 1602
 Db 2 AGAUCUACUUCAGAA 17
 RESULT 517
 ABQ99687
 ID ABQ99687 standard; DNA; 17 BP.
 XX
 AC ABQ99687;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Murine Ikbkap exon 27 acceptor site.
 XX
 KW Murine; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; ds;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; Carrier screening.
 XX
 OS Mus sp.
 XX
 PN WO200259381-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 07-JAN-2002; 2002WO-US000473.
 XX
 PR 06-JAN-2001; 2001US-0260080P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Slaugenhaupt S, Gusella JF;
 XX
 DR WPI; 2002-674806/72.
 XX
 PT New IKBKAP genes with mutations, useful for identifying a subject with
 PT familial dysautonomia (FD), or for rapid carrier screening in the
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
 PT prenatal diagnosis.
 XX
 PS Disclosure; Fig 11; 109pp; English.
 XX
 CC The present invention relates to methods and compositions useful for
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM
 CC 223900). It was found that mutations in the IKBKAP gene (see ABQ80565)
 CC are associated with FD. The mutation associated with the major haplotype
 CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
 CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
 CC patients, although they continue to express varying levels of wild-type
 CC message in a tissue-specific manner. The mutation associated with the
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
 CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
 CC This bp mutation causes an arginine to proline missense mutation (R696P)
 CC in the IKBKAP protein, which is predicted to disrupt a potential
 CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for

CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
 CC gene maps to chromosome 9q31. A mouse model of FD was created in an
 CC example from the invention. Expression of murine Ikbkap was examined
 CC using both mouse embryo and adult mouse multiple tissue Northern blots.
 CC The blots were probed with a 1045bp PCR fragment that contains exons 2
 CC through 11, which was generated using PCR primers ABQ80563-ABQ80564.
 CC ABQ99662-ABQ99733 are the murine Ikbkap exon and intron boundaries
 XX
 SQ Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2745 TTTTITTTTTTAAAGGA 2760
 Db 2 TTTTITTTTTTCAGGA 17
 RESULT 518
 ABT39218
 ID ABT39218 standard; DNA; 17 BP.
 XX
 AC ABT39218;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 4855.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004208.
 XX
 PR 17-SEP-2001; 2001PR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 601; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (antisense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these

CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX

SQ Sequence 17 BP; 9 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1727 GATCCTTAATCCCAA 1742
 DB 1 GATCATTAAATCCCAA 16

RESULT 519

ABZ59895
 ID ABZ59895 standard; RNA; 17 BP.

AC ABZ59895;

XX 21-MAR-2003 (first entry)

DE Human K-Ras DNzyme substrate #7.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US016940.

XX 29-MAY-2001; 2001US-0294140P.

PR 06-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J;

DR WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 85; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention

XX Sequence 17 BP; 3 A; 5 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 422 GCAGGCAGCAGCGCG 437
 DB 2 GGAGGCAGCAGCGCG 17

RESULT 520

ACC66553
 ID ACC66553 standard; DNA; 17 BP.

XX ACC66553;

XX 01-JUL-2003 (first entry)

XX Murine oligonucleotide associated with tumour supression, SEQ ID 3800.
 DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.

XX Mus musculus.

XX WO2003025176-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004210.

XX 17-SEP-2001; 2001FR-00011979.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-333167/31.

XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumours and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

XX Disclosure; Page 475; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC6806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia

XX Sequence 17 BP; 8 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2566 ATCAGTGTTTAAAAA 2581
 DB 2 ATCAGTCTTTAAAAA 17

RESULT 521

ACC64890
 ID ACC64890 standard; DNA; 17 BP.

XX ACC64890;

XX 01-JUL-2003 (first entry)

PS Disclosure; Page 310; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC sequence having at least 80% identity, after optimal alignment, with the

CC nucleotides, a sequence that hybridizes under stringent conditions with

CC the nucleotides, or the complement, or corresponding RNA, of the

CC nucleotides. The nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro

CC sense and antisense sequences, of nucleotides involved in tumour

CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as

CC experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors), the encoded polypeptides and antibodies

CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours

CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis

CC and/or prognosis of these diseases. The nucleotides and polypeptides can

CC also be used to screen for their specific interactive molecules,

CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.

XX SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2422 AGCTTCCCAATGAT 2437

DB 17 AGCTTCCCAATGAT 2

|||||||

RESULT 524

ADB40778

ID ADB40778 standard; DNA; 17 BP.

XX AC ADB40778;

XX 18-DEC-2003 (revised)

DT 04-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #1101.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

KW diagnosis.

XX Homo sapiens.

OS WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

PF 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

DR New nucleic acid encoding human prostate membrane-specific antigen,

XX useful e.g. for treatment of tumors and viral infection, also related

PT polypeptide and antibodies.

XX Disclosure; Page 160; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC sequence having at least 80% identity, after optimal alignment, with the

CC nucleotides, a sequence that hybridizes under stringent conditions with

CC the nucleotides, or the complement, or corresponding RNA, of the

CC nucleotides. The nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro

CC sense and antisense sequences, of nucleotides involved in tumour

CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as

CC experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors), the encoded polypeptides and antibodies

CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours

CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis

CC and/or prognosis of these diseases. The nucleotides and polypeptides can

CC also be used to screen for their specific interactive molecules,

CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.

XX SQ Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 821 GATCGAGTTCAGATC 836

DB 1 GATCGAGTTCAGATC 16

|||||||

RESULT 525

ADB44127/c

ID ADB44127 standard; DNA; 17 BP.

XX AC ADB44127;

XX 18-DEC-2003 (revised)

DT 04-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #4450.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

KW diagnosis.

XX Homo sapiens.

OS WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

PF 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

DR New nucleic acid encoding human prostate membrane-specific antigen,

XX useful e.g. for treatment of tumors and viral infection, also related

PT polypeptide and antibodies.

XX Disclosure; Page 552; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC sequence having at least 80% identity, after optimal alignment, with the

CC nucleotides, a sequence that hybridizes under stringent conditions with

CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX Sequence 17 BP; 4 A; 8 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 833 GATCAGCCACTCCGCA 848
 |||||
 Db 1 GATCAGCCACCCGCA 16

RESULT 528

ID ADB40890/C
 ID ADB40890 standard; DNA; 17 BP.

XX AC ADB40890;

XX XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #1213.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.

XX OS Homo sapiens.

XX PN WO2003040369-A2.

XX PD 15-MAY-2003.

XX PF 17-SEP-2002; 2002WO-IB004219.

XX PR 17-SEP-2001; 2001FR-00011981.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.

XX Disclosure; Page 173; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATC 2818

Db 16 AAAAAAAAAAAGATC 1

RESULT 529

ID ADE31052/C

ID ADE31052 standard; DNA; 17 BP.

XX AC ADE31052;

XX DT 29-JAN-2004 (first entry)

XX DE Cholesterol homeostasis/adipogenesis related DNA seq id 439.

XX expression vector; anorectic; antiarteriosclerotic; cardiant;
 KW anti-diabetic; elevated cholesterol; elevated lipid; adipogenesis;
 KW obesity; atherosclerosis; diabetes mellitus;
 KW coronary artery heart disease; cholesterol homeostasis; ss;
 KW differential expression.

XX OS Homo sapiens.

XX PN US2003180764-A1.

XX PD 25-SEP-2003.

XX PF 08-JAN-2003; 2003US-00339793.

XX PR 09-JAN-2002; 2002US-0347286P.

XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Shang J, Bowen B;

XX WPI; 2003-830986/77.

XX Polynucleotides differentially regulated in response to cholesterol and
 PT adipogenesis are useful to detect and treat associated conditions such as
 PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart
 PT disease.

PS Claim 8; SEQ ID NO 439; 59pp; English.

XX The invention describes a composition comprising at least one expression
 CC vector comprising a polynucleotide of the invention. The composition has
 CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.
 CC The invention is used to detect and treat conditions associated with
 CC elevated cholesterol and lipid or during adipogenesis, particularly
 CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart
 CC disease. This sequence represents a polynucleotide differentially
 CC expressed during cholesterol homeostasis and adipogenesis.

XX Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      2138 CTACTGCTTTAGAAAT 2153
Db      17  CTACTGCTTTAGAGAT 2

RESULT 530
ADF62143
ID      ADF62143 standard; DNA; 17 BP.
XX
AC      ADF62143;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Human PCCP1 DNA fragment SEQ ID 4-directed probe - SEQ ID 47.
XX
KW      chromatin organisation modifier; CHROMO domain; cytostatic; PCCP1;
KW      prostate cancer candidate protein 1; tumour; gene therapy; vaccine;
KW      human; ss; probe.
XX
OS      Homo sapiens.
XX
PN      WO2003050284-A1.
XX
PD      19-JUN-2003.
XX
PF      22-NOV-2002; 2002WO-US037506.
XX
PR      10-DEC-2001; 2001US-0339764P.
XX
PA      (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI      Guo J;
XX
DR      WPI; 2003-532916/50.
XX
PT      New prostate cancer candidate protein 1 (PCCP1), useful for preparing a
PT      composition for treating or preventing a disorder associated with
PT      decreased or increased expression or activity of PCCP1 e.g., tumor.
XX
PS      Example 2; SEQ ID NO 47; 164pp; English.
XX
CC      The invention relates to a novel isolated nucleic acid that encodes a
CC      protein with a chromatin organisation modifier (CHROMO) domain. The
CC      polynucleotide of the invention demonstrates cytostatic activity and may
CC      be useful for preparing a composition for treating or preventing a
CC      disorder associated with decreased or increased expression or activity of
CC      PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as
CC      during gene therapy and vaccine production procedures. The current
CC      sequence is that of the human PCCP1-related DNA fragment SEQ ID 4-
CC      directed probe of the invention. Note: The current sequence is not shown
CC      within the specification per se but was retrieved from the Wipoweb
CC      database.
XX
SQ      Sequence 17 BP; 3 A; 9 C; 5 G; 0 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCACG 631
Db      2 CGCGCGCACGCACGCACG 17

RESULT 531
ADF62144
ID      ADF62144 standard; DNA; 17 BP.
XX
AC      ADF62144;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Human PCCP1 DNA fragment SEQ ID 4-directed probe - SEQ ID 48.
XX

QY      2138 CTACTGCTTTAGAAAT 2153
Db      17  CTACTGCTTTAGAGAT 2

RESULT 530
ADF62143
ID      ADF62143 standard; DNA; 17 BP.
XX
AC      ADF62143;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Human PCCP1 DNA fragment SEQ ID 4-directed probe - SEQ ID 47.
XX
KW      chromatin organisation modifier; CHROMO domain; cytostatic; PCCP1;
KW      prostate cancer candidate protein 1; tumour; gene therapy; vaccine;
KW      human; ss; probe.
XX
OS      Homo sapiens.
XX
PN      WO2003050284-A1.
XX
PD      19-JUN-2003.
XX
PF      22-NOV-2002; 2002WO-US037506.
XX
PR      10-DEC-2001; 2001US-0339764P.
XX
PA      (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI      Guo J;
XX
DR      WPI; 2003-532916/50.
XX
PT      New prostate cancer candidate protein 1 (PCCP1), useful for preparing a
PT      composition for treating or preventing a disorder associated with
PT      decreased or increased expression or activity of PCCP1 e.g., tumor.
XX
PS      Example 2; SEQ ID NO 47; 164pp; English.
XX
CC      The invention relates to a novel isolated nucleic acid that encodes a
CC      protein with a chromatin organisation modifier (CHROMO) domain. The
CC      polynucleotide of the invention demonstrates cytostatic activity and may
CC      be useful for preparing a composition for treating or preventing a
CC      disorder associated with decreased or increased expression or activity of
CC      PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as
CC      during gene therapy and vaccine production procedures. The current
CC      sequence is that of the human PCCP1-related DNA fragment SEQ ID 4-
CC      directed probe of the invention. Note: The current sequence is not shown
CC      within the specification per se but was retrieved from the Wipoweb
CC      database.
XX
SQ      Sequence 17 BP; 3 A; 9 C; 5 G; 0 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCACG 631
Db      2 CGCGCGCACGCACGCACG 17

RESULT 532
ADI48299/C
ID      ADI48299 standard; DNA; 17 BP.
XX
AC      ADI48299;
XX
DT      15-APR-2004 (first entry)
XX
DE      Human tumour suppression/reversion-related DNA sequence SeqID802.
XX
KW      tumour suppression; tumour reversion; apoptosis; virus resistance;
KW      cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW      primer; PCR; gene chip; antisense; viral disease; tumour;
KW      cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS      Homo sapiens.
XX
PN      WO2003025177-A2.
XX
PD      27-MAR-2003.
XX
PF      17-SEP-2002; 2002WO-IB004523.
XX
SQ      Sequence 17 BP; 3 A; 8 C; 6 G; 0 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCACG 631
Db      1 CGCGCGCACGCACGCACG 16

RESULT 532
ADI48299/C
ID      ADI48299 standard; DNA; 17 BP.
XX
AC      ADI48299;
XX
DT      15-APR-2004 (first entry)
XX
DE      Human tumour suppression/reversion-related DNA sequence SeqID802.
XX
KW      tumour suppression; tumour reversion; apoptosis; virus resistance;
KW      cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW      primer; PCR; gene chip; antisense; viral disease; tumour;
KW      cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS      Homo sapiens.
XX
PN      WO2003025177-A2.
XX
PD      27-MAR-2003.
XX
PF      17-SEP-2002; 2002WO-IB004523.
XX
SQ      Sequence 17 BP; 3 A; 8 C; 6 G; 0 T; 0 U; 0 Other;
```

PR 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX
 PS Disclosure; SEQ ID NO 802; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2138 CTACTGCTTTAGAAAT 2153
 Db 17 CTACTGCTTTAGAGAT 2
 XX
 RESULT 533
 ADI49153/c
 ID ADI49153 standard; DNA; 17 BP.
 AC ADI49153;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID1656.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2003025177-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004523.
 PF
 XX 17-SEP-2001; 2001FR-00011980.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-313354/30.
 DR
 XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis

PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; SEQ ID NO 1656; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 512 CCGGCCTCTGTGGATC 527
 Db 16 CCGGCCTCTGTGGATC 1
 XX
 RESULT 534
 ADI50684/c
 ID ADI50684 standard; DNA; 17 BP.
 AC ADI50684;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID3187.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2003025177-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004523.
 PF
 XX 17-SEP-2001; 2001FR-00011980.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-313354/30.
 DR
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; SEQ ID NO 3187; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis

CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, indentifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration.
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 3 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 167 TCGGAGAGAGGATC 182
 |||||
 Db 16 TCGGAGAGAGGATC 1

RESULT 535
 ADI49419
 ID ADI49419 standard; DNA; 17 BP.
 AC ADI49419;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID1922.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523..
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 1922; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, indentifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration.
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 821 GATCGAGTTGAGATC 836
 |||||
 Db 1 GATCTGAGTTGAGATC 16

RESULT 536
 ADI52640
 ID ADI52640 standard; DNA; 17 BP.
 XX
 AC ADI52640;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID5143.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523..
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 5143; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, indentifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration.
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 4 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 821 GATCGAGTTCAGATC 836
 |||||
 Db 1 GATCTGAGTTCAGATC 16

RESULT 537
 ADI51580/c
 ID ADI51580 standard; DNA; 17 BP.
 XX
 AC ADI51580;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID4083.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosolic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 4083; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAACATC 2818
 |||||
 Db 16 AAAAAAAAAAGATC 1

RESULT 539
 ACC51571
 ID ACC51571 standard; DNA; 17 BP.
 XX
 AC ACC51571;
 XX

RESULT 538
 ADI52683/c
 ID ADI52683 standard; DNA; 17 BP.
 XX
 AC ADI52683;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID5186.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosolic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 5186; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 2 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 167 TGCAGAGAGAGATC 182
 |||||
 Db 16 TGAGGAGAGAGATC 1

RESULT 539
 ACC51571
 ID ACC51571 standard; DNA; 17 BP.
 XX
 AC ACC51571;
 XX

CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 12 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2798 ATGTGAAAAA 2813
DB 2 ATCTGAAAAA 17

RESULT 542
ADL49414/c
ID ADL49414 standard; RNA; 17 BP.
XX
AC ADL49414;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #528.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
XX
PN W0200281628-A2.
XX
PD 17-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010512.
PF
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
XX WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2947; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR

CC substrate sequence.
XX
SQ Sequence 17 BP; 5 A; 1 C; 1 G; 0 T; 10 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2570 GTGTTTAAAAA 2585
DB 16 GTCTTTAAAAA 1

RESULT 543
AAx63282
ID AAx63282 standard; RNA; 18 BP.
XX
AC AAx63282;
XX
DT 16-JUL-1999 (first entry)
XX
DE Delta-9 desaturase hairpin ribozyme substrate SEQ ID NO:1157.
XX
KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
OS Zea mays.
XX
XX WO9710328-A2.
PN
XX 20-MAR-1997.
PD
XX 12-JUL-1996; 96WO-US011689.
PF
XX 13-JUL-1995; 95US-0001135P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA (DWC) DOWELANCO.
XX
PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
PI Young SA, Folkerts O, Merlo DJ;
XX
XX WPI; 1997-202224/18.
DR
XX Ribozyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX
PS Claim 40; Page 93; 155pp; English.
XX
CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant
XX
SQ Sequence 18 BP; 0 A; 11 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 3e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 586 CTCGCCGCGCTCGCC 601
|:|||||:|||||

```

Db      2 CUCCCCGCCGCGCGCC 17

RESULT 544
AAZ222554
ID   AAZ222554 standard; DNA; 18 BP.
XX
AC   AAZ222554;
XX
DT   26-NOV-1999 (first entry)
XX
DE   Antisense oligonucleotide for inhibitor-kappa B kinase-alpha mRNA.
XX
KW   Human; inhibitor-kappa B kinase-alpha; antisense oligonucleotide;
KW   inflammation; asthma; diabetes; multiple sclerosis; dermatitis; leukemia;
KW   inflammatory bowel disease; rhinitis; allograft rejection; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5962673-A.
XX
PD   05-OCT-1999.
XX
PF   20-NOV-1998; 98US-00197360.
XX
PR   20-NOV-1998; 98US-00197360.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP, Cowseert LM;
XX
DR   WPI; 1999-571297/48.
XX
PT   Antisense inhibition of the gene encoding Inhibitor-kappa B Kinase-alpha,
PT   useful for treating diseases associated with an inflammatory response
PT   e.g. asthma, diabetes.
XX
PS   Example 13; Col 38; 32pp; English.
XX
CC   Antisense oligonucleotides AAZ22543-82, are 8-30 nucleotides in length,
CC   and are targeted to inhibitor-kappa B kinase-alpha mRNA. The antisense
CC   oligonucleotides may be used for treating diseases with an inflammatory
CC   component such as asthma, diabetes, multiple sclerosis, dermatitis,
CC   leukemia, inflammatory bowel disease, rhinitis and allograft rejection.
CC   They may also have diagnostic and research applications
XX
SQ   Sequence 18 BP; 4 A; 1 C; 1 G; 12 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   3727 TATTTTATGTTATGTC 3742
      |||||
Db    1 TATTTTATGTTATTC 16

RESULT 545
AAI8953/c
ID   AAX18953 standard; DNA; 18 BP.
XX
AC   AAX18953;
XX
DT   14-MAY-1999 (first entry)
XX
DE   Fructose:glucose ratio determining gene PCR MS6 primer.
XX
KW   Fructose:glucose ratio determining gene; mature tomato fruit; flavour;
KW   MS6 primer; MS8 primer; PCR primer; molecular marker; ss.
XX
OS   Synthetic.
XX

PN   WO9904621-A1.
XX
PD   04-FEB-1999.
XX
PF   16-JUL-1998; 98WO-11000336.
XX
PR   23-JUL-1997; 97IL-00121373.
XX
PA   (ISRA ) ISRAEL MIN AGRIC.
XX
PI   Levin I, Shaffer AA;
XX
DR   WPI; 1999-142457/12.
XX
PT   New molecular marker for a gene determining fructose:glucose ratio in
PT   mature tomatoes - useful for finding this gene and producing tomato
PT   seeds, plants and/or fruit with an increased fructose to glucose ratio.
XX
PS   Claim 2; Page 11; 17pp; English.
XX
CC   The present invention describes a molecular marker for a gene determining
CC   fructose:glucose ratio in mature tomatoes. Also described are: (1)
CC   breeding tomato plants that produce tomatoes having superior taste
CC   characteristics. At least one Lycopersicon esculentum plant is crossed
CC   with a Lycopersicon spp. to produce hybrid (F1) seeds, which grow into F1
CC   plants that produce seeds. These seeds produce plants, which produce ripe
CC   fruit, in which the fructose:glucose content is determined using the
CC   marker gene; and (2) tomato plants produced by the method, and their
CC   fruit and seeds. The marker is useful for finding (and cloning) genes
CC   that produce tomatoes having superior taste characteristics. The marker
CC   gene is also useful in a method of breeding tomato plants for selecting
CC   plants producing fruit having desired characteristics, including a higher
CC   fructose:glucose ratio than that of standard L. esculentum. The molecular
CC   marker enables the selection of tomato plants at the young seedling
CC   stage, and eliminates undesirable environmental effects on the plant
CC   phenotype, which can limit the effectiveness of selection for a phenotype
CC   characteristic. The present sequence represents a primer used in
CC   producing an amplification product for use as the marker
XX
SQ   Sequence 18 BP; 0 A; 10 C; 0 G; 8 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   66 GGGAGAGAAAGAGAGA 81
      |||||
Db    18 GGGAGAGAGAGAGAGA 3

RESULT 546
AAA58386/c
ID   AAA58386 standard; DNA; 18 BP.
XX
AC   AAA58386;
XX
DT   01-NOV-2000 (first entry)
XX
DE   Polynucleotide # 2 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999; 99WO-US026612.
XX
PR   10-NOV-1998; 98US-0107828P.
XX
OS   09-NOV-1999; 99US-00437076.
XX

```

PA (BIOC-) BIOCRYSTAL LTD.
 XX Barbera-Guillem E, Nelson MB, Castro S;
 XX WPI; 2000-376593/32.
 XX Functionalized nanocrystal carrying polynucleotide, used for detecting
 PT target analyte, forms dendrimers with complementary nanocrystals to
 PT amplify the fluorescent signal.
 XX
 XX Example 3; Page 69; 72pp; English.
 XX
 XX The present invention relates to functionalised nanocrystals for use in
 CC nonisotopic detection systems for biomolecules e.g. nucleic acids,
 CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands
 CC attached to their surfaces with one end of the polynucleotide extending
 CC outwardly from the nanocrystal. The present sequence is one such
 CC polynucleotide. These nanocrystals are used with a second series of
 CC nanocrystals, which have polynucleotides complementary to the first
 CC polynucleotides, so that the respective complementary strands hybridise
 CC to each other and form a dendrimer. This dendrimer produces a signal
 CC which can then be detected e.g. fluorescence. The present sequence is
 CC composed mainly of thymine bases. This sequence may therefore be used
 CC with a polynucleotide composed mainly of Adenine bases (AAA58385)
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 931 AAAAAAAAAACCAACC 946
 Db 17 AAAAAAAAAACCAACC 2
 RESULT 547
 ABL56900/c
 ID ABL56900 standard; DNA; 18 BP.
 XX
 AC ABL56900;
 XX
 DT 26-JUL-2002 (first entry)
 XX
 DE Nucleic acid probe c.
 XX
 KW Concentration; quantification; mutation detection; polymorphic;
 KW polymerase chain reaction; PCR; probe; ss.
 XX
 OS Unidentified.
 XX
 PN EP1046717-A2.
 XX
 PD 25-OCT-2000.
 XX
 PF 20-APR-2000; 2000EP-00108643.
 XX
 PR 20-APR-1999; 99JP-00111601.
 XX
 PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX
 DR WPI; 2000-657765/64.
 XX
 XX Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.
 XX
 XX Example 5; Page 21; 55pp; English.

XX
 CC The invention relates to the determination of the concentration of a
 CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.
 CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for
 CC quantifying microbial cells in co-cultures or symbiotic systems, for
 CC detecting gene mutations or polymorphisms, and for analysing melting
 CC curves of target nucleic acids to determine a Tm value. Methods of the
 CC invention allow target nucleic acids to be quantified quickly, easily and
 CC accurately. Particularly there is no need to remove unbound probe, and no
 CC materials are introduced that inhibit amplification by Taq polymerase (so
 CC conventional PCR conditions can be used). The specificity of PCR is kept
 CC high (amplification of primer dimers is delayed), and the limit of
 CC quantitation is reduced. Complex probes are not needed, and amplification
 CC can be monitored in real time. The working graph for data analysis
 CC (automatically generated by a computer) has a higher correlation
 CC coefficient than conventional graphs so more accurate quantitation is
 CC possible. The current sequence represents a nucleic acid probe of the
 CC invention that was used for investigating the base selectivity of a
 CC target nucleic acid
 XX
 SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1162 ATATATATTTTCTT 1177
 Db 18 ATATATATTTTCTT 3
 RESULT 548
 ABL57542/c
 ID ABL57542 standard; DNA; 18 BP.
 XX
 AC ABL57542;
 XX
 DT 26-JUL-2002 (first entry)
 XX
 DE Nucleic acid probe g.
 XX
 KW Concentration; quantification; mutation detection; polymorphic;
 KW polymerase chain reaction; PCR; probe; ss.
 XX
 OS Unidentified.
 XX
 PN EP1046717-A2.
 XX
 PD 25-OCT-2000.
 XX
 PF 20-APR-2000; 2000EP-00108643.
 XX
 PR 20-APR-1999; 99JP-00111601.
 XX
 PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX
 PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX
 DR WPI; 2000-657765/64.
 XX
 XX Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.
 XX
 XX Example 5; Page 21; 55pp; English.
 XX
 XX The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.
 CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for
 CC quantifying microbial cells in co-cultures or symbiotic systems, for
 CC detecting gene mutations or polymorphisms, and for analysing melting
 CC curves of target nucleic acids to determine a T_m value. Methods of the
 CC invention allow target nucleic acids to be quantified quickly, easily and
 CC accurately. Particularly there is no need to remove unbound probe, and no
 CC materials are introduced that inhibit amplification by Taq polymerase (so
 CC conventional PCR conditions can be used). The specificity of PCR is kept
 CC high (amplification of primer dimers is delayed), and the limit of
 CC quantitation is reduced. Complex probes are not needed, and amplification
 CC can be monitored in real time. The working graph for data analysis
 CC (automatically generated by a computer) has a higher correlation
 CC coefficient than conventional graphs so more accurate quantitation is
 CC possible. The current sequence represents a nucleic acid probe of the
 CC invention that was used for investigating the base selectivity of a
 CC target nucleic acid
 XX
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
 |||||
 Db 18 ATATATATTTTCTT 3

RESULT 549
 ABL56899/c
 ID ABL56899 standard; DNA; 18 BP.
 XX
 AC ABL56899;
 DT 26-JUL-2002 (first entry)
 XX
 DE Nucleic acid probe b.
 XX Concentration; quantification; mutation detection; polymorphic;
 KW polymerase chain reaction; PCR; probe; ss.
 XX Unidentified.
 XX EP1046717-A2.
 XX 25-OCT-2000.
 XX 20-APR-2000; 2000EP-00108643.
 XX 20-APR-1999; 99JP-00111601.
 XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX WPI; 2000-657765/64.
 DR
 XX
 PT Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.
 XX
 PS Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a
 CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for
 CC quantifying microbial cells in co-cultures or symbiotic systems, for
 CC detecting gene mutations or polymorphisms, and for analysing melting
 CC curves of target nucleic acids to determine a T_m value. Methods of the
 CC invention allow target nucleic acids to be quantified quickly, easily and
 CC accurately. Particularly there is no need to remove unbound probe, and no
 CC materials are introduced that inhibit amplification by Taq polymerase (so
 CC conventional PCR conditions can be used). The specificity of PCR is kept
 CC high (amplification of primer dimers is delayed), and the limit of
 CC quantitation is reduced. Complex probes are not needed, and amplification
 CC can be monitored in real time. The working graph for data analysis
 CC (automatically generated by a computer) has a higher correlation
 CC coefficient than conventional graphs so more accurate quantitation is
 CC possible. The current sequence represents a nucleic acid probe of the
 CC invention that was used for investigating the base selectivity of a
 CC target nucleic acid
 XX
 SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
 |||||
 Db 18 ATATATATTTTCTT 3

RESULT 550
 ABL57540/c
 ID ABL57540 standard; DNA; 18 BP.
 XX
 AC ABL57540;
 DT 26-JUL-2002 (first entry)
 XX
 DE Nucleic acid probe d.

XX Concentration; quantification; mutation detection; polymorphic;
 KW polymerase chain reaction; PCR; probe; ss.
 XX Unidentified.
 XX EP1046717-A2.
 XX 25-OCT-2000.
 XX 20-APR-2000; 2000EP-00108643.
 XX 20-APR-1999; 99JP-00111601.
 XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.

XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX WPI; 2000-657765/64.
 DR

XX
 PT Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.
 XX
 PS Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a
 CC nucleic acid target, using a fluorescently labeled probe which produces
 CC reduced fluorescence emission when hybridised to the target nucleic acid.
 CC The method comprises measuring the reduction in emission caused by
 CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a nucleic acid probe of the
CC invention that was used for investigating the base selectivity of a
CC target nucleic acid

SQ Sequence 18 BP; 14 A; 0 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 551
AAF75598/c
ID AAF75598 standard; DNA; 18 BP.
XX AAF75598;
XX
XX
DT 10-MAY-2001 (first entry)
DE Binary encoded sequence tag method anchored primer #3.
XX Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
XX Synthetic.
OS
XX
XX WO200112855-A2.
XX
XX
PD 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-US022164.
XX
XX 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX
XX (UYUA) UNIV YALE.
XX
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
PI WPI; 2001-202878/20.
DR
XX
XX Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX
XX Disclosure; Page 101; 101pp; English.
PS
XX
XX The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes

SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACA 2816
Db 18 TGAATAAAAAAAAAAAAA 3

RESULT 552
ABA97627/c
ID ABA97627 standard; DNA; 18 BP.
XX ABA97627;
AC
XX
DT 11-APR-2002 (first entry)
XX
DE Probe g.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
XX JP2001286300-A.
XX
XX 16-OCT-2001.
XX
XX 20-APR-2000; 2000JP-00120097.
PF
XX
XX 20-APR-1999; 99JP-00111601.
PR 24-AUG-1993; 99JP-00236666.
PR 30-AUG-1993; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
XX WPI; 2002-134193/18.
DR
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
XX Example 5; Page 17; 34pp; Japanese.
XX
XX This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid

SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCCTTTTATATATA 1168
Db 16 TTTTTCCTTTATATATA 1

RESULT 553
ABA97623/c
ID ABA97623 standard; DNA; 18 BP.
XX ABA97623;
AC
XX
DT 11-APR-2002 (first entry)
XX
DE Probe b.

XX ss; fluorochrome; nucleic acid probe; fluorescence.
XX Unidentified.
XX JP2001286300-A.
XX 16-OCT-2001.
XX 20-APR-2000; 2000JP-00120097.
XX 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEI2-) KEIZAI SANGYOSHOU SANGYO GIJUTSU SOGO KEN.
XX WPI; 2002-134193/18.
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX Example 5; Page 17; 34pp; Japanese.
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
XX Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 1153 TTCTTTTATATATA 1168
Db 16 TTTTATATATATA 1
XX
RESULT 554
ABL95900/c
ID ABL95900 standard; DNA; 18 BP.
XX
AC ABL95900;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe g for assaying nucleic acids.
XX
XX Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
XX Unidentified.
XX
XX WO200208414-A1.
XX
XX 31-JAN-2002.
XX
XX 27-JUN-2001; 2001WO-IB001147.
XX
XX 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
XX 31-JAN-2002.
XX
XX 27-JUN-2001; 2001WO-IB001147.
XX
XX 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI

PI Yokomaku T;
XX
XX WPI; 2002-195876/25.
XX
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
XX Example 12; Page 60; 152pp; Japanese.
XX
XX The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
XX Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1153 TTCTTTTATATATA 1168
Db 16 TTTTATATATATA 1
XX
RESULT 555
ABL95896/c
ID ABL95896 standard; DNA; 18 BP.
XX
AC ABL95896;
XX
DT 19-JUN-2002 (first entry)
XX
XX Probe b for assaying nucleic acids.
XX
XX Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
XX Unidentified.
XX
XX WO200208414-A1.
XX
XX 31-JAN-2002.
XX
XX 27-JUN-2001; 2001WO-IB001147.
XX
XX 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
XX WPI; 2002-195876/25.
XX
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
XX Example 12; Page 60; 152pp; Japanese.
XX


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RESULT 560
ADB54950
ID ADB54950 standard; DNA; 18 BP.
XX
XX ADB54950;
XX
XX 04-DEC-2003 (first entry)
XX
XX Hybridisation oligonucleotide 486 used to analyse genomic DNA region.
XX
XX colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytosinatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;
KW Probe.
XX
XX Unidentified.
XX
XX WO2003072821-A2.
XX
XX 04-SEP-2003.
XX
XX 27-FEB-2003; 2003WO-EP002035.
XX
XX 27-FEB-2002; 2002BP-00004551.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;
PI
XX WPI; 2003-731620/69.
XX
XX Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
XX Claim 36; Page 28; 74pp; English.
XX
XX The invention relates to a novel method for detecting and differentiating
XX between colon cell proliferative disorders associated with at least one
XX gene or its regulatory regions. The method comprises contacting a target
XX nucleic acid in a biological sample obtained from the subject with at
XX least one reagent or a series of reagents, where the reagent or series of
XX reagents, distinguishes between methylated and non methylated CpG
XX dinucleotides within the target nucleic acid. The molecules of the
XX invention demonstrate cytosinatic activity whilst the method may useful
XX for detecting and differentiating between colon cell proliferative
XX disorders, including cancers such as colon adenoma and colon carcinoma.
XX The PNA (peptide nucleic acid)-oligomers are useful as probes for
XX determining cytosine methylation state or single nucleotide
XX polymorphisms. The current sequence is that of the hybridisation
XX oligonucleotide of the invention which was used to analyse the genomic
XX DNA region.
XX
XX Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4130 AGTTTCGTTGAGTTT 4145
DB 3 AGTTTCGTTGAGTTT 18

RESULT 561
ADC70020/c
ID ADC70020 standard; DNA; 18 BP.
XX
XX ADC70020;
XX
XX 18-DEC-2003 (first entry)
XX

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XX
DE DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 509).
XX
XX PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
KW adenocarcinoma; squamous cell carcinoma; cytosinatic; probe; PNA-oligomer;
KW cytosine methylation state.
XX
XX Unidentified.
XX
XX WO2003052135-A2.
XX
XX 26-JUN-2003.
XX
XX 10-DEC-2002; 2002WO-EP014026.
XX
XX 14-DEC-2001; 2001DE-01061625.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;
PI Nimmrich I;
PI
XX WPI; 2003-533029/50.
XX
XX Detecting and differentiating cytosine methylation state of genomic DNA,
PT useful for diagnosing, treating prognosticating and/or monitoring lung
PT cell proliferative disorders e.g. adenocarcinoma and squamous cell
PT carcinoma.
XX
XX Claim 15; SEQ ID NO 509; 58pp; English.
XX
XX This invention relates to a novel method for detecting and
XX differentiating between lung cell proliferative disorders associated with
XX at least one gene and/or their regulatory regions. Specifically, it
XX refers to a method comprising contacting a target nucleic acid in a
XX biological sample with at least one reagent, wherein the reagent is able
XX to distinguish between methylated and non-methylated CpG dinucleotides
XX present in the target DNA. As such, it is possible to further
XX differentiate and diagnose medical conditions including adenocarcinoma
XX and squamous cell carcinoma, and their respective adjacent lung tissue.
XX The present invention describes cytosinatic oligomers and PNA-oligomers
XX that are useful as probes for determining the cytosine methylation state
XX or single nucleotide polymorphisms (SNPs) of the target sequence. This
XX oligonucleotide sequence is a primer oligomer used for the analysis of
XX CpG positions within genomic DNA, used in an exemplification of the
XX invention.
XX
XX Sequence 18 BP; 4 A; 0 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950
DB 16 AAAAAACAACCTTTC 1

RESULT 562
AAD61014
ID AAD61014 standard; DNA; 18 BP.
XX
XX AAD61014;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human inhibitor-kappa B kinase-alpha antisense oligo, ISIS 23503.
XX
XX Human; inhibitor-kappa B kinase-alpha; hyperproliferative condition;
KW cancer; inflammation; juvenile diabetes mellitus; myasthenia gravis;
KW Grave's disease; rheumatoid arthritis; allograft rejection; asthma;
KW systemic lupus erythematosus; bowel disease; multiple sclerosis;
KW psoriasis; dermatitis; rhinitis; antithyroid; neuroprotective; allergy;

```

KW immunosuppressive; therapy; phosphorothioate backbone; antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides; All cytidines are
FT methylcytidines"
FT modified_base 15..18
FT /*tag= C
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides; All cytidines are
FT methylcytidines"
XX US2003092654-A1.
XX 15-MAY-2003.
XX
XX 13-MAY-2002; 2002US-00145857.
XX PF
XX 20-NOV-1998; 98US-00197360.
XX PR
XX 22-JUL-1999; 99WO-US016603.
XX PR
XX 27-JUL-2001; 2001US-00856074.
XX
XX (MONI/) MONIA B P.
XX (COWS/) COWSERT L M.
XX PA
XX
XX Monia BP, Cowsert LM;
XX WPI; 2003-765489/72.
XX DR
XX Antisense compound targeted to a nucleic acid molecule encoding human
XX inhibitor-kappa B kinase-alpha, useful for treating human having a
XX disease or condition such as cancer, asthma, juvenile diabetes mellitus.
XX
XX Example 15; Page 21; Opp; English.
XX PS
XX The invention relates to an antisense compound targeted to a nucleic
XX acid molecule encoding human inhibitor-kappa B kinase-alpha where the
XX antisense compound inhibits the expression of human inhibitor-kappa B
XX kinase-alpha. The invention is useful for inhibiting expression of
XX inhibitor of kappa B kinase-alpha in human cells or tissues. The
XX invention is also useful for treating hyperproliferative condition such
XX as cancer, inflammatory conditions such as asthma, juvenile diabetes
XX mellitus, myasthenia gravis, Grave's disease, rheumatoid arthritis,
XX allograft rejection, inflammatory bowel disease, multiple sclerosis,
XX psoriasis, lupus erythematosus, systemic lupus erythematosus, contact
XX dermatitis, rhinitis and various allergies. The present sequence is an
XX antisense oligonucleotide targeted to human inhibitor-kappa B kinase-
XX alpha DNA
XX
XX Sequence 18 BP; 4 A; 1 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 3727 TATTTATGTTATGTC 3742
DB 1 TATTTATGTTATTC 16

RESULT 563
ADE84380/c
ID ADE84380 standard; DNA; 18 BP.
XX

AC ADE84380;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human lymphoid cell proliferative disorder gene CpG analysis oligo #86.
XX
XX Lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis; primer; ss.
XX
XX Homo sapiens.
OS
XX WO2003044226-A2.
XX PN
XX 30-MAY-2003.
XX PD
XX 25-NOV-2002; 2002WO-EP013265.
XX PF
XX 23-NOV-2001; 2001DE-01057491.
XX PR
XX 28-DEC-2001; 2001DE-01064501.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX
XX Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
XX WPI; 2003-457621/43.
XX DR
XX
XX Detecting and differentiating between lymphoid cell proliferative
XX disorders comprises contacting a target nucleic acid with at least one
XX reagent that distinguishes between methylated and non-methylated CpG
XX dinucleotides.
XX
XX Claim 30; SEQ ID NO 376; 448pp; English.
XX PS
XX
XX The invention relates to a method of detecting and differentiating
XX between lymphoid cell proliferative disorders associated with at least
XX one gene and/or their regulatory regions in a subject by contacting a
XX target nucleic acid in a biological sample obtained from the subject with
XX at least one reagent or series of reagents that distinguish between
XX methylated and non-methylated CpG dinucleotides within the target nucleic
XX acid. The genes and/or their regulatory regions are preferably selected
XX from MDRI, CSNK2B, BGR4, AR, CDK4, RB2, CDC25A, GPII beta, MYOD1, CDH3,
XX GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB12, TGFBR2, TP73, CDKN1C,
XX GSK3beta, ESRI, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
XX acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
XX of the genes are useful for detecting the methylation state of all the
XX CpG dinucleotides within one or more the sequences, or their complements,
XX for determining the cytosine methylation state and or single nucleotide
XX polymorphisms (SNPs), and for differentiating at least two of the medical
XX conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
XX chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
XX lymphoma. They are also useful for detecting of a predisposition to,
XX differentiation between subclasses, diagnosis, prognosis, treating and/or
XX monitoring of lymphoid cell proliferative disorder. This sequence
XX represents an oligonucleotide used to analyse of CpG positions within the
XX above mentioned genes.
XX
XX Sequence 18 BP; 4 A; 0 C; 5 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 935 AAAAAACAAACCTTTC 950
DB 16 AAAAAACAAACCTTC 1

RESULT 564
ADN74905/c

ADN74905 standard; DNA; 18 BP.
 ADN74905;
 29-JUL-2004 (first entry)
 Human CLCN2 gene 74-117 deletion identification PCR primer SEQ ID:18.
 voltage-gated chloride channel; CIC-2; CLCN2; human; chromosome 3;
 neurological disease; neuroprotective; anticonvulsant;
 idiopathic generalised epilepsy; childhood absence epilepsy;
 juvenile absence epilepsy; juvenile myoclonic epilepsy; epilepsy;
 grand mal seizure; PCR; primer; ss.
 Homo sapiens.
 Synthetic.
 WO2004039979-A1.
 13-MAY-2004.
 30-OCT-2003; 2003WO-EP012086.
 30-OCT-2002; 2002US-0422102P.
 (RHEI-) RHEINISCHE FRIEDRICH-WILHELMS-UNIV BONN.
 Heils A, Haug K;
 WPI; 2004-390325/36.
 New voltage-gated chloride channel CIC-2 polynucleotides and
 polypeptides, useful in diagnosing and treating a neurological disease or
 disorder such as idiopathic generalized epilepsy.
 Claim 19; SEQ ID NO 18; 124pp; English.
 The present invention describes a nucleic acid molecule (I) comprising a
 sequence encoding a polypeptide which has an amino acid sequence of a
 voltage-gated chloride channel CIC-2, where the glycine (Gly) residue
 corresponding to position 715 of the wild-type voltage-gated chloride
 channel CIC-2 comprising a 898 amino acid sequence of SEQ ID NO:2, is
 replaced by another amino acid residue. The voltage-gated chloride
 channel CIC-2 is encoded by the CLCN2 gene. The human CLCN2 gene is
 located on chromosome 3, more specifically to 3q26. Also described: (1) a
 vector comprising (1); (2) a host transformed with the vector of (1) or
 transformed with (1); (3) a method of producing the polypeptide encoded
 by (1); (4) a polypeptide encoded by (1) produced by the method of (3);
 (5) an antibody specifically directed to the polypeptide of (4), where
 the antibody specifically reacts with an epitope generated and/or formed
 by the mutation in the voltage-gated chloride channel CIC-2; (6) an
 aptamer specifically binding to (1) or to the polypeptide of (4); (7) a
 primer or pair of primers capable of specifically amplifying (1); (8) a
 composition comprising (1), the vector of (1), the polypeptide of (4),
 the antibody of (5), the aptamer of (6) and the primer or pair of primers
 of (7); (9) a method of diagnosing a neurological disease or a
 susceptibility to a neurological disease; (10) a pharmaceutical
 composition comprising (1); (11) a method of treating a neurological
 disease; (12) a kit comprising (1) the vector of (1), the host of (2),
 the polypeptide of (4), the antibody of (5), the aptamer of (6) and the
 primer or pair of primers of (7); (13) a method of identifying or
 screening for molecules capable of specifically interacting with the
 polypeptide of (4); (14) a method of characterising molecules capable of
 altering the characteristic of the polypeptide of (4); and (15) a method
 of producing a pharmaceutical composition. (1) has neuroprotective and
 anticonvulsant activities. The nucleic acid molecule, vector,
 polypeptide, antibody, aptamer and the primer or pair of primers from the
 present invention can be used in preparing a diagnostic or pharmaceutical
 composition for the detection and treatment of a neurological disease or
 disorder, i.e. idiopathic generalised epilepsy (IGE), e.g. childhood
 absence epilepsy (CAE), juvenile absence epilepsy (JAE), juvenile
 myoclonic epilepsy (JME) or epilepsy with grand mal seizures on awakening
 (EGMA). The present sequence represents a PCR primer for the human CLCN-2

CC gene, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. NO. 3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 96 GAGCTCTGGGGCAGGC 111
 Db 18 GAGCTCTGGGGCAGGC 3
 RESULT 565
 AD079612/C
 ID AD079612 standard; DNA; 18 BP.
 XX
 AC AD079612;
 DT
 DT 26-AUG-2004 (first entry)
 XX
 DE KIAA0783 extend primer #4.
 XX
 KW Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPFF3;
 KW CENPC1; SNP; single nucleotide polymorphism; PHF14;
 KW PHD finger protein 14; chromosome 7p21.3; zinc finger protein;
 KW transcription factor; extend; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004047514-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 25-NOV-2003; 2003WO-US037943.
 XX
 PR 25-NOV-2002; 2002US-0429136P.
 PR 24-JUL-2003; 2003US-0490234P.
 XX
 PA (SEQU-) SEQUENOM INC.
 XX
 PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
 XX
 DR WPI; 2004-441037/41.
 XX
 PT Identifying a subject at risk of breast cancer by detecting the presence
 of polymorphic variations in the DLG1, KIAA0783, DPFF3 or CENPC1 regions
 which are associated with breast cancer in a nucleic acid sample from a
 subject.
 PT
 PS
 XX
 XX Example 4; Page 78; 227pp; English.
 CC The present invention relates to a method for identifying a subject at
 risk of breast cancer. The method comprising detecting the presence or
 absence of one or more polymorphic variations associated with breast
 cancer in a nucleic acid sample from a subject. The nucleic acid sample
 comprises the DLG1 region (ADO79402), KIAA0783 region (ADO79403), DPFF3
 region (ADO79404) or CENPC1 region (ADO79405). The gene DLG1 (discs,
 large homolog 1 (Drosophila)) is also known as synapse-associated protein
 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
 gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783
 has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a
 novel gene with unknown function, however, being a zinc finger protein,
 it likely to be a transcription factor. The gene DPFF3 (D4, zinc and
 double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079
 and 2810403B03R1K. DPFF3 is a Rho family guanine-nucleotide exchange
 factor. CENPC1 has been mapped to chromosomal position 14q24.3-q31.1. The
 gene CENPC1 (centromere protein C1) is also known as Centromere
 autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-
 q13.3. CENPC1 is a centromere autoantigen and a component of the inner
 kinetochore plate. The CENPC1 protein is required for maintaining proper
 kinetochore size and a timely transition to anaphase. The method is
 useful for identifying a subject at risk of breast cancer, for early

CC diagnosis, prevention and treatment of breast cancer, to analyze and
 CC predict a response to a breast cancer treatment, and in clinical drug
 CC trials. The present sequence was used in an example from the invention.
 XX
 SQ Sequence 18 BP; 1 A; 8 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 66 GGGAGAGAAAGAGAGA 81
 Db 17 GTGAGAGAAAGAGAGA 2
 RESULT 566
 ADP46381/c
 ID ADP46381 standard; DNA; 18 BP.
 XX
 AC ADP46381;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Extend primer 10 used to genotype human NUMA1/FLJ20625/LOC220074 SNP.
 XX
 KW breast cancer; cytostatic; gene therapy; human; ss; primer; PCR; SNP;
 KW single nucleotide polymorphism; NUMA1; FLJ20625; LOC220074;
 KW chromosome 11q13.3; probe.
 XX
 OS Homo sapiens.
 XX
 PN WO2004047623-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 25-NOV-2003; 2003WO-US037948.
 PR 25-NOV-2002; 2002US-0429136P.
 PR 24-JUL-2003; 2003US-0490234P.
 XX
 PA (SEQU-) SEQUENOM INC.
 XX
 PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
 XX
 DR WPI; 2004-441051/41.
 XX
 PT Identifying a subject at risk of breast cancer by detecting the presence
 PT of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUMA1 or GALE
 PT regions which are associated with breast cancer in a nucleic acid sample
 PT from a subject.
 XX
 PS Example 7; Page 106; 289pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject at risk
 CC of breast cancer comprising detecting the presence or absence of one or
 CC more polymorphic variations associated with breast cancer in a nucleic
 CC acid sample from a subject. The method of the invention has cytostatic
 CC applications and may be useful for identifying a subject at risk of
 CC breast cancer, for early diagnosis, prevention and treatment of breast
 CC cancer, possibly via gene therapy, as well as to analyse and predict a
 CC response to a breast cancer treatment and in clinical drug trials. The
 CC current sequence is that of an Extend primer (also described as probe) of
 CC the invention which was used to genotype human NUMA1/FLJ20625/LOC220074
 CC region gDNA. FLJ20625 and LOC220074 have been mapped to chromosomal
 CC position 11q13.3.
 XX
 SQ Sequence 18 BP; 0 A; 5 C; 2 G; 11 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 927 GGAGAGAAAAAACA 942

Db 17 GGGGAAAAAACA 2
 RESULT 567
 ADS90062
 ID ADS90062 standard; DNA; 18 BP.
 XX
 AC ADS90062;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Oligonucleotide of the invention SEQ ID NO:1078.
 XX
 KW ss; cell proliferative disorder; breast; methylation; cytostatic;
 KW gene therapy; single nucleotide polymorphism; SNP.
 XX
 OS Unidentified.
 XX
 PN WO2004035803-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 01-OCT-2003; 2003WO-EP010881.
 XX
 PR 01-OCT-2002; 2002DE-01045779.
 PR 07-JAN-2003; 2003DE-01000096.
 PR 17-APR-2003; 2003DE-01017955.
 XX
 PA (EPTG-) EPIGENOMICS AG.
 XX
 PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
 PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
 XX
 DR WPI; 2004-348468/32.
 XX
 PT Predicting responsiveness of a subject with breast cell proliferative
 PT disorder, useful for treating or differentiating breast cell
 PT proliferative disorders comprises analyzing methylation pattern of a
 PT genomic DNA from the subject.
 XX
 PS Disclosure; SEQ ID NO 1078; 104pp; English.
 XX
 CC The invention relates to a novel method for predicting the responsiveness
 CC of a subject with a cell proliferative disorder of the breast tissues to
 CC a therapy comprising analysing the methylation pattern of a target
 CC nucleic acid by contacting at least one of the target nucleic acids in a
 CC biological sample obtained from the subject prior to or during treatment.
 CC The method of the invention has cytostatic activity, and may have a use
 CC in gene therapy. The set of oligonucleotides comprising at least two of
 CC the oligomers are useful for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
 CC methods, nucleic acid, oligonucleotide, and kit are useful for the
 CC treatment, characterisation, classification and/or differentiation, of
 CC breast cell proliferative disorders. The method is also useful for
 CC predicting the responsiveness of a subject with a cell proliferative
 CC disorder of the breast tissues to a therapy. The present sequence is used
 CC in the exemplification of the invention.
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4130 AGTTTGGTTGAGTTTT 4145
 Db 3 AGTTTGGTTGAGTTTT 18
 RESULT 568
 ADR78534/c
 ID ADR78534 standard; DNA; 18 BP.

XX ADR78534;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human apolipoprotein B (ApoB) oligonucleotide seqid 3019.
XX
XX antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
XX cytosolic; anticonvulsant; nootropic; muscular; anti-HIV;
XX RNA interference; RNA, antisense technology; lipid metabolism;
XX cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
XX coronary artery disease; CAD; coronary heart disease; CHD;
XX atherosclerosis; hepatic glucose production;
XX glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
XX colon cancer; lung cancer; neurological disease; Huntington disease;
XX spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS Homo sapiens.
XX
XX WO2004080406-A2.
XX
XX 23-SEP-2004.
XX
XX 08-MAR-2004; 2004WO-US007070.
XX
XX 07-MAR-2003; 2003US-0452682P.
XX PR 12-MAR-2003; 2003US-0454265P.
XX PR 13-MAR-2003; 2003US-0454962P.
XX PR 13-MAR-2003; 2003US-0455050P.
XX PR 14-APR-2003; 2003US-0462894P.
XX PR 17-APR-2003; 2003US-0463772P.
XX PR 25-APR-2003; 2003US-0465665P.
XX PR 25-APR-2003; 2003US-0465802P.
XX PR 09-MAY-2003; 2003US-0469612P.
XX PR 08-AUG-2003; 2003US-0493986P.
XX PR 11-AUG-2003; 2003US-0494597P.
XX PR 26-SEP-2003; 2003US-0506341P.
XX PR 09-OCT-2003; 2003US-0510246P.
XX PR 10-OCT-2003; 2003US-0510318P.
XX PR 07-NOV-2003; 2003US-0518453P.
XX
XX (ALNY-) ALNYLAM PHARM.
XX
XX Manoharan M, Bumcrot D;
XX WPI; 2004-677362/66.
XX
XX Interference RNA agent useful for treating dyslipidemias, coronary artery
XX disease, diabetes, cancer or neurological disease, comprises sense
XX sequence and antisense sequence which has specific modifications.
XX
XX Example 5; SEQ ID NO 3019; 378pp; English.
XX
XX The invention describes a RNA interference (iRNA) agent (I) comprising a
XX sense sequence and an antisense sequence, where the sense sequences have
XX one or more asymmetrical 2'-O alkyl modifications, the antisense
XX sequences have one or more asymmetrical phosphorothioate modifications
XX and the antisense sequence targets a human gene sequence. Also described
XX are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
XX levels or glucose-6-phosphatase levels in a subject; producing (I);
XX stabilising (I), involves selecting a sequence with activity and
XX introducing one or more asymmetrical modification in the sequence, where
XX the modification decreases nuclease sensitivity while not decreasing its
XX activity; a kit comprising (I) and instruction for its use; and a device
XX that can be dispense or administer a composition comprising (I). (I) is
XX useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
XX is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
XX The subject is suffering from a disorder characterised by elevated or
XX otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
XX levels of cholesterol, and/or dysregulation of lipid metabolism. The
XX disorder is chosen from the HDL/LDL cholesterol imbalance,
XX dyslipidaemias, hypercholesterolaemia, statin-resistant
XX hypercholesterolaemia, coronary artery disease (CAD), coronary heart

CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC can be used to control ApoB gene expression.
XX
XX Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3362 GAAGTGGCTGTTCATC 3377
DB 16 GAAGCGGCTGTTCATC 1
RESULT 569
ABZ88813/c
ID ABZ88813 standard; DNA; 20 BP.
XX
XX AC ABZ88813;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 4055; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 4.1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3264 TTTTTCCTTTTAAATT 3282
 Db 20 TTTTTCCTTTTAAATT 2
 RESULT 570
 ABD25043/C
 ID ABD25043 standard; DNA; 20 BP.
 XX AC ABD25043;
 XX 29-JUL-2004 (first entry)
 XX DE A1128305-derived oligonucleotide SEQ ID 4055.
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX Homo sapiens.
 XX OS
 XX WO200285309-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013143.
 XX 24-APR-2001; 2001US-0286036P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
 XX Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-093058/08.
 XX Pharmaceutical composition for treating asthma, has antisense
 PT nucleic acids containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX Claim 15; SEQ ID NO 4055; 763pp; English.
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 0.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 4.1e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3264 TTTTTCCTTTTAAATT 3282
 Db 20 TTTTTCCTTTTAAATT 2
 RESULT 571
 ABQ99687/C
 ID ABQ99687 standard; DNA; 17 BP.
 XX AC ABQ99687;
 XX 08-NOV-2002 (first entry)
 XX DT
 XX DE Murine Ikbkap exon 27 acceptor site.
 XX Murine; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; ds;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening.
 XX Mus sp.
 XX WO200259381-A2.
 XX 01-AUG-2002.
 XX 07-JAN-2002; 2002WO-US000473.
 XX 06-JAN-2001; 2001US-0260080P.
 XX (GEHO) GEN HOSPITAL CORP.
 XX Slaugenhaupt S, Gusella JF;
 XX WPI; 2002-674806/72.
 XX New IKBKAP genes with mutations, useful for identifying a subject with
 PT familial dysautonomia (FD), or for rapid carrier screening in the
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
 PT prenatal diagnosis.
 XX Disclosure; Fig 11; 109pp; English.
 XX The present invention relates to methods and compositions useful for
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM
 CC 223900). It was found that mutations in the IKBKAP gene (see ABQ0565)
 CC are associated with FD. The mutation associated with the major haplotype

CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
 CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
 CC patients, although they continue to express varying levels of wild-type
 CC message in a tissue-specific manner. The mutation associated with the
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
 CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
 CC This bp mutation causes an arginine to proline missense mutation (R696P)
 CC in the IKBKAP protein, which is predicted to disrupt a potential
 CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
 CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
 CC gene maps to chromosome 9q31. A mouse model of FD was created in an
 CC example from the invention. Expression of murine Ikbkap was examined
 CC using both mouse embryo and adult mouse multiple tissue Northern blots.
 CC The blots were probed with a 1045bp PCR fragment that contains exons 2
 CC through 11, which was generated using PCR primers ABQ80563-ABQ80564.
 CC ABQ99662-ABQ99733 are the murine Ikbkap exon and intron boundaries
 XX
 SQ Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
 DB 14 TGAATAAAAAAAAAA 1

RESULT 572
 ID ADB40890
 AC ADB40890 standard; DNA; 17 BP.
 AC ADB40890;
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX Tumour suppression/reversion associated nucleotide #1213.
 XX cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO2003040369-A2.
 XX 15-MAY-2003.
 XX 17-SEP-2002; 2002WO-IB004219.
 XX 17-SEP-2001; 2001FR-00011981.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-441574/41.
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX Disclosure; Page 173; 771pp; French.
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and/or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2742 ATCTTTT TTTT 2755
 DB 2 ATCTTTT TTTT 15

RESULT 573
 ADI51580
 ID ADI51580 standard; DNA; 17 BP.
 XX ADI51580;
 XX 15-APR-2004 (first entry)
 DT 15-APR-2004 (first entry)
 XX Human tumour suppression/reversion-related DNA sequence SeqID4083.
 DE Human tumour suppression/reversion-related DNA sequence SeqID4083.
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytostatic; virucide; neuroprotective; nontropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO2003025177-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004523.
 XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; SEQ ID NO 4083; 30pp; French.
 XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC nontropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that

KW	restenosis; asthma; Crohn's disease; diabetes; obesity;
KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW	allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW	substrate, ds.
XX	
OS	Unidentified.
XX	
FN	W0200281628-A2.
XX	
PD	17-OCT-2002.
XX	
PF	03-APR-2002; 2002W0-US010512.
XX	
PR	05-APR-2001; 2001US-00827395.
PR	29-MAY-2001; 2001US-0294412P.
PR	28-AUG-2001; 2001US-0315315P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
XX	
PI	Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX	
DR	WPI; 2003-058513/05.
XX	
PT	Novel enzymatic nucleic acid that down-regulates expression of neurite
PT	growth inhibitor receptor, prostaglandin D2 receptor. IkappaB kinase or
PT	protein kinase PKR genes, for treating cancer and inflammatory disease.
XX	
PS	Claim 59; SEQ ID NO 2942; 317pp; English.
XX	
CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC	that down regulate the expression or inhibit the function of a receptor
CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC	IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC	invention are useful for treating: cerebrovascular accident, central
CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC	disease, lupus, multiple sclerosis, transplant/graft rejection,
CC	ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC	nucleic acids of the invention are also useful for down-regulating the
CC	expression of a target gene and as a diagnostic tool to examine genetic
CC	drifts and mutations within diseased cells or to detect the presence of a
CC	target RNA in a cell. The present RNA sequence represents a human PKR
CC	substrate sequence.
XX	
SQ	Sequence 17 BP; 2 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
Query Match	0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity	17.6%; Pred. No. 3.2e+02;
Matches	3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
Qy	2741 CATCTTTTITTTTAA 2757
Db	: : : : : : : : : :
	1 CUUUUUUUUUUUUUUA 17
RESULT 578	
ADP86176/c	
ID	ADP86176 standard; DNA; 17 BP.
XX	
AC	ADP86176;
XX	
DT	09-SEP-2004 (first entry)
XX	
DE	CpG immunostimulatory oligonucleotide #47.
XX	
KW	CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW	viral infection; bacterial infection; cancer; lymphoma;
KW	intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW	carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX	

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OS Unidentified.
XX Key Location/Qualifiers
FH modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX WO2004053104-A2.
XX
XX PD 24-JUN-2004.
XX
XX PF 11-DEC-2003; 2003WO-US039775.
XX
XX PR 11-DEC-2002; 2002US-0432409P.
XX
XX PR 25-SEP-2003; 2003US-0506108P.
XX
XX PA (COLE-) COLEY PHARM GROUP INC.
XX
XX PA (COLE-) COLEY PHARM GMBH.
XX
XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX
XX DR WPI; 2004-487902/46.
XX
XX PT New oligonucleotides, useful for treating allergy or asthma, viral and
XX bacterial infections, and cancer, e.g. biliary tract cancer, breast
XX cancer, cervical cancer.
XX
XX PS Example; SEQ ID NO 47; 104pp; English.
XX
XX CC The invention relates to a class of CpG immunostimulatory
XX oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
XX are useful for stimulating an immune response. Oligonucleotides and
XX compositions of the invention are useful for treating allergy or asthma,
XX viral and bacterial infections and cancer e.g. biliary tract cancer,
XX breast cancer, cervical cancer, choriocarcinoma, colon cancer,
XX endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
XX liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
XX neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
XX rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
XX and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
XX Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
XX testicular cancer, as well as other carcinomas and sarcomas. The
XX invention is also useful in gene therapy. The present sequence is a CpG
XX immunostimulatory oligonucleotide.
XX
XX SQ Sequence 17 BP; 11 A; 1 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.3%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 3.2e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1032 TTTTCTTTTAAAGGA 1048
XX |||||
DB 17 TTTTCTTTTAAACGA 1
XX
RESULT 579
ADL49414
ID ADL49414 standard; RNA; 17 BP.
XX
XX AC ADL49414;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human PKR substrate sequence #528.
XX
XX KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX reestenosis; asthma; Crohn's disease; diabetes; obesity;
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KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
XX OS Unidentified.
XX
XX PN WO200281628-A2.
XX
XX PD 17-OCT-2002.
XX
XX PF 03-APR-2002; 2002WO-US010512.
XX
XX PR 05-APR-2001; 2001US-00827395.
XX
XX PR 29-MAY-2001; 2001US-0294412P.
XX
XX PR 28-AUG-2001; 2001US-0315315P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
XX DR WPI; 2003-058513/05.
XX
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX PS Claim 59; SEQ ID NO 2947; 317pp; English.
XX
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX disease, lupus, multiple sclerosis, transplant/graft rejection,
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX nucleic acids of the invention are also useful for down-regulating the
XX expression of a target gene and as a diagnostic tool to examine genetic
XX drifts and mutations within diseased cells or to detect the presence of a
XX target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.
XX
XX SQ Sequence 17 BP; 5 A; 1 C; 1 G; 0 T; 10 U; 0 Other;
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 29.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 10; Mismatches 2; Indels 0; Gaps 0;
```

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QY 2746 TTTTCTTTTAAAGGA 2762
XX ::::::::::|||
DB 1 UUUUUUUUUUAAAGACA 17
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Search completed: February 25, 2005, 09:48:43
Job time : 28 secs

